



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 119468

TO: Sean McGarry
Location: 2d19/3c18
Wednesday, April 21, 2004
Art Unit: 1635
Phone: 272-0761
Serial Number: 10 / 006430

2018

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
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Search Notes

6

107	15	1.0	15	1	1	CF313320	ACCESSION:CF313320	C 180	14	0.9	14	1	1	CF334281	ACCESSION:CF334281
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C 315	12	0.8	12	1	12	1	CF301075	ACCSSION:CF301075	C 388	11	0.7	11	1	11	1	CF301744	ACCSSION:CF301744
C 316	12	0.8	12	1	12	1	CF301489	ACCSSION:CF301489	C 389	11	0.7	11	1	11	1	CF302896	ACCSSION:CF302896
C 317	12	0.8	12	1	12	1	CF301940	ACCSSION:CF301940	C 390	11	0.7	11	1	11	1	CF307845	ACCSSION:CF307845
C 318	12	0.8	12	1	12	1	CF302029	ACCSSION:CF302029	C 391	11	0.7	11	1	11	1	CF309987	ACCSSION:CF309987
C 319	12	0.8	12	1	12	1	CF302122	ACCSSION:CF302122	C 392	11	0.7	11	1	11	1	CF311911	ACCSSION:CF311911
C 320	12	0.8	12	1	12	1	CF302289	ACCSSION:CF302289	C 393	11	0.7	11	1	11	1	CF311912	ACCSSION:CF311912
C 321	12	0.8	12	1	12	1	CF302486	ACCSSION:CF302486	C 394	11	0.7	11	1	11	1	CF314533	ACCSSION:CF314533
C 322	12	0.8	12	1	12	1	CF308112	ACCSSION:CF308112	C 395	11	0.7	11	1	11	1	CF318741	ACCSSION:CF318741
C 323	12	0.8	12	1	12	1	CF311835	ACCSSION:CF311835	C 396	11	0.7	11	1	11	1	CF326997	ACCSSION:CF326997
C 324	12	0.8	12	1	12	1	CF311836	ACCSSION:CF311836	C 397	11	0.7	11	1	11	1	CF326998	ACCSSION:CF326998
C 325	12	0.8	12	1	12	1	CF313356	ACCSSION:CF313356	C 398	11	0.7	11	1	11	1	CF327885	ACCSSION:CF327885

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c 399      11      0.7      11      1      CF328618      ACCESSION:CF328618
c 400      11      0.7      11      1      CF328619      ACCESSION:CF328619
c 401      11      0.7      11      1      CF329242      ACCESSION:CF329242
c 402      11      0.7      11      1      CF329344      ACCESSION:CF329344
c 403      11      0.7      11      1      CF329345      ACCESSION:CF329345
c 404      11      0.7      11      1      CF331049      ACCESSION:CF331049
c 405      11      0.7      11      1      CF331066      ACCESSION:CF331066
c 406      11      0.7      11      1      CF331814      ACCESSION:CF331814
c 407      11      0.7      11      1      CF331815      ACCESSION:CF331815

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ALIGNMENTS

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RESULT 1
CF302409/c
LOCUS      CF302409      18 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--07-N19-g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-N19, mRNA sequence.
ACCESSION      CF302409
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa

```

```

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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FEATURES
source
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Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-N19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site:1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match      1.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1479      CTAATAAAAAAAAAAAAAA 1496
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      18      CTAATAAAAAAAAAAAAAA 1

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RESULT 2
AZ450180
LOCUS      AZ450180      19 bp      DNA      linear      GSS 04-OCT-2000
DEFINITION      1M0248K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0248K13 R, genomic survey sequence.
ACCESSION      AZ450180
VERSION      AZ450180.1      GI:10604710
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus

```

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired ends from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0248 row: K column: 13
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES
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Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0248K13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI:4732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match      1.2%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1479      CTAATAAAAAAAAAAAAAA 1496
      |||
      1      CTAATAAAAAAAAAAAAAA 18

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RESULT 3
BQ590128/c
LOCUS      BQ590128      17 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION      E012843-024-019-E19-T7 MP12-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-E19 3-PTIME, mRNA sequence.
ACCESSION      BQ590128
VERSION      BQ590128.1      GI:26119711
KEYWORDS      EST.
SOURCE      Beta vulgaris
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Anaranthaceae; Beta.
 1 (bases 1 to 17)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 12472698
 Contact: Weisshaar B
 ADIS DNA core facility at MPZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 17 Std Error: 0.00
 Plate: 19 row: E column: 19
 Seq primer: T7; GTAATACGACTCATTATAGGCG.

FEATURES

source
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 Location/Qualifiers
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 /db_xref="taxon:161934"
 /clone="024-019-E19"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-storage root"
 /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCAGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.1%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
 |||||
 DB 17 TAAAAAAAAAAAAAAAAA 1

RESULT 4

CF294668/c
 LOCUS 30DGS--04-E17-g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 DEFINITION sativa cDNA clone 30DGS--04-E17, mRNA sequence.
 ACCESSION CF294668
 VERSION CF294668.1 GI:33663701
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 17)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Query Match 1.1%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496

Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES

source
 1. 17
 Location/Qualifiers
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 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--04-E17"
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 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
 |||||
 DB 17 TAAAAAAAAAAAAAAAAA 1

RESULT 5

CF295988/c
 LOCUS 30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 DEFINITION sativa cDNA clone 30DGS--06-C17, mRNA sequence.
 ACCESSION CF295988
 VERSION CF295988.1 GI:33665021
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 17)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES

source
 1. 17
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 /organism="Oryza sativa"
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 /clone="30DGS--06-C17"
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 /dev_stage="30 days after germination"
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 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496

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Db      17 TAAAAAAAAAAAAAAAAA 1
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CF336950      17 bp mRNA linear EST 18-AUG-2003
JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.
CF336950
VERSION      CF336950.1 GI:33822280
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
JOURNAL
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
              Location/Qualifiers
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              /cultivar="Nackdong"
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              /tissue_type="leaf"
              /dev_stage="14 days after germination"
              /lab_host="E.coli DH10B"
              /clone_lib="AtJMT-overexpressing transgenic rice plasmid
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              /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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              prepared from Arabidopsis Jasmonate Carboxyl
              methyltransferase overexpression line."
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              Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1480 TAAAAAAAAAAAAAAAAA 1496
|||||
Db      17 TAAAAAAAAAAAAAAAAA 1
|||||
CF301151/c
LOCUS      7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--05-005, mRNA sequence.
ACCESSION      CF301151
VERSION      CF301151.1 GI:33672912
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
JOURNAL

RESULT 6
CF336950/c
LOCUS      17 bp mRNA linear EST 18-AUG-2003
DEFINITION      library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.
ACCESSION      CF336950
VERSION      CF336950.1 GI:33822280
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
JOURNAL
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
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              /lab_host="E.coli DH10B"
              /clone_lib="AtJMT-overexpressing transgenic rice plasmid
              cDNA library (JMT)"
              /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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              prepared from Arabidopsis Jasmonate Carboxyl
              methyltransferase overexpression line."
              Query Match      1.1%; Score 17; DB 1; Length 17;
              Best Local Similarity 100.0%; Pred. No. 28;
              Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1480 TAAAAAAAAAAAAAAAAA 1496
|||||
Db      17 TAAAAAAAAAAAAAAAAA 1
|||||
CF301151/c
LOCUS      7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--05-005, mRNA sequence.
ACCESSION      CF301151
VERSION      CF301151.1 GI:33672912
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
JOURNAL

COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
              Location/Qualifiers
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              /tissue_type="leaf"
              /dev_stage="7 days after germination"
              /lab_host="E.coli DH10B"
              /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
              /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
              with oligoribonucleotides and then used as templates for
              RT-PCR."
              Query Match      1.1%; Score 17; DB 1; Length 18;
              Best Local Similarity 100.0%; Pred. No. 35;
              Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1480 TAAAAAAAAAAAAAAAAA 1496
|||||
Db      18 TAAAAAAAAAAAAAAAAA 2
|||||
RESULT 8
CF320046/c
LOCUS      HD--10-M11.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION      library (HD) Oryza sativa cDNA clone HD--10-M11, mRNA sequence.
ACCESSION      CF320046
VERSION      CF320046.1 GI:33691807
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
JOURNAL
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
              Location/Qualifiers
              1..18
              /organism="Oryza sativa"
              /mol_type="mRNA"
              /cultivar="Nackdong"
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              /clone="HD--10-M11"
              /tissue_type="callus"
              /dev_stage="proliferated callus on 2N6 media for 2 weeks"
              /lab_host="E.coli DH10B"
              /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
              cDNA library (HD)"
              /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
              treated with ABA(20um) for 1hr. Oligo-capped mRNA was
              reverse transcribed and then used for PCR. mRNA was
              derived from rice Histone Deacetylase overexpression
              line."

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Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
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 Db 17 TAAAAAAAAAAAAAAAAA 1

RESULT 9
 AZ345795
 LOCUS
 DEFINITION IM0080H09R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UUGC1M0080H09 R, genomic survey sequence.

ACCESSION AZ345795
 VERSION AZ345795.1 GI:10425032
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Duna,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: H column: 09
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 1. .19
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080H09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male); was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
 |||||
 Db 2 TAAAAAAAAAAAAAAAAA 18

RESULT 10
 AZ650575
 LOCUS
 DEFINITION IM0520P13R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UUGC1M0520P13 R, genomic survey sequence.

ACCESSION AZ650575
 VERSION AZ650575.1 GI:11785200
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0520 row: P column: 13
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 1. .19
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0520P13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male); was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.1%; Score 17; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1496
|||||
Db 2 TAAAAAATAAAAA 18

RESULT 11
AL587759/c
LOCUS
DEFINITION AL587759 BP Chicken Brain Library EST 02-MAR-2001
ROS061G06, mRNA sequence.

ACCESSION AL587759.1 GI:13192793
VERSION
KEYWORDS Gallus gallus (chicken)
SOURCE
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 20)
AUTHORS Murray, F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk

CGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
Location/Qualifiers
1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS061G06"
/tissue type="Brain"
/dev stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCACCTCGAG 3'; 3' adaptor sequence: 5'
CGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"

FEATURES
source

RESULT 13
AZ486784/c
LOCUS
DEFINITION IM0315C20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0315C20 F, genomic survey sequence.
ACCESSION AZ486784.1 GI:10653898
VERSION
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn, D., Oyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: C column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1496
|||||
Db 20 TAAAAAATAAAAA 4

RESULT 12
CF299570/c
LOCUS
DEFINITION 7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-K09, mRNA sequence.

ACCESSION CF299570
VERSION
KEYWORDS Oryza sativa
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 20)
AUTHORS Kim, J.-S., Jun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C.,
Song, S.-I., Kim, J.-K., Kim, Y.-K. and Nahm, B.-H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-K09"
/tissue type="leaf"
/dev stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1496
|||||
Db 17 TAAAAAATAAAAA 1

RESULT 13
AZ486784/c
LOCUS
DEFINITION IM0315C20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0315C20 F, genomic survey sequence.
ACCESSION AZ486784.1 GI:10653898
VERSION
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn, D., Oyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: C column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"

RESULT 13

AZ486784/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source


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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315C20"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1480 TAAAAA...AAAAA 1496
Db 20 TAAAAA...AAAAA 4

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```

RESULT 14
AZ849506
LOCUS
DEFINITION
2M0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0150P21 R, genomic survey sequence.
ACCESSION
AZ849506
VERSION
AZ849506.1 GI:13033596
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

```

```

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

```

```

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```

```

Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACAGGAACAGCTATGACC

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Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20

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FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

```

```

/db_xref="taxon:10090"
/clone="UUGC2M0150P21"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1480 TAAAAA...AAAAA 1496
Db 2 TAAAAA...AAAAA 18

```

```

RESULT 15
AZ858419
LOCUS

```

```

DEFINITION
2M0163003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0163003 R, genomic survey sequence.
ACCESSION
AZ858419
VERSION
AZ858419.1 GI:13051545
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

```

```

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

```

```

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```

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Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: O column: 03
Seq primer: CACACAGGAACAGCTATGACC

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Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20

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FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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/clone="UUGC2M0163003"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA... 1496
 Db 1 TAAAAA... 17

RESULT 16
 CF291665/c
 LOCUS
 DEFINITION 19 bp mRNA linear EST 14-AUG-2003
 sativa cDNA clone 14ROOT--02-D01, mRNA sequence.

ACCESSION CF291665
 VERSION CF291665.1 GI:33660698
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1. .19
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ROOT--02-D01"
 /tissue_type="root"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"
 /note="Vector: PCR4-TOPO; Site:1; EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA... 1496
 Db 18 CAAAAA... 1

RESULT 17
 CF295672/c

LOCUS

DEFINITION 19 bp mRNA linear EST 14-AUG-2003
 sativa cDNA clone 30DGS--05-L12, mRNA sequence.

ACCESSION CF295672

VERSION CF295672.1 GI:33664705

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1. .19
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--05-L12"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
 /note="Vector: PCR4-TOPO; Site:1; EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1476 ATGCTAAA... 1493
 Db 18 ATGTTAAA... 1

RESULT 18
 CF298396/c

LOCUS

DEFINITION 19 bp mRNA linear EST 15-AUG-2003
 sativa cDNA clone 7LEAF--01-M05, mRNA sequence.

ACCESSION CF298396

VERSION CF298396.1 GI:33670157

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

1. 19
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--01-M05"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA... 1496
 Db 19 CAAAAA... 2

RESULT 19

CF302456/c
 LOCUS
 DEFINITION 7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--07-P22, mRNA sequence.
 CF302456
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

1. 19
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--07-P22"
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 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FEATURES

1. 19
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 /cultivar="Nackdong"
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 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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 RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA... 1496
 Db 19 CAAAAA... 2

RESULT 21

BQ590166/c
 LOCUS
 DEFINITION E012844-024-019-K18-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-K18 3-PRIME, mRNA sequence.
 BQ590166
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
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 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

1. 19
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
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FEATURES

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 Location/Qualifiers
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 /clone="7LEAF--01-M05"
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 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA... 1496
 Db 19 CAAAAA... 2

RESULT 20

CF327587/c
 LOCUS
 DEFINITION NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--02-C04, mRNA sequence.
 CF327587
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

1. 19
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
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 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
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 RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
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FEATURES

1. 19
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 /clone="7LEAF--01-M05"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA... 1496
 Db 19 CAAAAA... 2

RESULT 21

BQ590166/c
 LOCUS
 DEFINITION E012844-024-019-K18-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-K18 3-PRIME, mRNA sequence.
 BQ590166
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Unpublished (2003)
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

1. 16
 Location/Qualifiers
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="Beta vulgaris"
 /db_xref="taxon:4530"
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 /tissue_type="root"
 /dev_stage="storage"
 /lab_host="E.coli DH10B"
 /clone_lib="MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-K18 3-PRIME, mRNA sequence."
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL MEDLINE Plant J. 32 (5), 845-857 (2002)

PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 19 row: K column: 18
Seq primer: T7; GTAATACGACTCATTATAGGC.
Location/Qualifiers
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/db_xref="taxon:161934"
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/tissue_type="storage root"
/lab_host="EMDH108"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES
source
1. .16
Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 22
BQ590507/c
LOCUS E012844-024-019-M04-T7 MPZ-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
ACCESSION BQ590507
VERSION BQ590507.1 GI:26120090
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL MEDLINE Plant J. 32 (5), 845-857 (2002)

PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ

Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCATTATAGGC.
Location/Qualifiers
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/clone="024-019-M04"
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MPZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
|||||
Db 16 TAAAAAAAAAAAAA 1

RESULT 23
BQ592600
LOCUS S013686-024-028-F08-SP6R MPZ-ADIS-024-developing root Beta
DEFINITION vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.
ACCESSION BQ592600
VERSION BQ592600.1 GI:26122183
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL MEDLINE Plant J. 32 (5), 845-857 (2002)

PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
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/clone_lib="MPIZ-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 24
BQ592965/c
LOCUS
DEFINITION
S013324-024-028-A01-T7 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-028-A01 3-PRIME, mRNA sequence.
ACCESSION
BQ592965
VERSION
BQ592965.1 GI:26122548
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 28 row: A column: 01
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/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 25
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LOCUS
DEFINITION
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cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION
BQ595369
VERSION
BQ595369.1 GI:26124952
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: P column: 02
Seq primer: T7; GTAATACGACTCTACTATAGGC.
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line)"
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/db_xref="taxon:161934"
/clone="024-022-P02"
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/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.
Location/Qualifiers
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/organism="Oryza sativa"
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/clone="30DGS--06-F22"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1495
Db 16 TAAAAAATAAAAAAAAAA 1

RESULT 29
CF311057/c
LOCUS
DEFINITION
ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Song,S.I., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Kim,J.S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
source
1. .16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--02-G01"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
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derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 TAAAAAATAAAAAAAAAA 1

RESULT 31
CF314377/c
LOCUS
DEFINITION
HD--02-001.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--02-001, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
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1. .16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--06-C03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAATAAAAAAAAAA 1496

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RESULT 37
CF329320/c
LOCUS       NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION  sativa cDNA clone NACL--04-J17, mRNA sequence.
ACCESSION   CF329320
VERSION     CF329320.1 GI:33806877
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="NACL--04-J17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1495
Db 16 TAAAAAATAAAAA 1

RESULT 38
CF333386
LOCUS       JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION  library (JMT) Oryza sativa cDNA clone JMT--02-E05, mRNA sequence.
ACCESSION   CF333386
VERSION     CF333386.1 GI:33815044
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="NACL--04-J17"
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                     /dev_stage="proliferated callus on 2N6 media for 30 days"
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1495
Db 16 TAAAAAATAAAAA 1

RESULT 39
BQ590687
LOCUS       S013717-024-018-B24-T7 MP12-ADIS-024-storage root Beta vulgaris
DEFINITION  cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
ACCESSION   BQ590687
VERSION     BQ590687.1 GI:26120270
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
             Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
             and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
             fingerprinting allows access to 25 000 potential sugar beet genes
             Plant J. 32 (5), 845-857 (2002)
JOURNAL     22362189
MEDLINE     12472698
PUBMED      12472698
COMMENT     Contact: Weisshaar B
             ADIS DNA core facility at MP1Z
             Max-Planck-Institute for Plant Breeding Research
             Carl-von-Linne Weg 10, 50829 Koeln, Germany
             Fax: 00492215062851
             Email: weisshaar@mpiz-koeln.mpg.de
             Insert Length: 17 Std Error: 0.00
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             Seq primer: T7; GTAATACGACCTCATATAGGCG.

FEATURES             Location/Qualifiers
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                     /clone="024-018-B24"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MP12-ADIS-024-storage root"
                     /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:

```

```

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--02-E05"
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     prepared from Arabidopsis Jasmonate Carboxyl
                     methyltransferase overexpression line."

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAATAAAAA 1496
Db 1 AAAAAAATAAAAA 16

RESULT 39
BQ590687
LOCUS       S013717-024-018-B24-T7 MP12-ADIS-024-storage root Beta vulgaris
DEFINITION  cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
ACCESSION   BQ590687
VERSION     BQ590687.1 GI:26120270
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
             Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
             and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
             fingerprinting allows access to 25 000 potential sugar beet genes
             Plant J. 32 (5), 845-857 (2002)
JOURNAL     22362189
MEDLINE     12472698
PUBMED      12472698
COMMENT     Contact: Weisshaar B
             ADIS DNA core facility at MP1Z
             Max-Planck-Institute for Plant Breeding Research
             Carl-von-Linne Weg 10, 50829 Koeln, Germany
             Fax: 00492215062851
             Email: weisshaar@mpiz-koeln.mpg.de
             Insert Length: 17 Std Error: 0.00
             Plate: 18 row: B column: 24
             Seq primer: T7; GTAATACGACCTCATATAGGCG.

FEATURES             Location/Qualifiers
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                     /clone="024-018-B24"
                     /tissue_type="storage root"
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                     /clone_lib="MP12-ADIS-024-storage root"
                     /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:

```

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 |||||
 Db 1 AAAAAAAAAAAAAA 16

RESULT 40

LOCUS BQ591177/c
 DEFINITION E012715-024-017-B22-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 CDNA clone 024-017-B22 3-PRIME, mRNA sequence.

ACCESSION BQ591177
 VERSION BQ591177.1
 KEYWORDS GI:26120760
 SOURCE EST.

ORGANISM

Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 17)

REFERENCE Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

PUBMED 12472698

COMMENT

ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 17 Std Error: 0.00
 Plate: 17 row: B column: 22
 Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES

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 /db_xref="taxon:161934"
 /clone="024-017-B22"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 |||||
 Db 17 AAAAAAAAAAAAAA 2

RESULT 41

LOCUS BQ591181/c
 DEFINITION E012715-024-017-H16-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 CDNA clone 024-017-H16 3-PRIME, mRNA sequence.

ACCESSION BQ591181
 VERSION BQ591181.1
 KEYWORDS GI:26120764
 SOURCE EST.

ORGANISM

Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE

1 (bases 1 to 17)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

PUBMED 12472698

COMMENT

ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 17 Std Error: 0.00
 Plate: 17 row: H column: 16
 Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES

source

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 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
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 /db_xref="GABI:188932"
 /db_xref="taxon:161934"
 /clone="024-017-H16"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
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 Db 16 TAAAAAAAAAAAAA 1

RESULT 42

LOCUS CF290854/c
 DEFINITION E012715-024-017-H16-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 CDNA clone 024-017-H16 3-PRIME, mRNA sequence.

17 bp mRNA linear EST 14-AUG-2003

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DEFINITION 14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION sativa cDNA clone 14ROOT--01-A21, mRNA sequence.
VERSION CF290854
KEYWORDS CF290854.1 GI:33659887
SOURCE EST.
ORGANISM Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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          /lab_host="E.coli DH10B"
          /clone_lib="Rice root plasmid cDNA library (14ROOT)"
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          with oligoribonucleotides and then used as templates for
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Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 43
CF295807/c
LOCUS CF295807
DEFINITION 30DGS--05-O12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
ACCESSION sativa cDNA clone 30DGS--05-O12, mRNA sequence.
VERSION CF295807
KEYWORDS CF295807.1 GI:33664840
SOURCE EST.
ORGANISM Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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          /mol_type="mRNA"
          /cultivar="Nackdong"
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          /dev_stage="7 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 44
CF298589/c
LOCUS CF298589
DEFINITION 7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION sativa cDNA clone 7LEAF--02-A18, mRNA sequence.
VERSION CF298589
KEYWORDS CF298589.1 GI:33670350
SOURCE EST.
ORGANISM Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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          /organism="Oryza sativa"
          /mol_type="mRNA"
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          /clone="30DGS--05-O12"
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          /lab_host="E.coli DH10B"
          /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 44
CF298589/c
LOCUS CF298589
DEFINITION 7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION sativa cDNA clone 7LEAF--02-A18, mRNA sequence.
VERSION CF298589
KEYWORDS CF298589.1 GI:33670350
SOURCE EST.
ORGANISM Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
          1..17
          /organism="Oryza sativa"
          /mol_type="mRNA"
          /cultivar="Nackdong"
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          /tissue_type="leaf"
          /dev_stage="7 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 45
CF299639/c

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LOCUS	CF299639	17 bp	mRNA	linear	EST 15-AUG-2003				
DEFINITION	7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-L20, mRNA sequence.								
ACCESSION	CF299639								
VERSION	CF299639.1	GI:33671400							
KEYWORDS	EST.								
SOURCE	Oryza sativa								
ORGANISM	Oryza sativa								
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.								
AUTHORS	1 (bases 1 to 17)								
TITLE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.								
JOURNAL	Large-scale Sequencing Analysis of Rice ESTs								
COMMENT	Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnaahm@gbio.com, bhnaahm@bio.myongji.ac.kr.								
FEATURES	Location/Qualifiers								
source	1..17								
	/organism="Oryza sativa"								
	/mol_type="mRNA"								
	/cultivar="Nackdong"								
	/db_xref="taxon:4530"								
	/clone="7LEAF-03-L20"								
	/tissue_type="leaf"								
	/dev_stage="7 days after germination"								
	/lab_host="E.coli DH10B"								
	/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"								
	/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."								
Query Match	1.1%; Score 16; DB 1; Length 17;								
Best Local Similarity	100.0%; Pred. No. 52;								
Matches	16;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;				
QY	1481	AAAAAAAAAAAAAAAAAAAA 1496							
Db	16	AAAAAAAAAAAAAAAAAAAA 1							
RESULT 46									
CF302447/c									
LOCUS	CF302447	17 bp	mRNA	linear	EST 15-AUG-2003				
DEFINITION	7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-P11, mRNA sequence.								
ACCESSION	CF302447								
VERSION	CF302447.1	GI:33674208							
KEYWORDS	EST.								
SOURCE	Oryza sativa								
ORGANISM	Oryza sativa								
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.								
AUTHORS	1 (bases 1 to 17)								
TITLE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.								
JOURNAL	Large-scale Sequencing Analysis of Rice ESTs								
COMMENT	Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnaahm@gbio.com, bhnaahm@bio.myongji.ac.kr.								
FEATURES	Location/Qualifiers								

```

RESULT 48
CF311499/c
LOCUS
DEFINITION
ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.
ACCESSION
CF311499
VERSION
CF311499.1 GI:33683260
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
/lab_host="E.coli DH10B"
/dev_stage="14 days after germination"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--06-L20"
/tissue_type="leaf"
/lab_host="E.coli DH10B"
/dev_stage="14 days after germination"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1495
Db 16 TAAAAAATAAAAA 1

RESULT 49
CF313013/c
LOCUS
DEFINITION
ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-P19, mRNA sequence.
ACCESSION
CF313013
VERSION
CF313013.1 GI:33684774
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
/lab_host="E.coli DH10B"
/dev_stage="14 days after germination"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1495
Db 16 TAAAAAATAAAAA 1

RESULT 49
CF313013/c
LOCUS
DEFINITION
ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-P19, mRNA sequence.
ACCESSION
CF313013
VERSION
CF313013.1 GI:33684774
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
/lab_host="E.coli DH10B"
/dev_stage="14 days after germination"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1495
Db 16 TAAAAAATAAAAA 1

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..17

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--08-P19"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 1.1%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAATAAAAA 1496

Db 16 AAAAAAATAAAAA 1

RESULT 50

CF319075/c

LOCUS

DEFINITION

HD--09-H06.g1 OshDACL-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--09-H06, mRNA sequence.

ACCESSION

CF319075

VERSION

CF319075.1 GI:33690836

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

/lab_host="E.coli DH10B"

/dev_stage="14 days after germination"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 1.1%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAATAAAAA 1496

Db 16 AAAAAAATAAAAA 1

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..17

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HD--09-H06"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDACL-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression line."

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1480 TAAAAAATAAAAAAAAAA 1495
DB 16 TAAAAAATAAAAAAAAAA 1

RESULT 51
CFP334566/c
LOCUS
DEFINITION
JMT--03-013.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT-03-013, mRNA sequence.

ACCESSION
CFP334566
VERSION
CFP334566.1 GI:33817460
KEYWORDS
EST.

SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1. 17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT-03-013"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAATAAAAAAAAAA 1496
DB 17 AAAAAAATAAAAAAAAAA 2

RESULT 52
AL048754
LOCUS
DEFINITION
DKFP566L173_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
library (JMT) Oryza sativa cDNA clone JMT-03-013, mRNA sequence.
ACCESSION
AL048754
VERSION
AL048754.1 GI:4727825
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
AUTHORS
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE
EST (Koehler, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source
1. 18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP566L173"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMPl; Site 1: NotI; Site 2: SalI"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAATAAAAAAAAAA 1496
DB 3 AAAAAAATAAAAAAAAAA 18

RESULT 53

BQ582676/c
LOCUS
DEFINITION
R01281-024-007-P18-SP6 MP12-ADIS-024-inflorescence Beta vulgaris
cDNA clone 024-007-P18 5-PRIME, mRNA sequence.

ACCESSION
BQ582676
VERSION
BQ582676.1 GI:26112253
KEYWORDS
EST.

SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
22362189
PUBMED
12472698

COMMENT
Contact: Weisshaar B

ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de

Insert Length: 18 Std Error: 0.00

Plate: 7 row: P column: 18

Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

source
1. 18
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:184018"
/db_xref="taxon:161934"
/clone="024-007-P18"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-inflorescence"

/notes=Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 54
BQ590027/c
LOCUS
DEFINITION BQ590027 18 bp mRNA linear EST 06-DEC-2002
cDNA clone 024-019-E24-T7 MP1Z-ADIS-024-storage root Beta vulgaris

ACCESSION BQ590027
VERSION BQ590027.1 GI:26119610
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 18)
AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL MEDLINE
PUBMED 22362189
COMMENT 12472698
CONTACT: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 19 row: E column: 24
Seq primer: T7; GTAATACGACTACTATAGGCG.

FEATURES
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/mol_type="mRNA"
/cultivar="KWS22320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:190095"
/db_xref="taxon:161934"
/clone="024-019-E24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes=Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 55
CF277873/c
LOCUS
DEFINITION CF277873 18 bp mRNA linear EST 14-AUG-2003
Oryza sativa cDNA clone 14ETL--03-J04, mRNA sequence.

ACCESSION CF277873
VERSION CF277873.1 GI:33655259
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 18)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE Unpublished (2003)
JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--03-J04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note=Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 56
CF297446/c
LOCUS
DEFINITION CF297446 18 bp mRNA linear EST 14-AUG-2003
30DGS--08-F02.g1 Rice leaf plasmid cDNA library 1 (30DGS) Oryza
sativa cDNA clone 30DGS--08-F02, mRNA sequence.

ACCESSION CF297446
VERSION CF297446.1 GI:33666479
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.


```

REFERENCE 1 (bases 1 to 18)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES   source
            Location/Qualifiers
            1..18
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="30DGS--08-F02"
            /tissue_type="leaf"
            /dev_stage="30 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
            /notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 57
CF298591/c
LOCUS     7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION
ACCESSION CF298591.1 GI:33670352
VERSION   EST.
KEYWORDS  Oryza sativa
SOURCE    Oryza sativa
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES   source
            Location/Qualifiers
            1..18
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="7LEAF--02-A20"
            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 59
CF299674/c
LOCUS     7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION
ACCESSION CF299674.1 GI:33671435
VERSION   EST.
KEYWORDS  Oryza sativa
SOURCE    Oryza sativa
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.

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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
DB 16 TAAAAAAAAAAAAA 1

RESULT 58
CF299027/c
LOCUS     7LEAF--02-N14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION
ACCESSION CF299027.1 GI:33670788
VERSION   EST.
KEYWORDS  Oryza sativa
SOURCE    Oryza sativa
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES   source
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            1..18
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            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="7LEAF--02-N14"
            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 59
CF299674/c
LOCUS     7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION
ACCESSION CF299674.1 GI:33671435
VERSION   EST.
KEYWORDS  Oryza sativa
SOURCE    Oryza sativa
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-M14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
DB 18 AAAAAAAAAAAAAA 3

RESULT 60
CF300456/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF300456 18 bp mRNA linear EST 15-AUG-2003
7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-N23, mRNA sequence.

CF300456
CF300456.1 GI:33672217
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-N23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
DB 16 AAAAAAAAAAAAAA 1

RESULT 61
CF301057/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF301057 18 bp mRNA linear EST 15-AUG-2003
7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M05, mRNA sequence.

CF301057
CF301057.1 GI:33672818
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-M05"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
DB 17 AAAAAAAAAAAAAA 2

RESULT 62
CF301325/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF301325 18 bp mRNA linear EST 15-AUG-2003
7LEAF--06-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-C12, mRNA sequence.

CF301325
CF301325.1 GI:33673086
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
 1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .18
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--06-C12"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496

Db 18 AAAAAAAAAAAAAA 3

RESULT 63

CF301760/c

LOCUS 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--06-L22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--06-L22, mRNA sequence.

ACCESSION CF301760

VERSION CF301760.1 GI:33673521

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 18)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .18
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--06-L22"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496

Db 18 AAAAAAAAAAAAAA 3

RESULT 64

CF309376/c

LOCUS 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa cDNA clone ABF--03-I19, mRNA sequence.

ACCESSION CF309376

VERSION CF309376.1 GI:33681137

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 18)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .18
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="ABF--03-I19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495

Db 16 TAAAAAAAAAAAAA 1

RESULT 65

CF320418/c

LOCUS 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--11-E22.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD--11-E22, mRNA sequence.

ACCESSION CF320418

VERSION CF320418.1 GI:33692179


```

LOCUS      BE230585                      15 bp      mRNA      linear      EST 07-JUL-2000
DEFINITION 99AS799 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa
            (indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION  BE230585
VERSION     BE230585.1 GI:8956782
KEYWORDS   EST.
SOURCE      Oryza sativa (indica cultivar-group)
            Oryza sativa (indica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
            Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of ESTs from Rice Seedling
JOURNAL    Unpublished (1999)
COMMENT    Contact: Eun M.Y.
            Department of Cytogenetics
            National Inst. of Agri. Sci. and Tech, RDA
            Suwon, Kyunggido, Korea
            Tel: 82 331 290 0301
            Fax: 82 331 290 0307
            Email: myeun@sun20.asti.re.kr.
FEATURES   Location/Qualifiers
            1..15
                /organism="Oryza sativa (indica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Milyang23"
                /db_xref="taxon:39946"
                /clone="99AS799"
                /dev_stage="5 days after pollination"
                /lab_host="E. coli SOLR"
                /clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
                /notes="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
                XhoI; Directional cDNA library inserted into lambda ZAPII
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Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      1 AAAAAAAAAAAAAA 15

RESULT 72
BQ582543/c
LOCUS      BQ582543                      15 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION 'S013300-024-007-B02-T7 MP1Z-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-007-B02 3-PRIME, mRNA sequence.
ACCESSION  BQ582543
VERSION     BQ582543.1 GI:26112120
KEYWORDS   EST.
SOURCE      Beta vulgaris
            Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
            1 (bases 1 to 15)
            Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
JOURNAL    22362189
MEDLINE    12472698
PUBMED     12472698
COMMENT    Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851

TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL    Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT    Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851

```

```

Email: weisshaar@mpiz-koeln.mpg.de
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Plate: 7 row: B column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.
FEATURES   Location/Qualifiers
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                /lab_host="EMDH10B"
                /clone_lib="MP1Z-ADIS-024-inflorescence"
                /note="Vector: pCMVSPORT6; Site.1: SalI; Site.2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
                b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                orientation:
                SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Best
                Project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      15 AAAAAAAAAAAAAA 1

RESULT 73
BQ585820/c
LOCUS      BQ585820                      15 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION E012533-024-014-H17-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
            024-014-H17 5-PRIME, mRNA sequence.
ACCESSION  BQ585820
VERSION     BQ585820.1 GI:26115402
KEYWORDS   EST.
SOURCE      Beta vulgaris
            Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
            1 (bases 1 to 15)
            Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
JOURNAL    22362189
MEDLINE    12472698
PUBMED     12472698
COMMENT    Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert Length: 15 Std Error: 0.00
            Plate: 14 row: H column: 17
            Seq primer: SP6; CATACGATTGATGTCGACACTATAG.
FEATURES   Location/Qualifiers
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                /organism="Beta vulgaris"
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                /cultivar="KWS2320 (double haploid, monogerm breeding
                line)"

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/db xref="taxon:161934"
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/clone lib="MP12-ADIS-024-leaf"
/notes="Vector: pCMVSPORT6; Site:1: Sali; Site:2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 74
BO590410/c 15 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
E012844-024-019-M08-T7 MP12-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-M08 3-PRIME, mRNA sequence.
ACCESSION
BO590410
VERSION
BO590410.1 GI:26119993
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 15)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
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Seq primer: T7: GTAATACGACTCATTAGGCG.

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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 75
BO590656/c 15 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
S015086-024-018-L13-SP6 MP12-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-L13 5-PRIME, mRNA sequence.
ACCESSION
BO590656
VERSION
BO590656.1 GI:26120239
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 15)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
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Seq primer: SP6: CATACGATTAGTGCACACTATAG.

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line)"
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/clones="024-018-L13"
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/notes="Vector: pCMVSPORT6; Site:1: Sali; Site:2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCACTATAGGCG.

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/tissue_type="storage root"
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/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: Sali; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 79
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LOCUS
DEFINITION BQ594689 15 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-024-M05-T7 MPZ-ADIS-024-developing root Beta vulgaris
ACCESSION BQ594689
VERSION BQ594689.1 GI:26124272
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 15)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPZ

Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES

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/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site_1: Sali; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 80
CF277319/c
LOCUS
DEFINITION CF277319 15 bp mRNA linear EST 14-AUG-2003
Oryza sativa CDNA clone 14ETL--02-M23, mRNA sequence.
ACCESSION CF277319
VERSION CF277319.1 GI:33654705
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES

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1. .15
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/db_xref="taxon:4530"
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/dev_stage="14 days after germination"

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/clone lib="Rice etiolated leaf plasmid cDNA library
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 81
CF281923/c
LOCUS
DEFINITION
14ETL--09-D04_g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-D04, mRNA sequence.
ACCESSION
CF281923
VERSION
CF281923.1 GI:33659310
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 82
CF290920/c
LOCUS
DEFINITION
14ROOT--01-C09_b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-C09, mRNA sequence.
ACCESSION
CF290920
VERSION
CF290920.1 GI:33659953

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KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

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Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 83
CF291029/c
LOCUS
DEFINITION
14ROOT--01-E19_b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION
CF291029
VERSION
CF291029.1 GI:33660062
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
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/cultivar="Nackdong"
/db_xref="taxon:4530"

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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 84
CF291103/c
LOCUS      15 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-G10, mRNA sequence.
ACCESSION  CF291103
VERSION     CF291103.1 GI:33660136
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1. .15
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RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 85
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LOCUS      15 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-E04, mRNA sequence.
ACCESSION  CF291717

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VERSION      CF291717.1 GI:33660750
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1. .15
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 86
CF291798/c
LOCUS      15 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-G02.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-G02, mRNA sequence.
ACCESSION  CF291798
VERSION     CF291798.1 GI:33660831
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 87
CF292458/c
LOCUS      15 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 30DGS--01-E17, mRNA sequence.
ACCESSION CF292458
VERSION    CF292458.1 GI:33661491
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 89
CF295100/c
LOCUS      15 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 30DGS--04-002, mRNA sequence.
ACCESSION CF295100
VERSION    CF295100.1 GI:33664133
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 88
CF292461/c
LOCUS      15 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 30DGS--01-E19, mRNA sequence.
ACCESSION CF292461
VERSION    CF292461.1 GI:33661494
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1480 TAAAAAATAAAAAA 1494
Db 15 TAAAAAATAAAAAA 1

RESULT 90
CF298148/c      15 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
7LEAF--01-G17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-G17, mRNA sequence.
CF298148
VERSION
CF298148.1 GI:33669909
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
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OY 1481 AAAAAAATAAAAAA 1495
Db 15 AAAAAAATAAAAAA 1

RESULT 92
CF298733/c      15 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-E20, mRNA sequence.
CF298733
VERSION
CF298733.1 GI:33670494
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
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JOURNAL
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COMMENT
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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAATAAAAAA 1495
Db 15 AAAAAAATAAAAAA 1

RESULT 91
CF298630/c      15 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-B23, mRNA sequence.
CF298630
VERSION
CF298630.1 GI:33670391
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAATAAAAAA 1495
Db 15 AAAAAAATAAAAAA 1

RESULT 92
CF298733/c      15 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-E20, mRNA sequence.
CF298733
VERSION
CF298733.1 GI:33670494
KEYWORDS
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ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Db 15 AAAAAAATAAAAAA 1

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 93
CF298805/c
LOCUS
DEFINITION
7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-G20, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

Query Match          1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 15 AAAAAAAAAAAAAA 1

RESULT 94
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DEFINITION
7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-L01, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

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DEFINITION
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sativa cDNA clone 7LEAF--02-J09, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
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ORGANISM
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Query Match          1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 95
CF299602/c
LOCUS
DEFINITION
7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-L01, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
RT-PCR."

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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1. .15
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cDNA library (ABF)"
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 105

CF311907/c

LOCUS ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--07-G04, mRNA sequence.

ACCESSION CF311907

VERSION CF311907

KEYWORDS EST.

SOURCE CF311907.1 GI:33683668

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

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1. .15
/organism="Oryza sativa"
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/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 106

CF313319/c

LOCUS HD--01-G13.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.

ACCESSION CF313319

VERSION CF313319.1

KEYWORDS EST.

SOURCE CF313319.1 GI:33685080

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

```

1. .15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--01-G13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDACL1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 107

CF313320

LOCUS HD--01-G13.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.

ACCESSION CF313320

VERSION CF313320.1

KEYWORDS EST.

SOURCE CF313320.1 GI:33685081

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

REFERENCE
AUTHORS      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
TITLE        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL      Large-scale Sequencing Analysis of Rice ESTs
COMMENT      Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .15
   /organism="Oryza sativa"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:4530"
   /clone="HD--01-G13"
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   /lab_host="E.coli DH10B"
   /clone_lib="OSHADAC1-overexpressing transgenic rice plasmid
   cDNA library (HD)"
   /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
   treated with ABA(20um) for 1hr. Oligo-capped mRNA was
   reverse transcribed and then used for PCR. mRNA was
   derived from rice Histone Deacetylase overexpression
   line."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      1 AAAAAAAAAAAAAA 15

RESULT 108
CF316251
LOCUS      CF316251
DEFINITION      HD--05-H15.b1 OSHADAC1-overexpressing transgenic rice plasmid cDNA
               library (HD) Oryza sativa cDNA clone HD--05-H15, mRNA sequence.
ACCESSION      CF316251
VERSION        CF316251.1 GI:33688012
KEYWORDS       EST.
SOURCE        Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .15
   /organism="Oryza sativa"
   /mol_type="mRNA"
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   /db_xref="taxon:4530"
   /clone="HD--05-H15"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 2 weeks"
   /lab_host="E.coli DH10B"
   /clone_lib="OSHADAC1-overexpressing transgenic rice plasmid
   cDNA library (HD)"
   /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
   treated with ABA(20um) for 1hr. Oligo-capped mRNA was
   reverse transcribed and then used for PCR. mRNA was
   derived from rice Histone Deacetylase overexpression
   line."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      1 AAAAAAAAAAAAAA 15

RESULT 109
CF318035/c
LOCUS      CF318035
DEFINITION      HD--07-P06.b1 OSHADAC1-overexpressing transgenic rice plasmid cDNA
               library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence.
ACCESSION      CF318035
VERSION        CF318035.1 GI:33689796
KEYWORDS       EST.
SOURCE        Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .15
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   /mol_type="mRNA"
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   /tissue_type="callus"
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   /lab_host="E.coli DH10B"
   /clone_lib="OSHADAC1-overexpressing transgenic rice plasmid
   cDNA library (HD)"
   /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
   treated with ABA(20um) for 1hr. Oligo-capped mRNA was
   reverse transcribed and then used for PCR. mRNA was
   derived from rice Histone Deacetylase overexpression
   line."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      1 AAAAAAAAAAAAAA 15

RESULT 110
CF318035/c
LOCUS      CF318035
DEFINITION      HD--07-P06.b1 OSHADAC1-overexpressing transgenic rice plasmid cDNA
               library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence.
ACCESSION      CF318035
VERSION        CF318035.1 GI:33689796
KEYWORDS       EST.
SOURCE        Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .15
   /organism="Oryza sativa"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:4530"
   /clone="HD--07-P06"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 2 weeks"
   /lab_host="E.coli DH10B"
   /clone_lib="OSHADAC1-overexpressing transgenic rice plasmid
   cDNA library (HD)"
   /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
   treated with ABA(20um) for 1hr. Oligo-capped mRNA was
   reverse transcribed and then used for PCR. mRNA was
   derived from rice Histone Deacetylase overexpression
   line."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      1 AAAAAAAAAAAAAA 15

```


b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:

SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-TV; Note: Sequencing granted in the context of the GABI-Best Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 116

CF318894/c

LOCUS

DEFINITION HD--09-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-D06, mRNA sequence.

ACCESSION

CF318894

VERSION

CF318894.1

GI:33690655

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..16

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HD--09-D06"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr_ Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

ACCESSION

CF327923

VERSION

CF327923.1

GI:33804096

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..16

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--02-J18"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..16

/organism="Oryza sativa"

RESULT 117

CF327923/c

LOCUS

DEFINITION NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza

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/db_xref="taxon:4530"
/clone="NACL--03-A10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 100.0%; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 119
CF291802/c
LOCUS
DEFINITION
14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION
CF291802
VERSION
CF291802.1 GI:33660835
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-A10"
/clone_lib="Rice callus plasmid cDNA library (14ROOT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Best Local Similarity 100.0%; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 121
AW248457/c
LOCUS
DEFINITION
2820576.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820576 3',
mRNA sequence.
ACCESSION
AW248457
VERSION
AW248457.1 GI:6591450
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 16)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2820576.5prime
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center

```

PHRAP suite. Poly-T identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu/LowQuality> Sequence: 16 contiguous PHRD high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LfCM4 row: J column: 1
High quality sequence stop: 16.

FEATURES

source

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  /cell_line="MGC3"
  /lab_host="DH10B (phage-resistant)"
  /clone_lib="NIH_MGC_7"

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/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1475 CATGCTAAAAAAA 1490

Db 16 CATCCTAAAAAAA 1

RESULT 122

CF317778/c

LOCUS 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--07-J13.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--07-J13, mRNA sequence.

ACCESSION CF317778

VERSION 1 GI:33689539

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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1. .16
Location/Qualifiers
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  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="HD--07-J13"
  /tissue_type="callus"
  /dev_stage="proliferated callus on 2N6 media for 2 weeks"
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/lab_host="E.coli DH10B"
/clone_lib="OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496

Db 16 AAAAAAAAAAAAAA 1

RESULT 123

BQ586422/c

LOCUS

DEFINITION BQ586422 14 bp mRNA linear EST 06-DEC-2002
024-013-002 T7 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone

ACCESSION BQ586422

VERSION BQ586422.1 GI:26116004

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)

Hervig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

Contact: Weishaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

Plate: 13 row: 0 column: 02

Seq primer: T7; GTAATACGACTCCTATAGGCG.

FEATURES

source

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/cultivar="KWS2320 (double haploid, monogerm breeding line)"

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/db_xref="taxon:161934"

/clone="024-013-002"

/tissue_type="leaf"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-leaf"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:<http://gabi.rzpd.de>

Query Match 0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 124
BQ587890/c

LOCUS
DEFINITION BQ587890 14 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-009-B02-T7 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone

ACCESSION 024-009-B02 3-PRIME, mRNA sequence.

VERSION BQ587890.1 GI:26117472
KEYWORDS EST.
SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Anaranthaceae; Beta.

1 (bases 1 to 14)
Herwig.R., Schulz.B., Weisshaar.B., Hennig.S., Steinfath.M.,
Drungowski.M., Stahl.D., Wruck.W., Menze.A., O'Brien.J., Lehrach.H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
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Seq primer: T7; GTAATACGACTCCTACTATAGGC.

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Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
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Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 125
BQ589191/c

LOCUS
DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Anaranthaceae; Beta.

1 (bases 1 to 14)

Herwig.R., Schulz.B., Weisshaar.B., Hennig.S., Steinfath.M.,

Drungowski.M., Stahl.D., Wruck.W., Menze.A., O'Brien.J., Lehrach.H.

and Radelof,U.

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fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
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Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
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Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Best Local Similarity 100.0%; Pred. No. 81;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 126

BQ590242/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

BQ590242 14 bp mRNA linear EST 06-DEC-2002

E012840-024-019-E16-SP6 MP1Z-ADIS-024-storage root Beta vulgaris

CDNA clone 024-019-E16 5-PRIME, mRNA sequence.

ACCESSION BQ590242

VERSION BQ590242.1 GI:26119825

KEYWORDS EST.

SOURCE Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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REFERENCE
AUTHORS      Caryophyllales; Amaranthaceae; Beta.
              1 (bases 1 to 14)
              Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weishaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weishaar@piz-koeln.mpg.de
              Insert Length: 14 Std Error: 0.00
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              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
              orientation:
              SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Best
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"
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QY          1481 AAAAAAAAAAAAAA 1494
Db          14 AAAAAAAAAAAAAA 1

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LOCUS      E012944-024-019-K14-T7 MPIZ-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-019-K14 3-PRIME, mRNA sequence.
ACCESSION  BQ590261
VERSION     BQ590261.1 GI:26119844
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Beta vulgaris
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weishaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaar@piz-koeln.mpg.de
            Insert Length: 14 Std Error: 0.00
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            Seq primer: T7; GTAATACGACTCCTACTATAGGC.
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            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Best
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"
            Query Match      0.9%; Score 14; DB 1; Length 14;
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            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db          14 AAAAAAAAAAAAAA 1

RESULT 128
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LOCUS      E012713-024-017-H18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-017-H18 3-PRIME, mRNA sequence.
ACCESSION  BQ591168
VERSION     BQ591168.1 GI:26120751
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weishaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaar@piz-koeln.mpg.de
            Insert Length: 14 Std Error: 0.00
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            b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Best
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"
            Query Match      0.9%; Score 14; DB 1; Length 14;
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Db          14 AAAAAAAAAAAAAA 1

RESULT 129
BQ591168/c
LOCUS      E012713-024-017-H18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-017-H18 3-PRIME, mRNA sequence.
ACCESSION  BQ591168
VERSION     BQ591168.1 GI:26120751
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weishaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaar@piz-koeln.mpg.de
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            Prof. Christian Jung; Sequence submission managed by
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            Query Match      0.9%; Score 14; DB 1; Length 14;
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Db          14 AAAAAAAAAAAAAA 1

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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 129
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LOCUS
DEFINITION
E012715-024-017-N20-T7 MPZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-N20 3-PRIME, mRNA sequence.
ACCESSION
BQ591176
VERSION
BQ591176.1 GI:26120759
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 14)
Hewig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radloff,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 130
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DEFINITION
E012715-024-017-B04-T7 MPZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-B04 3-PRIME, mRNA sequence.
ACCESSION
BQ591207
VERSION
BQ591207.1 GI:26120790
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 14)
Hewig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radloff,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert length: 14 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCCTACTATAGGC.

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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 131
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 E012714-024-017-B15-T7 MP12-ADIS-024-storage root Beta vulgaris
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ACCESSION BQ591380
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE
 AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
 MEDLINE
 PUBMED

COMMENT

Contact: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaa@mpiz-koeln.mpg.de
 Insert Length: 14 Std Error: 0.00
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 Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES

Location/Qualifiers

1..14
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 Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

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 DB 14 AAAAAAAAAAAAAA 1

RESULT 132

BQ591482/c

LOCUS

DEFINITION

BQ591482 14 bp mRNA linear EST 06-DEC-2002

E012713-024-017-M04-T7 MP12-ADIS-024-storage root Beta vulgaris

CDNA clone 024-017-M04 3-PRIME, mRNA sequence.

ACCESSION BQ591482

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS

1 (bases 1 to 14)

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaa@mpiz-koeln.mpg.de

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Seq primer: T7; GTAATACGACTCACTATAGGCG.

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Location/Qualifiers

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 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

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RESULT 133

BQ593052/c

LOCUS

DEFINITION

BQ593052 14 bp mRNA linear EST 06-DEC-2002

E012375-024-028-C03-SP6 MP12-ADIS-024-developing root Beta vulgaris

CDNA clone 024-028-C03 5-PRIME, mRNA sequence.

ACCESSION BQ593052

VERSION

KEYWORDS

SOURCE

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS

1 (bases 1 to 14)

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaa@mpiz-koeln.mpg.de

ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT ADIS DNA core facility at MPiZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
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 Kleinzellenecker Saatzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
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QY 1481 AAAAAAAAAAAAAA 1494
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 Db 14 AAAAAAAAAAAAAA 1
 RESULT 134
 CF277935/c
 LOCUS 14 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ETL--03-K11-g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 ORYZA SATIVA cDNA clone 14ETL--03-K11, mRNA sequence.
 ACCESSION CF277935
 VERSION CF277935.1 GI:33655321
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
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 Db 14 AAAAAAAAAAAAAA 1

RESULT 135
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 ORYZA SATIVA cDNA clone 14ETL--03-L21, mRNA sequence.
 ACCESSION CF278001
 VERSION CF278001.1 GI:33655387
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 136
CF278452/c
LOCUS 1481 AAAAAAAAAAAAAA 1494 bp mRNA linear EST 14-AUG-2003
DEFINITION Oryza sativa cDNA clone 14ETL--04-F22, mRNA sequence.
ACCESSION CF278452
VERSION 1
KEYWORDS EST.
SOURCE 1 GI:33655838
ORGANISM Oryza sativa
Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 14 AAAAAAAAAAAAAA 1

RESULT 137
CF279473/c
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DEFINITION Oryza sativa cDNA clone 14ETL--05-M14, mRNA sequence.
ACCESSION CF279473
VERSION 1
KEYWORDS EST.
SOURCE 1 GI:33656859
ORGANISM Oryza sativa
Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```

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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 14 AAAAAAAAAAAAAA 1

RESULT 138
CF279992/c
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DEFINITION Oryza sativa cDNA clone 14ETL--06-I01, mRNA sequence.
ACCESSION CF279992
VERSION 1
KEYWORDS EST.
SOURCE 1 GI:33657378
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 14 AAAAAAAAAAAAAA 1

RESULT 139
CF279992/c
LOCUS 1481 AAAAAAAAAAAAAA 1494 bp mRNA linear EST 14-AUG-2003
DEFINITION Oryza sativa cDNA clone 14ETL--06-I01, mRNA sequence.
ACCESSION CF279992
VERSION 1
KEYWORDS EST.
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ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for RT-PCR."

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DB 14 AAAAAAAAAAAAAA 1

RESULT 139
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DEFINITION Oryza sativa cDNA clone 14ETL--09-D24, mRNA sequence.
ACCESSION CF281958
VERSION CF281958.1 GI:33659345
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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DB 14 AAAAAAAAAAAAAA 1

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LOCUS 14ETL--09-N05.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.
ACCESSION CF282350
VERSION CF282350.1 GI:33659737
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Euphorbiaceae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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DB 14 AAAAAAAAAAAAAA 1

RESULT 141
CF294449/c

LOCUS 14 bp mRNA linear EST 14-AUG-2003
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ACCESSION CF294449
VERSION CF294449.1 GI:33663482
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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QY 1481 AAAAAAAAAAAAAA 1494
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Db 14 AAAAAAAAAAAAAA 1

RESULT 142
CF295570/c 14 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION sativa cDNA clone 30DGS--05-J06, mRNA sequence.

ACCESSION CF295570
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

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/organism="Oryza sativa"
/mol_type="mRNA"
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RT-PCR."

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 143
CF296120/c 14 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION sativa cDNA clone 30DGS--06-F17, mRNA sequence.

ACCESSION CF296120
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Db 14 AAAAAAAAAAAAAA 1

RESULT 144
CF297969/c

LOCUS
DEFINITION sativa cDNA clone 7LEAF--01-C16, mRNA sequence.

ACCESSION CF297969
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 145
CF298109/c
LOCUS      14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-F19, mRNA sequence.
ACCESSION  CF298109
VERSION     CF298109.1 GI:33669870
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
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            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
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            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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        RT-PCR."

REFERENCE  1 (bases 1 to 14)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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Db 14 AAAAAAAAAAAAAA 1

RESULT 146
CF299368/c
LOCUS      14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-F21, mRNA sequence.
ACCESSION  CF299368
VERSION     CF299368.1 GI:33671129
KEYWORDS   EST.

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Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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Db 14 AAAAAAAAAAAAAA 1

RESULT 147
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DEFINITION 7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION  CF300542
VERSION     CF300542.1 GI:33672303
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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Db 14 AAAAAAAAAAAAAA 1

RESULT 151
CF302675/c
LOCUS      14 bp mRNA linear EST 15-AUG-2003
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sativa cDNA clone 7LEAF--08-G18, mRNA sequence.
ACCESSION  CF302675
VERSION     CF302675.1 GI:33674436
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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Db 14 AAAAAAAAAAAAAA 1

RESULT 152
CF302846/c
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DEFINITION 7LEAF--08-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-M05, mRNA sequence.
ACCESSION  CF302846

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VERSION      CF302846.1 GI:33674607
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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RT-PCR."

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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RESULT 153
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LOCUS      14 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-K10, mRNA sequence.
ACCESSION  CF308006
VERSION     CF308006.1 GI:33679767
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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then used for PCR. mRNA was prepared from ABA-responsive
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line."
Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 154
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LOCUS
DEFINITION
ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.
ACCESSION
CF308220
VERSION
CF308220.1 GI:33679981
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
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line."
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QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 154
CF308220/c
LOCUS
DEFINITION
ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.
ACCESSION
CF308220
VERSION
CF308220.1 GI:33679981
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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element binding transcription factor 3 overexpression
line."

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Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
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QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

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RESULT 155
CF308445/c
LOCUS
DEFINITION
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library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.
ACCESSION
CF308445
VERSION
CF308445.1 GI:33680206
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
CONTACT: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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/organism="Oryza sativa"
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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cDNA library (ABF)"
/notes=Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

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RESULT 156
CF308918/c
LOCUS
DEFINITION
ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--02-O16, mRNA sequence.
ACCESSION
CF308918
VERSION
CF308918.1 GI:33680679
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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FEATURES
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line."
Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

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FEATURES

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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 157

CF310714/c

LOCUS

DEFINITION ABF--05-111.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--05-111, mRNA sequence.

ACCESSION CF310714

VERSION CF310714.1

GI:33682475

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

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FEATURES

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/organism="Oryza sativa"
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element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 159

CF311813/c

LOCUS

DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.

ACCESSION CF311813

VERSION CF311813.1

GI:33683574

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 158

CF311201/c

LOCUS

DEFINITION ABF--06-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-F09, mRNA sequence.

ACCESSION CF311201

VERSION CF311201.1

GI:33682962

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 159

CF311813/c

LOCUS

DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.

ACCESSION CF311813

VERSION CF311813.1

GI:33683574

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Contact: Nahm B.H.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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/organism="Oryza sativa"
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cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

source

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Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 160

CF318323/c
LOCUS HD--08-G13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-G13, mRNA sequence.
DEFINITION
ACCESSION CF318323
VERSION
KEYWORDS EST.
SOURCE
ORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

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Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 161

CF318450/c
LOCUS HD--08-J08.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-J08, mRNA sequence.
DEFINITION
ACCESSION CF318450
VERSION
KEYWORDS EST.
SOURCE
ORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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Best Local Similarity 100.0%; Pred. No. 81;
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Db 14 AAAAAAAAAAAAAA 1

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
 Db 14 AAAAAAAAAAAAAA 1

RESULT 165
 CF327119/c
 LOCUS
 DEFINITION NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--01-H14, mRNA sequence.

ACCESSION CF327119
 VERSION CF327119.1 GI:33802493
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 14)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
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 Tel: 82 31 330 6193
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FEATURES
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QY 1481 AAAAAAAAAAAAAA 1494
 Db 14 AAAAAAAAAAAAAA 1

RESULT 166
 CF327445/c
 LOCUS
 DEFINITION NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--01-O24, mRNA sequence.

ACCESSION CF327445
 VERSION CF327445.1 GI:33803149
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 14)
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 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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FEATURES
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QY 1481 AAAAAAAAAAAAAA 1494
 Db 14 AAAAAAAAAAAAAA 1

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FEATURES
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
 Db 14 AAAAAAAAAAAAAA 1

RESULT 167
 CF328490/c
 LOCUS
 DEFINITION NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--03-G21, mRNA sequence.

ACCESSION CF328490
 VERSION CF328490.1 GI:33805226
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 14)
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 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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FEATURES
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 /organism="Oryza sativa"
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 14;
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QY 1481 AAAAAAAAAAAAAA 1494
 Db 14 AAAAAAAAAAAAAA 1


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Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 168
CF328540/C
LOCUS CF328540 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-H24, mRNA sequence.
ACCESSION CF328540
VERSION CF328540.1 GI:33805324
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 170
CF328994/C
LOCUS CF328994 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-C11, mRNA sequence.
ACCESSION CF328994
VERSION CF328994.1 GI:33806228
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 169
CF328669/C
LOCUS CF328669 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-K23, mRNA sequence.
ACCESSION CF328669
VERSION CF328669.1 GI:33805587
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

```

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Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 170
CF328994/C
LOCUS CF328994 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-C11, mRNA sequence.
ACCESSION CF328994
VERSION CF328994.1 GI:33806228
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 171
CF329217/c
LOCUS      14 bp mRNA linear EST 18-AUG-2003
DEFINITION sativa cDNA clone NACL--04-H10, mRNA sequence.
ACCESSION  CF329217.1 GI:33806672
VERSION     EST.
KEYWORDS    Oryza sativa
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/clone="NACL--05-111"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 14

RESULT 173
CF330784/c
LOCUS      14 bp mRNA linear EST 18-AUG-2003
DEFINITION sativa cDNA clone NACL--06-K10, mRNA sequence.
ACCESSION  CF330784
VERSION     EST.
KEYWORDS    Oryza sativa
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 172
CF329990
LOCUS      14 bp mRNA linear EST 18-AUG-2003
DEFINITION sativa cDNA clone NACL--05-111, mRNA sequence.
ACCESSION  CF329990
VERSION     EST.
KEYWORDS    Oryza sativa
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
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 Db 14 AAAAAAAAAAAAAA 1

RESULT 174
 CF3311272/c
 LOCUS NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza EST 18-AUG-2003
 DEFINITION sativa cDNA clone NACL--07-F09, mRNA sequence.
 ACCESSION CF331272
 VERSION CF331272.1 GI:33810755
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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 with oligoribonucleotides and then used as templates for
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 Best Local Similarity 100.0%; Pred. No. 81;
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QY 1481 AAAAAAAAAAAAAA 1494
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 Db 14 AAAAAAAAAAAAAA 1

RESULT 175
 CF331861/c
 LOCUS NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza EST 18-AUG-2003
 DEFINITION sativa cDNA clone NACL--08-C10, mRNA sequence.
 ACCESSION CF331861
 VERSION CF331861.1 GI:33811945
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
 |||||
 Db 14 AAAAAAAAAAAAAA 1

RESULT 176
 CF333214/c
 LOCUS JMT--02-A10.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
 DEFINITION
 ACCESSION CF333214
 VERSION CF333214.1 GI:33814707
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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 /note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA"


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/lab host="E.coli DH10B"
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/notes="vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match          0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 180
CF334281/c
LOCUS
DEFINITION
JMT--03-105.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--03-105, mRNA sequence.
ACCESSION
CF334281
VERSION
CF334281.1 GI:33816894
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/lab host="E.coli DH10B"
/clone lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match          0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 181
CF334290/c
LOCUS
DEFINITION
JMT--03-111.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--03-111, mRNA sequence.
ACCESSION
CF334290
VERSION
CF334290.1 GI:33816914
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-111"
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/lab host="E.coli DH10B"
/clone lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match          0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 182
CF335781/c
LOCUS
DEFINITION
JMT--05-J13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--05-J13, mRNA sequence.
ACCESSION
CF335781
VERSION
CF335781.1 GI:33819936
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Fax: 82 31 321 6355

```

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .14
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--05-J13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 183

CF336094/c

LOCUS

DEFINITION 14 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa cDNA clone JMT--06-A10, mRNA sequence.

CF336094

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

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of Bioscience and Bioinformatics, Myongji University

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Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .14
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 184

CF336106/c

LOCUS

DEFINITION 14 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa cDNA clone JMT--06-A17, mRNA sequence.

CF336106

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .14
Location/Qualifiers
/organism="Oryza sativa"
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/tissue_type="leaf"
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Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 185

CF336287/c

LOCUS

DEFINITION 14 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa cDNA clone JMT--06-E15, mRNA sequence.

CF336287

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

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JOURNAL COMMENT
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Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 186
CF336906/c
LOCUS
DEFINITION
JMT--07-C05.b1 AtJMT-overexpressing transgenic rice plasmid
library (JMT) Oryza sativa cDNA clone JMT--07-C05, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
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cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 187
CF296652/c
LOCUS
DEFINITION
30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--07-C02, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa"
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/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
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RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 188
CF329379/c
LOCUS
DEFINITION
NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-K23, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 187
CF296652/c
LOCUS
DEFINITION
30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--07-C02, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="30DGS--07-C02"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 188
CF329379/c
LOCUS
DEFINITION
NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-K23, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
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RT-PCR."
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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAAAAAAAAA 1494
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DB 15 AAAAAAAAAAAAAA 2
RESULT 189
CF291803
LOCUS
DEFINITION
14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION
CF291803
VERSION
CF291803.1 GI:33660836
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
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COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"

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RT-PCR."
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1481 AAAAAAAAAAAAAA 1494
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DB 3 AAAAAAAAAAAAAA 16
RESULT 190
CF312586/c
LOCUS
DEFINITION
ABF--08-G13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-G13, mRNA sequence.
ACCESSION
CF312586
VERSION
CF312586.1 GI:33684347
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
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JOURNAL
Unpublished (2003)
COMMENT
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Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1480 TAAAAAAAAAAAAA 1493
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DB 14 TAAAAAAAAAAAAA 1
RESULT 191
CF290849
LOCUS
DEFINITION
14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION
CF290849
VERSION
CF290849.1 GI:33659882
KEYWORDS
EST.

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1..16
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SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 193
CF291030
LOCUS
DEFINITION
15 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION
CF291030.1 GI:33660063
VERSION
EST.
KEYWORDS
Oryza sativa
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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1..15
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/clone="14ROOT--01-E19"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 192
CF291030
LOCUS
DEFINITION
15 bp mRNA linear EST 14-AUG-2003
sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION
CF291030.1 GI:33660063
VERSION
EST.
KEYWORDS
Oryza sativa
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
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JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 AAAAAAAAAAAAAA 15

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BQ583549
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BQ583549
CDNA clone 024-005-C14-SP6 MP12-ADIS-024-inflorescence Beta vulgaris
ACCESSION
BQ583549
VERSION
BQ583549.1 GI:26113126

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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 193
CF301470
LOCUS
DEFINITION
15 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--06-F15, mRNA sequence.
ACCESSION
CF301470
VERSION
EST.
KEYWORDS
Oryza sativa
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAACA 1

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LOCUS
DEFINITION
13 bp mRNA linear EST 06-DEC-2002
BQ583549
CDNA clone 024-005-C14-SP6 MP12-ADIS-024-inflorescence Beta vulgaris
ACCESSION
BQ583549
VERSION
BQ583549.1 GI:26113126

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KEYWORDS
SOURCE      Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.

TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@piz-koeln.mpg.de
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            /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
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Db       1 AAAAAAAAAAAAAA 13

RESULT 195
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LOCUS      S014009-024-015-122-T7 MPZ-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-015-122 3-PRIME, mRNA sequence.
ACCESSION  BQ589180
VERSION     BQ589180.1 GI:26118763
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.

TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851

KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.

TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851

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Email: weishaa@piz-koeln.mpg.de
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 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Db 1 AAAAAAAAAAAAAA 13

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CF278426/c
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 DEFINITION 14ETL--04-F09.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa cDNA clone 14ETL--04-F09, mRNA sequence.

ACCESSION CF278426

VERSION CF278426.1 GI:33655812

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 198

CF280420/c

LOCUS

DEFINITION 14ETL--07-B11.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

Oryza sativa cDNA clone 14ETL--07-B11, mRNA sequence.

ACCESSION CF280420

VERSION CF280420.1 GI:33657806

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Db 13 AAAAAAAAAAAAAA 1

RESULT 199

CF280707/c

LOCUS

DEFINITION 14ETL--07-H19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

Oryza sativa cDNA clone 14ETL--07-H19, mRNA sequence.

ACCESSION CF280707

VERSION CF280707.1 GI:33658093

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

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13 AAAAAAAAAAAAAA 1

RESULT 200

CF280757/c

LOCUS

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Oryza sativa cDNA clone 14ETL--07-121, mRNA sequence.

CF280757

CF280757.1 GI:33658143

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

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13 AAAAAAAAAAAAAA 1

RESULT 201

CF282369/c

LOCUS

DEFINITION

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Oryza sativa cDNA clone 14ETL--09-N16, mRNA sequence.

CF282369

CF282369.1 GI:33659756

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

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13 AAAAAAAAAAAAAA 1

RESULT 202

CF290970/c

LOCUS

DEFINITION

14ROOT--01-D13.b1 Rice root plasmid cDNA library (14ROOT) Oryza

sativa cDNA clone 14ROOT--01-D13, mRNA sequence.

CF290970

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VERSION      CF290970.1  GI:33660003
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      13 AAAAAAAAAAAAAA 1

RESULT 203
CF290971
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DEFINITION 14ROOT--01-D13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
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ACCESSION  CF290971.1 GI:33660004
VERSION     CF290971
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      13 AAAAAAAAAAAAAA 1

RESULT 204
CF291011/c
LOCUS      13 bp mRNA linear EST 14-AUG-2003
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ACCESSION  CF291011.1 GI:33660044
VERSION     CF291011
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES     source
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                /db_xref="taxon:4530"
                /tissue_type="root"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."
Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 205
CF291060/c
LOCUS      13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza
              sativa cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION  CF291060.1 GI:33660044
VERSION     CF291060
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES     source
              1..13
                Location/Qualifiers
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /tissue_type="root"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."
Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 206
CF291060/c
LOCUS      13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza
              sativa cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION  CF291060.1 GI:33660044
VERSION     CF291060
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES     source
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                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /tissue_type="root"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."
Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

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ACCESSION   CF291060
VERSION     CF291060.1  GI:33660093
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa

REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-F11"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 206
CF291061
LOCUS       CF291061
DEFINITION  14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION   CF291061
VERSION     CF291061.1  GI:33660094
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa

REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-F11"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 206
CF291061
LOCUS       CF291061
DEFINITION  14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION   CF291061
VERSION     CF291061.1  GI:33660094
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa

REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-F11"
/tissue_type="root"
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 207
CF291167/c
LOCUS       CF291167
DEFINITION  14ROOT--01-H20.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-H20, mRNA sequence.
ACCESSION   CF291167
VERSION     CF291167.1  GI:33660200
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa

REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:4530"
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                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 208
CF291214/c
LOCUS       CF291214
DEFINITION  14ROOT--01-I22.b1 Rice root plasmid cDNA library (14ROOT) Oryza

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LOCUS       CF291596               13 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION   14ROOT--02-B12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
VERSION      CF291596
ACCESSION   CF291596
SOURCE      CF291596.1 GI:33660629
            Oryza sativa
            Oryza sativa
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
            1..13
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="14ROOT--02-B12"
            /tissue_type="root"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice root plasmid cDNA library (14ROOT)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
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            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUERY MATCH
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 215
CF291597
LOCUS       CF291597               13 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION   14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
VERSION      CF291597
ACCESSION   CF291597
SOURCE      CF291597.1 GI:33660630
            Oryza sativa
            Oryza sativa
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="14ROOT--02-B12"
            /tissue_type="root"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice root plasmid cDNA library (14ROOT)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
            0.9%; Score 13; DB 1; Length 13;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 216
CF291726
LOCUS       CF291726               13 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION   14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
VERSION      CF291726
ACCESSION   CF291726
SOURCE      CF291726.1 GI:33660759
            Oryza sativa
            Oryza sativa
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
            1..13
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            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
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            /tissue_type="root"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice root plasmid cDNA library (14ROOT)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
            0.9%; Score 13; DB 1; Length 13;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 217
CF291726/c
LOCUS       CF291726/c             13 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION   14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
VERSION      CF291726/c
ACCESSION   CF291726/c
SOURCE      CF291726/c
            Oryza sativa
            Oryza sativa
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
            1..13
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            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="14ROOT--02-B12"
            /tissue_type="root"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice root plasmid cDNA library (14ROOT)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
            0.9%; Score 13; DB 1; Length 13;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

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RESULT 220
CF298736/c
LOCUS
DEFINITION 13 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--02-E22, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS 1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--02-E22"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 221
CF298764/c
LOCUS
DEFINITION 13 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--02-F20, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS 1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--02-F20"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 222
CF298795/c
LOCUS
DEFINITION 13 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--02-G14, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS 1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="7LEAF--02-G14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

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RESULT 223
CF298908/c
LOCUS       CF298908               13 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF298908
VERSION     CF298908.1 GI:33670669
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-K03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 224
CF299133/c
LOCUS       CF299133               13 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299133
VERSION     CF299133.1 GI:33670894
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-K03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 225
CF299359/c
LOCUS       CF299359               13 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299359
VERSION     CF299359.1 GI:33671120
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

```

Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

```

FEATURES             Location/Qualifiers
     source           1..13
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 225
CF299359/c
LOCUS       CF299359               13 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299359
VERSION     CF299359.1 GI:33671120
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

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RESULT 226
LOCUS CF299937/c 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--04-C12, mRNA sequence.
ACCESSION CF299937
VERSION CF299937.1 GI:33671698
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-C12"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/notes="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

RESULT 227
LOCUS CF300118/c 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-G10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--04-G10, mRNA sequence.
ACCESSION CF300118
VERSION CF300118.1 GI:33671879
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="7LEAF--04-G10"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/notes="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

RESULT 228
LOCUS CF300587/c 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-C01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-C01, mRNA sequence.
ACCESSION CF300587
VERSION CF300587.1 GI:33672348
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-C01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/notes="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

Db 13 AAAAAAAAAAAAAA 1
|||||

RESULT 232
CF301286/c
LOCUS
DEFINITION
7LEAF--06-B15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-B15, mRNA sequence.

ACCESSION
VERSION
CF301286.1 GI:33673047
KEYWORDS
SOURCE
EST.

Oryza sativa
Oryza sativa

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 13)

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source

1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--06-B15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 233
CF302158/c
LOCUS
DEFINITION
7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-G20, mRNA sequence.

ACCESSION
VERSION
CF302158.1 GI:33673919
KEYWORDS
SOURCE
EST.

Oryza sativa
Oryza sativa

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 13)

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source

1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-G20"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 234
CF302830/c

LOCUS
DEFINITION
7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-L16, mRNA sequence.

ACCESSION
VERSION
CF302830.1 GI:33674591
KEYWORDS
SOURCE
EST.

Oryza sativa
Oryza sativa

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 13)

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

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COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source

1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--08-L16"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1481 AAAAAAAAAAAAAA 1493
      |||||||
Db      13 AAAAAAAAAAAAAA 1

RESULT 235
CF302898/c
LOCUS   7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION
sativa cDNA clone 7LEAF--08-N08, mRNA sequence.
ACCESSION
VERSION CF302898.1 GI:33674659
KEYWORDS
SOURCE   Oryza sativa
ORGANISM Oryza sativa
          13 bp mRNA linear EST 15-AUG-2003
          7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
          sativa cDNA clone 7LEAF--08-N08, mRNA sequence.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
JOURNAL
COMMENT  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
      source
      Location/Qualifiers
          1..13
          /organism="Oryza sativa"
          /mol_type="mRNA"
          /cultivar="Nackdong"
          /db_xref="taxon:4530"
          /clone="7LEAF--08-N08"
          /tissue_type="leaf"
          /dev_stage="7 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="ABF3-overexpressing transgenic rice plasmid
          cDNA library (ABF)"
          /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
      |||||||
Db      13 AAAAAAAAAAAAAA 1

RESULT 237
CF310517
LOCUS   ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION
VERSION CF310517.1 GI:33682278
KEYWORDS
SOURCE   Oryza sativa
ORGANISM Oryza sativa
          13 bp mRNA linear EST 15-AUG-2003
          ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
          library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
JOURNAL
COMMENT  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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      Location/Qualifiers
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          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="ABF3-overexpressing transgenic rice plasmid
          cDNA library (ABF)"
          /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
          for 2hrs. Oligo-capped mRNA was reverse transcribed and
          then used for PCR. mRNA was prepared from ABA-responsive
          element binding transcription factor 3 overexpression
          line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
      |||||||
Db      13 AAAAAAAAAAAAAA 1

RESULT 237
CF310517
LOCUS   ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION
VERSION CF310517.1 GI:33682278
KEYWORDS
SOURCE   Oryza sativa
ORGANISM Oryza sativa
          13 bp mRNA linear EST 15-AUG-2003
          ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
          library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
JOURNAL
COMMENT  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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          /clone_lib="ABF3-overexpressing transgenic rice plasmid
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          /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
          for 2hrs. Oligo-capped mRNA was reverse transcribed and
          then used for PCR. mRNA was prepared from ABA-responsive
          element binding transcription factor 3 overexpression
          line."

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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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          /lab_host="E.coli DH10B"
          /clone_lib="ABF3-overexpressing transgenic rice plasmid
          cDNA library (ABF)"
          /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
          for 2hrs. Oligo-capped mRNA was reverse transcribed and
          then used for PCR. mRNA was prepared from ABA-responsive
          element binding transcription factor 3 overexpression
          line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
      |||||||
Db      13 AAAAAAAAAAAAAA 1

RESULT 237
CF310517
LOCUS   ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION
VERSION CF310517.1 GI:33682278
KEYWORDS
SOURCE   Oryza sativa
ORGANISM Oryza sativa
          13 bp mRNA linear EST 15-AUG-2003
          ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
          library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
JOURNAL
COMMENT  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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          cDNA library (ABF)"
          /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
          for 2hrs. Oligo-capped mRNA was reverse transcribed and
          then used for PCR. mRNA was prepared from ABA-responsive
          element binding transcription factor 3 overexpression
          line."

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element binding transcription factor 3 overexpression
line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1481 AAAAAAAAAAAAAA 1493
Db  1 AAAAAAAAAAAAAA 13

RESULT 238
CF312721/c
LOCUS      13 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-J13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--08-J13, mRNA sequence.
ACCESSION  CF312721
VERSION     CF312721.1 GI:33684482
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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     /clone_lib="ABF3-overexpressing transgenic rice plasmid
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     element binding transcription factor 3 overexpression
     line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1481 AAAAAAAAAAAAAA 1493
Db  13 AAAAAAAAAAAAAA 1

RESULT 239
CF313171/c
LOCUS      13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--01-D10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.
ACCESSION  CF313171
VERSION     CF313171.1 GI:33684932
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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     element binding transcription factor 3 overexpression
     line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1481 AAAAAAAAAAAAAA 1493
Db  13 AAAAAAAAAAAAAA 1

RESULT 240
CF314239/c
LOCUS      13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-L01.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--02-L01, mRNA sequence.
ACCESSION  CF314239
VERSION     CF314239.1 GI:33686000
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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     reverse transcribed and then used for PCR. mRNA was
     derived from rice Histone Deacetylase overexpression
     line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1481 AAAAAAAAAAAAAA 1493
Db  13 AAAAAAAAAAAAAA 1

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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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     line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1481 AAAAAAAAAAAAAA 1493
Db  13 AAAAAAAAAAAAAA 1

RESULT 240
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LOCUS      13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-L01.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--02-L01, mRNA sequence.
ACCESSION  CF314239
VERSION     CF314239.1 GI:33686000
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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     /lab_host="E.coli DH10B"
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     /note="vector: PCR4-TOPO; Site_1: EcoRI; Callus was
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     line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1481 AAAAAAAAAAAAAA 1493
Db  13 AAAAAAAAAAAAAA 1

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cDNA library (HD)"
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
| | | | | | | | | |
Db 13 AAAAAAAAAAAAAA 1

RESULT 241
CF314874/c
LOCUS
DEFINITION
HD--03-J07.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--03-J07, mRNA sequence.
ACCESSION
CF314874
VERSION
CF314874.1 GI:33686635
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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/mol_type="mRNA"
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cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
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Db 13 AAAAAAAAAAAAAA 1

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FEATURES
Location/Qualifiers
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/lab_host="E.coli DH10B"
/clone lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
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Db 13 AAAAAAAAAAAAAA 1

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RESULT 242
CF315395/c
LOCUS
DEFINITION
HD--04-E20.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--04-E20, mRNA sequence.
ACCESSION
CF315395
VERSION
CF315395.1 GI:33687156
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
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Db 13 AAAAAAAAAAAAAA 1

RESULT 243
CF316439/c
LOCUS
DEFINITION
HD--05-l17.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--05-l17, mRNA sequence.
ACCESSION
CF316439
VERSION
CF316439.1 GI:33688200
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

1. .13
Location/Qualifiers

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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD-05-L17"
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cDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 244

CF316440

LOCUS HD--05-L17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--05-L17, mRNA sequence.

ACCESSION CF316440

VERSION 1

KEYWORDS Unpublished (2003)

SOURCE Contact: Nahm B.H.

ORGANISM

Oryza sativa
Oryza sativa
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

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Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

1. .13
Location/Qualifiers

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD-05-L17"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 1 AAAAAAAAAAAAAA 13

RESULT 245

CF316637/c

LOCUS HD--06-A04.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--06-A04, mRNA sequence.

ACCESSION CF316637

VERSION 1

KEYWORDS Unpublished (2003)

SOURCE Contact: Nahm B.H.

ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

1. .13
Location/Qualifiers

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cDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 246

CF318290/c

LOCUS HD--08-F19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--08-F19, mRNA sequence.

ACCESSION CF318290

VERSION 1

KEYWORDS Unpublished (2003)

SOURCE Contact: Nahm B.H.

ORGANISM

Oryza sativa
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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/lab_host="E.coli DH10B"
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cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 247

CF319066/c

LOCUS HD--09-H02.b1 OSHDAc1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--09-H02, mRNA sequence.

ACCESSION CF319066

VERSION CF319066.1 GI:33690827

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 248

CF319531/c

LOCUS HD--10-B03.b1 OSHDAc1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.

ACCESSION CF319531

VERSION CF319531.1 GI:33691292

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .13

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone="HD--10-B03"

/tissue_type="callus"

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/lab_host="E.coli DH10B"

/clone_lib="OSHDAc1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

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RESULT 249
CF319532      13 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION HD--10-B03.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.
ACCESSION CF319532
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
location/Qualifiers
1..13
/organism="Oryza sativa"
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/lab_host="E.coli DH10B"
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cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 250
CF319919      13 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION HD--10-J17.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-J17, mRNA sequence.
ACCESSION CF319919
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
location/Qualifiers
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cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
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line."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 251
CF320017      13 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION HD--10-L20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.
ACCESSION CF320017
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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location/Qualifiers
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 251
CF320017      13 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION HD--10-L20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.
ACCESSION CF320017
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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location/Qualifiers
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derived from rice Histone Deacetylase overexpression
line."

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Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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QY 1481 AAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAA 1

RESULT 252
CF320018
LOCUS
DEFINITION HD--10-L20.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.
ACCESSION CF320018
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
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derived from rice Histone Deacetylase overexpression
line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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QY 1481 AAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAA 1

RESULT 254
CF320938/c
LOCUS
DEFINITION HD--12-A06.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--12-A06, mRNA sequence.
ACCESSION CF320938
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAA 1

RESULT 253
CF320143/c
LOCUS
DEFINITION HD--10-O13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-O13, mRNA sequence.
ACCESSION CF320143
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAA 1

RESULT 254
CF320938/c
LOCUS
DEFINITION HD--12-A06.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--12-A06, mRNA sequence.
ACCESSION CF320938
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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cDNA library (HD)"
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derived from rice Histone Deacetylase overexpression
line."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAA 1

RESULT 253
CF320143/c
LOCUS
DEFINITION HD--10-O13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-O13, mRNA sequence.
ACCESSION CF320143
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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 /notes="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
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 line."

Query Match 0.9%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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Qy 1481 AAAAAAAAAAAAAA 1493
 Db 13 AAAAAAAAAAAAAA 1

RESULT 255
 CF326844/c
 LOCUS
 DEFINITION NACL--01-B12.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--01-B12, mRNA sequence.

ACCESSION
 VERSION CF326844.1 GI:33801943
 KEYWORDS
 SOURCE EST.

ORGANISM
 Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
 Db 13 AAAAAAAAAAAAAA 1

RESULT 256
 CF327070/c
 LOCUS
 DEFINITION NACL--01-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--01-G09, mRNA sequence.
 CF327070
 VERSION
 KEYWORDS CF327070.1 GI:33802396
 SOURCE EST.

ORGANISM
 Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 with oligoribonucleotides and then used as templates for
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
 Db 13 AAAAAAAAAAAAAA 1

RESULT 257
 CF327339/c

LOCUS
 DEFINITION NACL--01-M15.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--01-M15, mRNA sequence.

ACCESSION
 VERSION CF327339.1 GI:33802936
 KEYWORDS
 SOURCE EST.

ORGANISM
 Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

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 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .13
 /organism="Oryza sativa"


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FEATURES
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Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1481 AAAAAAAAAAAAAA 1493
Db  1 AAAAAAAAAAAAAA 13

RESULT 267
CF329417/c
LOCUS
DEFINITION
  NACL--04-L19, b1 Rice callus plasmid cDNA library (NACL) Oryza
  sativa cDNA clone NACL--04-L19, mRNA sequence.
ACCESSION
  CF329417
VERSION
  CF329417.1 GI:33807072
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzeae; Oryza.
  1 (bases 1 to 13)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1481 AAAAAAAAAAAAAA 1493
Db  1 AAAAAAAAAAAAAA 13

RESULT 269
CF329729/c
LOCUS
DEFINITION
  NACL--05-C14, g1 Rice callus plasmid cDNA library (NACL) Oryza
  sativa cDNA clone NACL--05-C14, mRNA sequence.
ACCESSION
  CF329729
VERSION
  CF329729.1 GI:33807674
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzeae; Oryza.
  1 (bases 1 to 13)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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      RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1481 AAAAAAAAAAAAAA 1493
Db  1 AAAAAAAAAAAAAA 13

RESULT 268
CF329460/c
LOCUS
DEFINITION
  NACL--04-M18, b1 Rice callus plasmid cDNA library (NACL) Oryza
  sativa cDNA clone NACL--04-M18, mRNA sequence.
ACCESSION
  CF329460
VERSION
  CF329460.1 GI:33807156
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzeae; Oryza.
  1 (bases 1 to 13)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1481 AAAAAAAAAAAAAA 1493
Db  1 AAAAAAAAAAAAAA 13

RESULT 269
CF329729/c
LOCUS
DEFINITION
  NACL--05-C14, g1 Rice callus plasmid cDNA library (NACL) Oryza
  sativa cDNA clone NACL--05-C14, mRNA sequence.
ACCESSION
  CF329729
VERSION
  CF329729.1 GI:33807674
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzeae; Oryza.
  1 (bases 1 to 13)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Query Match      0.9%; Score 13; DB 1; Length 13;
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Oy  1481 AAAAAAAAAAAAAA 1493
Db  1 AAAAAAAAAAAAAA 13

```

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 270
CF329800/c
LOCUS
DEFINITION
NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-E04, mRNA sequence.

ACCESSION
CF329800
VERSION
CF329800.1 GI:33807817
KEYWORDS
EST.

SOURCE
Oryza sativa

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 13)

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
Unpublished (2003)

COMMENT
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Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
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Db 13 AAAAAAAAAAAAAA 1

RESULT 271

CF329801

LOCUS

DEFINITION

NACL--05-E04.g1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--05-E04, mRNA sequence.

ACCESSION

CF329801

VERSION

CF329801.1 GI:33807819

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 13)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

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JOURNAL

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COMMENT

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Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

Location/Qualifiers

1. .13

/organism="Oryza sativa"

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Query Match 0.9%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

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Db 1 AAAAAAAAAAAAAA 13

RESULT 272

CF329869/c

LOCUS

DEFINITION

NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--05-F18, mRNA sequence.

ACCESSION

CF329869

VERSION

CF329869.1 GI:33807959

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 13)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

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JOURNAL

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COMMENT

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FEATURES

source

1. .13
/organism="Oryza sativa"
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/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 273

CF329946/c

LOCUS
DEFINITION NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-H12, mRNA sequence.

ACCESSION CF329946

VERSION CF329946.1 GI:33808114

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

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1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 274

CF329988/c

LOCUS
DEFINITION NACL--05-I10.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-I10, mRNA sequence.

ACCESSION CF329988

VERSION CF329988.1 GI:33808198

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

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/organism="Oryza sativa"
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 275

CF330023/c

LOCUS
DEFINITION NACL--05-J05.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-J05, mRNA sequence.

ACCESSION CF330023

VERSION CF330023.1 GI:33808268

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAA 1493
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 DB 13 AAAAAAAAAAAAA 1

RESULT 276

CF330725
 LOCUS
 DEFINITION
 NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-J01, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
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 Tel: 82 31 330 6193
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 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAA 1493
 |||||

Db 1 AAAAAAAAAAAAA 13
 RESULT 277
 CF331041/c
 LOCUS
 DEFINITION
 NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--07-A04, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
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 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
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 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAA 1493
 |||||
 DB 13 AAAAAAAAAAAAA 1

RESULT 278

CF331266/c
 LOCUS
 DEFINITION
 NACL--07-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--07-F06, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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    /mol_type="mRNA"
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    with oligoribonucleotides and then used as templates for
    RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1481 AAAAAAAAAAAAAA 1493

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Db 13 AAAAAAAAAAAAAA 1

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RESULT 279
LOCUS CF331273
DEFINITION NACL--07-F09.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION CF331273
VERSION CF331273.1 GI:33810757
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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    /notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1481 AAAAAAAAAAAAAA 1493

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Db 1 AAAAAAAAAAAAAA 13

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RESULT 280
LOCUS CF331903/c
DEFINITION NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-D07, mRNA sequence.
ACCESSION CF331903
VERSION CF331903.1 GI:33812027
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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    RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1481 AAAAAAAAAAAAAA 1493

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Db 13 AAAAAAAAAAAAAA 1

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RESULT 281
LOCUS CF332079/c
DEFINITION NACL--08-H04.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-H04, mRNA sequence.
ACCESSION CF332079
VERSION CF332079.1 GI:33812379
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
Location/Qualifiers

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1. .13
/organism="Oryza sativa"
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/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 282

CF332695/c
LOCUS
DEFINITION
JMT--01-E21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.

CF332695

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source
1. .13
/organism="Oryza sativa"
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/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 283

CF332696
LOCUS
DEFINITION
JMT--01-E21.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.

CF332696

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

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1. .13
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
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Db 1 AAAAAAAAAAAAAA 13

RESULT 284

CF333486/c
LOCUS
DEFINITION
JMT--02-G11.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-G11, mRNA sequence.

CF333486

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
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 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

TITLE
JOURNAL
COMMENT

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 cDNA library (JMT)"
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 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

RESULT 286
CF333973
LOCUS
DEFINITION 13 bp mRNA linear EST 18-AUG-2003
 JMT--03-B12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.
ACCESSION
VERSION CF333973.1 GI:33816251
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 /cultivar="Nackdong"
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 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
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Db 13 AAAAAAAAAAAAAA 1

RESULT 285
CF333972/c
LOCUS
DEFINITION 13 bp mRNA linear EST 18-AUG-2003
 JMT--03-B12.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.
ACCESSION
VERSION CF333972.1 GI:33816249
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 /cultivar="Nackdong"
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 /clone="JMT--03-B12"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"

RESULT 287
CF334347/c
LOCUS
DEFINITION 13 bp mRNA linear EST 18-AUG-2003
 JMT--03-J19.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--03-J19, mRNA sequence.
ACCESSION
VERSION CF334347.1 GI:33817022
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--03-B12"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
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 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
 |||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 287
CF334347/c
LOCUS
DEFINITION 13 bp mRNA linear EST 18-AUG-2003
 JMT--03-J19.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--03-J19, mRNA sequence.
ACCESSION
VERSION CF334347.1 GI:33817022
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 1. .13
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--03-B12"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"

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SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 289
CF337022/c
LOCUS
CF337022
DEFINITION
NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa CDNA clone NACL--01-J16, mRNA sequence.
ACCESSION
CF337022
VERSION
CF337022.1 GI:33802665
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 290
CF301021
LOCUS
CF301021
DEFINITION
NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa CDNA clone NACL--01-J16, mRNA sequence.
ACCESSION
CF301021
VERSION
CF301021.1 GI:33802665
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 289
CF337022/c
LOCUS
CF337022
DEFINITION
NACL--07-E22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa CDNA clone JMT--07-E22, mRNA sequence.
ACCESSION
CF337022
VERSION
CF337022.1 GI:33822426
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1. .13
/organism="Oryza sativa"
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methyltransferase overexpression line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 289
CF337022/c
LOCUS
CF337022
DEFINITION
NACL--07-E22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa CDNA clone JMT--07-E22, mRNA sequence.
ACCESSION
CF337022
VERSION
CF337022.1 GI:33822426
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 289
CF337022/c
LOCUS
CF337022
DEFINITION
NACL--07-E22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa CDNA clone JMT--07-E22, mRNA sequence.
ACCESSION
CF337022
VERSION
CF337022.1 GI:33822426
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 289
CF337022/c
LOCUS
CF337022
DEFINITION
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library (JMT) Oryza sativa CDNA clone JMT--07-E22, mRNA sequence.
ACCESSION
CF337022
VERSION
CF337022.1 GI:33822426
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing
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DEFINITION 7LEAF--05-L10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-L10, mRNA sequence.

ACCESSION CF301021
VERSION CF301021.1 GI:33672782
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

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/note="Vector: pCR4-TOPO; Site 1: EcorI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 12.4; DB 1; Length 14;
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 1 AAAAAAAAAAAAAA 14

RESULT 291

CF297251

LOCUS 30DGS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--07-P12, mRNA sequence.

DEFINITION

ACCESSION CF297251
VERSION CF297251.1 GI:33666284
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

1..17

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--07-P12"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcorI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGA 1102

Db 1 TTTTGTGTTTGTCTGA 17

RESULT 292

AL048754/c

LOCUS 18 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFP566L173.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFP566L173, mRNA sequence.

ACCESSION AL048754

VERSION AL048754.1 GI:4727825

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 18)

AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE ESR (Koehrer, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES source

1..18
/organism="Homo sapiens"
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/clone="DKFP566L173"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGA 1102

Db 17 TTTTGTGTTTGTCTGA 1

RESULT 293

CF291665

LOCUS 19 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-D01, mRNA sequence.

ACCESSION CF291665

VERSION CF291665.1 GI:33660698

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

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Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-D01"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12.2; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTGTTCTGA 1102
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Db 3 TTTTGTGTTTCTTGA 19

RESULT 294
BG668943
LOCUS
DEFINITION DRN03E05 Rat DRG Library Rattus norvegicus cDNA clone DRN03E05 5',
mRNA sequence.
ACCESSION BG668943
VERSION BG668943.1 GI:13890865
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 12)
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,P.X., Bao,L., Lu,Y.J., Guo,C.,
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
TITLE Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axotomy model of neuropathic pain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
MEDLINE 22056133
PUBMED 12060780
COMMENT Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguog (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T3

BACKWARD: T7
Seq primer: T3
POLYA=No.

FEATURES

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Location/Qualifiers
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/db_xref="taxon:10116"
/clone="DRN03E05"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
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Db 1 AAAAAAAAAA 12

RESULT 295
BG582536/c
LOCUS
DEFINITION

BQ582536 12 bp mRNA linear EST 06-DEC-2002
S013300-024-007-P01-T7 MP12-ADIS-024-inflorescence Beta vulgaris
cDNA clone 024-007-P01 3-PRIME, mRNA sequence.

ACCESSION BQ582536
VERSION BQ582536.1 GI:26112113
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,K., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B

ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weishaar@piz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCCTACTATAGGC.

FEATURES

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/db_xref="taxon:161934"
/clone="024-007-P01"
/tissue_type="inflorescence"
/lab_host="EMDH108"
/clone_lib="MP12-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

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Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary Database: http://gabi.rzpd.de"

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
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QY 1481 AAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAA 1

RESULT 296
LOCUS BQ594698/c
DEFINITION S013713-024-014-P24-T7 MP12-ADIS-024-storage root Beta vulgaris
ACCESSION BQ594698
VERSION 1
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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Seq primer: T7; GTAATACGACTCCTACTATAGGC.
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/clone="024-014-P24"
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/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary Database: http://gabi.rzpd.de"

Query Match      0.8%; Score 12; DB 1; Length 12;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 AAAAAAAAAAAAA 1

RESULT 297
LOCUS BQ594698/c
DEFINITION S012404-024-024-E05-T7 MP12-ADIS-024-developing root Beta vulgaris
ACCESSION BQ594698
VERSION 1
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCCTACTATAGGC.
FEATURES
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/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary Database: http://gabi.rzpd.de"

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAA 1

RESULT 298
LOCUS CF279278/c
DEFINITION 14ETU--05-110.bl Rice etiolated leaf plasmid cDNA library (14ETL)
ACCESSION CF279278
Oryza sativa cDNA clone 14ETL--05-110, mRNA sequence.

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CF279278.1  GI:33656664
EST.
SOURCE
ORGANISM
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .12
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Db 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS
DEFINITION
14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION
CF291428
VERSION
CF291428.1 GI:33660461
KEYWORDS
EST.
SOURCE
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Db 12 AAAAAAAAAA 1

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LOCUS
DEFINITION
14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION
CF291428
VERSION
CF291428.1 GI:33660461
KEYWORDS
EST.
SOURCE
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Oryza sativa"
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Db 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS
DEFINITION
14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION
CF291428
VERSION
CF291428.1 GI:33660461
KEYWORDS
EST.
SOURCE
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .12
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
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QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

RESULT 299
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LOCUS
DEFINITION
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ACCESSION
CF291428
VERSION
CF291428.1 GI:33660461
KEYWORDS
EST.
SOURCE
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .12
/organism="Oryza sativa"
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/clone_lib="Rice etiolated leaf plasmid cDNA library
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Db 12 AAAAAAAAAA 1

RESULT 299
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LOCUS
DEFINITION
14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION
CF291428
VERSION
CF291428.1 GI:33660461
KEYWORDS
EST.
SOURCE
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
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/dev stage="14 days after germination"
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(14ETL)"
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QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS
DEFINITION
14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION
CF291428
VERSION
CF291428.1 GI:33660461
KEYWORDS
EST.
SOURCE
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Oryza sativa"
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Query Match
Best Local
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DEFINITION 14ROOT--02-M21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
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VERSION CF292107
SOURCE CF292107.1 GI:33661140
KEYWORDS EST.
ORGANISM Oryza sativa
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          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
          1..12
          /organism="Oryza sativa"
          /mol_type="mRNA"
          /cultivar="Nackdong"
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          /tissue_type="root"
          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice root plasmid cDNA library (14ROOT)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

RESULT 305
CF295593/c
LOCUS 30DGS--05-J18.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION sativa cDNA clone 30DGS--05-J18, mRNA sequence.
ACCESSION CF295593
VERSION CF295593.1 GI:33664626
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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          /cultivar="Nackdong"
          /db_xref="taxon:4530"
          /clone="14ROOT--02-M21"
          /tissue_type="root"
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          /lab_host="E.coli DH10B"
          /clone_lib="Rice root plasmid cDNA library (14ROOT)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

RESULT 305
CF295593/c
LOCUS 30DGS--05-J18.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION sativa cDNA clone 30DGS--05-J18, mRNA sequence.
ACCESSION CF295593
VERSION CF295593.1 GI:33664626
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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          /db_xref="taxon:4530"
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          /tissue_type="root"
          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice root plasmid cDNA library (14ROOT)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--05-J18"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

RESULT 306
CF298686/c
LOCUS 7LEAF--02-D15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--02-D15, mRNA sequence.
ACCESSION CF298686
VERSION CF298686.1 GI:33670447
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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          /mol_type="mRNA"
          /cultivar="Nackdong"
          /db_xref="taxon:4530"
          /clone="7LEAF--02-D15"
          /tissue_type="leaf"
          /dev_stage="7 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

RESULT 307
CF298672/c

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LOCUS       CF298872               12 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--02-117.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF298872
VERSION     CF298872.1 GI:33670633
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
            1..12
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            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="7LEAF--02-117"
            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAA 1492
Db  12 AAAAAAAAAAAAA 1

RESULT 308
CF299343
LOCUS       CF299343               12 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--03-F06.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299343
VERSION     CF299343.1 GI:33671104
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
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            /mol_type="mRNA"
            /cultivar="Nackdong"
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            /clone="7LEAF--03-F06"
            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAA 1492
Db  12 AAAAAAAAAAAAA 1

RESULT 308
CF299343
LOCUS       CF299343               12 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--03-F06.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299343
VERSION     CF299343.1 GI:33671104
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
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            /organism="Oryza sativa"
            /mol_type="mRNA"
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            /tissue_type="leaf"
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            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAA 1492
Db  12 AAAAAAAAAAAAA 1

RESULT 310
CF299514
LOCUS       CF299514               12 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--03-J03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299514
VERSION     CF299514.1 GI:33671275
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
            1..12
            /organism="Oryza sativa"
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            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="7LEAF--03-J03"
            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAA 1492
Db  12 AAAAAAAAAAAAA 1

RESULT 310

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source
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAA 1492
Db  12 AAAAAAAAAAAAA 12

RESULT 309
CF299514/c
LOCUS       CF299514               12 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--03-J03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299514
VERSION     CF299514.1 GI:33671275
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
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            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAA 1492
Db  12 AAAAAAAAAAAAA 1

RESULT 310

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CF300272/c
LOCUS       CF300272                12 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--04-J19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--04-J19, mRNA sequence.
ACCESSION   CF300272
VERSION     CF300272.1   GI:33672033
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-J19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
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                     Oryza sativa
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
     REFERENCE       1 (bases 1 to 12)
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                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
     AUTHORS          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
     TITLE            Large-scale Sequencing Analysis of Rice ESTs
     JOURNAL          Unpublished (2003)
     COMMENT          Contact: Nahm B.H.
                     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355
                     Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

CF300420/c
LOCUS       CF300420                12 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--04-M23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--04-M23, mRNA sequence.
ACCESSION   CF300420
VERSION     CF300420.1   GI:33672181
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

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FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-M23"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
     ORGANISM        Oryza sativa
                     Oryza sativa
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
     REFERENCE       1 (bases 1 to 12)
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
     AUTHORS          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
     TITLE            Large-scale Sequencing Analysis of Rice ESTs
     JOURNAL          Unpublished (2003)
     COMMENT          Contact: Nahm B.H.
                     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355
                     Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAA 1492
Db      12 AAAAAAAAAA 1

RESULT 312
CF300558/c
LOCUS       CF300558                12 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--05-B09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--05-B09, mRNA sequence.
ACCESSION   CF300558
VERSION     CF300558.1   GI:33672319
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 12)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-B09"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
     ORGANISM        Oryza sativa
                     Oryza sativa
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
     REFERENCE       1 (bases 1 to 12)
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
     AUTHORS          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
     TITLE            Large-scale Sequencing Analysis of Rice ESTs
     JOURNAL          Unpublished (2003)
     COMMENT          Contact: Nahm B.H.
                     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355
                     Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAA 1492
Db      12 AAAAAAAAAA 1

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RESULT 313
CF300881/c
LOCUS
DEFINITION 12 bp mRNA linear EST 15-AUG-2003
7LEAF--05-I10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-I10, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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1 (bases 1 to 12)
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
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/organism="Oryza sativa"
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/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAAA 1

RESULT 315
CF301075/c
LOCUS
DEFINITION 12 bp mRNA linear EST 15-AUG-2003
7LEAF--05-M15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M15, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..12
/organism="Oryza sativa"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAAA 1

RESULT 316
CF301006/c
LOCUS
DEFINITION 12 bp mRNA linear EST 15-AUG-2003
7LEAF--05-L02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-L02, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-L02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAAA 1

RESULT 317
CF301006/c
LOCUS
DEFINITION 12 bp mRNA linear EST 15-AUG-2003
7LEAF--05-L02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-L02, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..12
/organism="Oryza sativa"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAAA 1

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RESULT 316
CF301489/c
LOCUS       12 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION  7LEAF--06-G01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-G01, mRNA sequence.
ACCESSION   CF301489
VERSION     CF301489.1  GI:33673250
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAAA 1

RESULT 317
CF301940/c
LOCUS       12 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION  7LEAF--07-A01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-A01, mRNA sequence.
ACCESSION   CF301940
VERSION     CF301940.1  GI:33673701
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAAA 1

RESULT 318
CF302029/c
LOCUS       12 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION  7LEAF--07-C18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-C18, mRNA sequence.
ACCESSION   CF302029
VERSION     CF302029.1  GI:33673790
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
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                     with oligoribonucleotides and then used as templates for
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Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAAA 1

RESULT 319
CF302029/c
LOCUS       12 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION  7LEAF--07-C18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-C18, mRNA sequence.
ACCESSION   CF302029
VERSION     CF302029.1  GI:33673790
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAAA 1

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RESULT 319
CF302122/c
LOCUS
DEFINITION
12 bp mRNA linear EST 15-AUG-2003
7LEAF--07-F15.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-F15, mRNA sequence.

ACCESSION
CF302122
VERSION
CF302122.1 GI:33673883
KEYWORDS
EST.

SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 (bases 1 to 12)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..12
/organism="Oryza sativa"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
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Db 12 AAAAAAAAAAAAA 1

RESULT 320
CF302289/c
LOCUS
DEFINITION
12 bp mRNA linear EST 15-AUG-2003
7LEAF--07-K10.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-K10, mRNA sequence.

ACCESSION
CF302289
VERSION
CF302289.1 GI:33674050
KEYWORDS
EST.

SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 (bases 1 to 12)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..12
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-K10"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
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Db 12 AAAAAAAAAAAAA 1

RESULT 321
CF302486/c
LOCUS
DEFINITION
12 bp mRNA linear EST 15-AUG-2003
7LEAF--08-B02.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-B02, mRNA sequence.

ACCESSION
CF302486
VERSION
CF302486.1 GI:33674247
KEYWORDS
EST.

SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 (bases 1 to 12)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--08-B02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
|||||

then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
|||||
Db 1 AAAAAAAAAA 12

RESULT 325
CF313356/c
LOCUS
DEFINITION
HD--01-H09.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-H09, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE
JOURNAL
COMMENT

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source

1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--01-H09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
|||||
Db 12 AAAAAAAAAA 1

RESULT 326
CF315565/c
LOCUS
DEFINITION
HD--04-I14.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--04-I14, mRNA sequence.

ACCESSION
VERSION
KEYWORDS

EST.

SOURCE
ORGANISM

Oryza sativa
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source

1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--04-I14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
|||||
Db 12 AAAAAAAAAA 1

RESULT 327

CF317551/c

LOCUS

DEFINITION

HD--07-E16.b1 OsHDAC1-overexpressing transgenic rice plasmid
library (HD) Oryza sativa cDNA clone HD--07-E16, mRNA sequence.

ACCESSION

CF317551

VERSION

CF317551.1

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

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FEATURES
source

1..12
/organism="Oryza sativa"
/mol_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--07-E16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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```

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAA 1492
    |||||
Db 12 AAAAAAAAAA 1

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```

RESULT 328
CF317798/c
LOCUS
DEFINITION
HD--07-J24.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--07-J24, mRNA sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

```

REFERENCE
AUTHORS
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)

```

```

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

```

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of Bioscience and Bioinformatics, Myongji University
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```

```

FEATURES
Location/Qualifiers

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1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--07-J24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAA 1492
    |||||
Db 12 AAAAAAAAAA 1

```

```

RESULT 329
CF320426/c

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```

LOCUS
DEFINITION
HD--11-F02.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--11-F02, mRNA sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

```

REFERENCE
AUTHORS
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)

```

```

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

```

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```

```

FEATURES
source

```

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1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--11-F02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1481 AAAAAAAAAA 1492
    |||||
Db 12 AAAAAAAAAA 1

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```

RESULT 330
CF324793/c

```

```

LOCUS
DEFINITION
JMT1--01-H22.g1 AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--01-H22, mRNA
sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

```

REFERENCE
AUTHORS
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)

```

```

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

```


COMMENT

Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .12

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT1-01-H22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ATJMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/notes="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5',
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492

Db 12 AAAAAAAAAAAAA 1

RESULT 331

CF326913/c

LOCUS
DEFINITION
NACL--01-D01.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-D01, mRNA sequence.

ACCESSION CF326913

VERSION CF326913.1 GI:33802082

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .12

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--01-D01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10S"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492

Db 12 AAAAAAAAAAAAA 1

RESULT 332

CF327376/c

LOCUS
DEFINITION
NACL--01-N10.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-N10, mRNA sequence.

ACCESSION CF327376

VERSION CF327376.1 GI:33803011

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .12

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--01-N10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10S"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492

Db 12 AAAAAAAAAAAAA 1

RESULT 333

CF327962/c

LOCUS
DEFINITION
NACL--02-K14.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-K14, mRNA sequence.

ACCESSION CF327962

VERSION CF327962.1 GI:33804174

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

```

1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--02-K14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
```

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1492
|||||
Db 12 AAAAAAAAAAAAAA 1

RESULT 334

CF328229 12 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--03-A13.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--03-A13, mRNA sequence.

ACCESSION CF328229
VERSION CF328229.1 GI:33804704

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source

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1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-A13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1492
|||||
Db 1 AAAAAAAAAAAAAA 12

RESULT 335

CF329141/c 12 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--04-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--04-F18, mRNA sequence.

ACCESSION CF329141
VERSION CF329141.1 GI:33806519

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

```

1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-F18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1492
|||||
Db 12 AAAAAAAAAAAAAA 1

RESULT 336

CF329142 12 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--04-F18.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--04-F18, mRNA sequence.

ACCESSION CF329142
VERSION CF329142.1 GI:33806520

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

```

REFERENCE
AUTHORS      1 (bases 1 to 12)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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QY      1481 AAAAAAAAAAAAAA 1492
Db      1 AAAAAAAAAAAAAA 12

RESULT 337
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LOCUS      CF329346
DEFINITION NACL--04-K07.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF329346
VERSION     CF329346.1 GI:33806928
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
REFERENCE   1 (bases 1 to 12)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      1 AAAAAAAAAAAAAA 12

RESULT 337
CF329346/c
LOCUS      CF329346
DEFINITION NACL--04-K07.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF329346
VERSION     CF329346.1 GI:33806928
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
REFERENCE   1 (bases 1 to 12)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Db      1 AAAAAAAAAAAAAA 12

RESULT 339
CF329929/c
LOCUS      CF329929
DEFINITION NACL--05-H03.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF329929
VERSION     CF329929.1 GI:33808079
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAAA 1

RESULT 338
CF329872/c
LOCUS      CF329872
DEFINITION NACL--05-F19.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF329872
VERSION     CF329872.1 GI:33807965
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
REFERENCE   1 (bases 1 to 12)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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   RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
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RESULT 339
CF329929/c
LOCUS      CF329929
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ACCESSION  CF329929
VERSION     CF329929.1 GI:33808079
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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/note=Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
DB 12 AAAAAAAAAAAAA 1

RESULT 341
CF331858 12 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--08-C08.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--08-C08, mRNA sequence.
ACCESSION CF331858
VERSION CF331858.1 GI:33811939
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
DB 12 AAAAAAAAAAAAA 1

RESULT 340
CF331241/c 12 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--07-E15.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--07-E15, mRNA sequence.
ACCESSION CF331241
VERSION CF331241.1 GI:33810705
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
DB 12 AAAAAAAAAAAAA 1

RESULT 342
CF331904 12 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--08-D07.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--08-D07, mRNA sequence.
ACCESSION CF331904
VERSION CF331904.1 GI:33812029
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS 1 (bases 1 to 12)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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/clone_lib="Rice callus plasmid cDNA library (NACL)"
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492

Db 1 AAAAAAAAAAAAA 12

RESULT 343

CF331950/c

LOCUS NACL--08-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--08-E07, mRNA sequence.

ACCESSION CF331950

VERSION CF331950.1 GI:33812121

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492

Db 12 AAAAAAAAAAAAA 1

RESULT 344

CF332993/c

LOCUS JMT--01-L10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

DEFINITION library (JMT) Oryza sativa cDNA clone JMT--01-L10, mRNA sequence.

ACCESSION CF332993

VERSION CF332993.1 GI:33814228

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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methyltransferase overexpression line."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
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Qy 1481 AAAAAAAAAAAAA 1492

Db 12 AAAAAAAAAAAAA 1

RESULT 345

CF333992/c

LOCUS JMT--03-B22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA

DEFINITION library (JMT) Oryza sativa cDNA clone JMT--03-B22, mRNA sequence.

ACCESSION CF333992

VERSION CF333992.1 GI:33816288

KEYWORDS EST.

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SOURCE
ORGANISM      Oryza sativa
              Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnamhggbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
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RESULT 346
BQ591949/c
LOCUS      BQ591949
DEFINITION BQ591949
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            cDNA clone 024-016-C15 5-PRIME, mRNA sequence.
ACCESSION  BQ591949
VERSION     BQ591949.1 GI:26121532
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
            1 (bases 1 to 14)
            Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
            22362189
            12472698
            Contact: Weisshaar B
            ADIS DNA core facility at MPZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
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    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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    RT-PCR."

Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
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    Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Best
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.8%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAA 1492
Db       13 AAAAAAAAAAAAA 2

RESULT 347
CF330198/c
LOCUS      CF330198
DEFINITION CF330198
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            sativa cDNA clone NACL--05-N04, mRNA sequence.
ACCESSION  CF330198
VERSION     CF330198.1 GI:33808624
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 14)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnamhggbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1..14
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="NACL--05-N04"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

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Query Match      0.8%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
Db 14 AAAAAAAAAA 3

RESULT 348
LOCUS CF299997 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF299997
VERSION CF299997.1 GI:33671758
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1086 TTTTGTTTGTCT 1100
Db 3 TTTTGTCTTCT 17

RESULT 349
LOCUS CF300456 18 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF300456
VERSION CF300456.1 GI:33672217
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-N23"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1086 TTTTGTTTGTCT 1100
Db 4 TTTTGTCTTCT 18

RESULT 350
LOCUS CF329285 18 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-122.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF329285
VERSION CF329285.1 GI:33806806
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"
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/db_xref="taxon:4530"
/clone="NACL--04-122"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match      0.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCT 1100
DB 3 TTTTGTGTTTGTCT 17

RESULT 351
CF298591
LOCUS
DEFINITION      18 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--02-A20, mRNA sequence.
ACCESSION      CF298591
VERSION        CF298591.1 GI:33670352
KEYWORDS
SOURCE
ORGANISM        Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..18
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone="7LEAF--02-A20"
/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 11.6; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGAA 1103
DB 1 TTTTGTGTTTGTCTGAA 18

RESULT 352
AZ345795/c
LOCUS
DEFINITION      19 bp DNA linear GSS 29-SEP-2000
1M0080H09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080H09 R, genomic survey sequence.
ACCESSION      AZ345795
VERSION        AZ345795.1 GI:10425032
KEYWORDS
SOURCE
ORGANISM        Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: H column: 09
Seq primer: CACACAGGNAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="genomic DNA"
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWB42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.8%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGAA 1103
DB 18 TTTTGTGTTTGTCTGAA 1

RESULT 353
AZ650575/c
LOCUS
DEFINITION      19 bp DNA linear GSS 14-DEC-2000
1M0520P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0520P13 R, genomic survey sequence.
ACCESSION      AZ650575
VERSION        AZ650575.1 GI:11785200
KEYWORDS
SOURCE
ORGANISM        Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,

```


Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: P column: 13
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES source

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGAA 1103
|||||
Db 18 TTTTGTGTTTGTCTGAA 1

RESULT 354

AZ849506/c 20 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0150P21 R, genomic survey sequence.

ACCESSION AZ849506
VERSION AZ849506.1 GI:13033596

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE

AUTHORS Dunn, D., Ayagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE JOURNAL COMMENT

Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES source

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/organism="Mus musculus"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 11.6; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGAA 1103
|||||
Db 18 TTTTGTGTTTGTCTGAA 1

RESULT 355

CF291168

LOCUS 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-H20.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-H20, mRNA sequence.

ACCESSION CF291168

VERSION CF291168.1 GI:33660201

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

```

JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
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Query Match      0.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 356
CF327120
LOCUS      13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-H14.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-H14, mRNA sequence.
ACCESSION  CF327120
VERSION     CF327120.1 GI:33802495
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
  Location/Qualifiers
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      /organism="Oryza sativa"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:4530"
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      /tissue_type="callus"
      /dev_stage="proliferated callus on 2N6 media for 30 days"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice callus plasmid cDNA library (NACL)"
      /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."

Query Match      0.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 356
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LOCUS      13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-H14.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-H14, mRNA sequence.
ACCESSION  CF327120
VERSION     CF327120.1 GI:33802495
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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      /mol_type="mRNA"
      /cultivar="KWS2320 (double haploid, monogerm breeding
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      /db_xref="taxon:161934"
      /clone="024-019-O15"
      /tissue_type="storage root"
      /lab_host="EMDH108"
      /clone_lib="MP1Z-ADIS-024-storage root"
      /note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
      cDNA library from sugar beet, library provided by KWS
      Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
      orientation:
      SP6-Sali-CCACGCGTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:
      Sequencing granted in the context of the GABI-Beet
      project, local PI: Dr. Katharina Schneider, coordinator:
      Prof. Christian Jung; Sequence submission managed by
      RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.7%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTG 1101
Db 1 TTTTGTGTTTGTCTG 16

RESULT 358
CF318894

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JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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      with oligoribonucleotides and then used as templates for
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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 356
CF327120
LOCUS      13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-H14.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-H14, mRNA sequence.
ACCESSION  CF327120
VERSION     CF327120.1 GI:33802495
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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      /db_xref="taxon:161934"
      /clone="024-019-O15"
      /tissue_type="storage root"
      /lab_host="EMDH108"
      /clone_lib="MP1Z-ADIS-024-storage root"
      /note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
      cDNA library from sugar beet, library provided by KWS
      Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
      orientation:
      SP6-Sali-CCACGCGTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:
      Sequencing granted in the context of the GABI-Beet
      project, local PI: Dr. Katharina Schneider, coordinator:
      Prof. Christian Jung; Sequence submission managed by
      RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.7%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTG 1101
Db 1 TTTTGTGTTTGTCTG 16

RESULT 358
CF318894

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RESULT 361
CF295807
LOCUS
DEFINITION
  CF295807 17 bp mRNA linear EST 14-AUG-2003
  sativa cDNA clone 30DGS--05-012, mRNA sequence.
ACCESSION
  CF295807
VERSION
  CF295807.1 GI:33664840
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 17)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
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  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 1086 TTTTGTGTTTGTCTG 1101
  Db 2 TTTTGTGTTTGTCTG 17

RESULT 362
CF299639
LOCUS
DEFINITION
  CF299639 17 bp mRNA linear EST 15-AUG-2003
  sativa cDNA clone 7LEAF--03-L20, mRNA sequence.
ACCESSION
  CF299639
VERSION
  CF299639.1 GI:33671400
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 17)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
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    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
  Query Match 0.7%; Score 11.2; DB 1; Length 17;
  Best Local Similarity 81.2%; Pred. No. 5.1e+02;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 1086 TTTTGTGTTTGTCTG 1101
  Db 2 TTTTGTGTTTGTCTG 17

RESULT 363
CF298341
LOCUS
DEFINITION
  CF298341 17 bp mRNA linear EST 15-AUG-2003
  sativa cDNA clone 7LEAF--01-K24, mRNA sequence.
ACCESSION
  CF298341
VERSION
  CF298341.1 GI:33670102
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 17)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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    /mol_type="mRNA"
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  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 1086 TTTTGTGTTTGTCTG 1101
  Db 2 TTTTGTGTTTGTCTG 17

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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    RT-PCR."
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  Best Local Similarity 81.2%; Pred. No. 5.1e+02;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 1086 TTTTGTGTTTGTCTG 1101
  Db 2 TTTTGTGTTTGTCTG 17

RESULT 363
CF298341
LOCUS
DEFINITION
  CF298341 17 bp mRNA linear EST 15-AUG-2003
  sativa cDNA clone 7LEAF--01-K24, mRNA sequence.
ACCESSION
  CF298341
VERSION
  CF298341.1 GI:33670102
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 17)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
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  QY 1086 TTTTGTGTTTGTCTG 1101
  Db 2 TTTTGTGTTTGTCTG 1101

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Db      1 TTTTGTGTTTTGTTCTG 16

RESULT 364
CF291802
LOCUS      17 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
VERSION     sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
CF291802
ACCESSION   CF291802.1 GI:33660835
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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            /clone_lib="Rice root plasmid cDNA library (14ROOT)"
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Query Match      0.7%; Score 11.2; DB 1; Length 17;
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1085 GTTTGTTTTGTTCT 1100
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Db      2 GTTTTGTGTTTTTTT 17

RESULT 365
CF298396
LOCUS      19 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
VERSION     sativa cDNA clone 7LEAF--01-M05, mRNA sequence.
CF298396
ACCESSION   CF298396.1 GI:33670157
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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            RT-PCR."

Query Match      0.7%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1086 TTTTGTGTTTTGTTCTG 1101
            ||||| ||||| |||
Db      4 TTTTGTGTTTTTTG 19

RESULT 366
CF302456
LOCUS      19 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
VERSION     sativa cDNA clone 7LEAF--07-P22, mRNA sequence.
CF302456
ACCESSION   CF302456.1 GI:33674217
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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            RT-PCR."

Query Match      0.7%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1086 TTTTGTGTTTTGTTCTG 1101
            ||||| ||||| |||

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..19
/organism="Oryza sativa"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTTGTTCTG 1101

||||| ||||| |||
Db 4 TTTTGTGTTTTTTG 19

RESULT 366

CF302456

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF302456 19 bp mRNA linear EST 15-AUG-2003
7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-P22, mRNA sequence.
CF302456
CF302456.1 GI:33674217
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..19
/organism="Oryza sativa"
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Query Match 0.7%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTTGTTCTG 1101

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..19
/organism="Oryza sativa"
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RT-PCR."

Query Match 0.7%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1085 GTTTGTTTTGTTCT 1100

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Db 2 GTTTTGTGTTTTTTT 17

RESULT 365

CF298396

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF298396 19 bp mRNA linear EST 15-AUG-2003
7LEAF--01-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-M05, mRNA sequence.
CF298396
CF298396.1 GI:33670157
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Query Match 0.7%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.3%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1085 GTTTGTTTTGTTCT 1100

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Db 2 GTTTTGTGTTTTTTT 17

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Db      4  |||| |||| |||| ||||
         4  TTTT TTTT TTTT TTTG 19

RESULT 367
CF327587
LOCUS   NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION
sativa cDNA clone NACL--02-C04, mRNA sequence.
ACCESSION   CF327587
VERSION     CF327587.1
KEYWORDS    GI:33803426
SOURCE      Oryza sativa
ORGANISM   Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,F.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      2  TTTT TTTT TTTT TTTG 17

RESULT 368
BQ589109
LOCUS   S013715-024-015-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION
cDNA clone 024-015-B24 3-PRIME, mRNA sequence.
ACCESSION   BQ589109
VERSION     BQ589109.1
KEYWORDS    GI:26118692
SOURCE      Beta vulgaris
ORGANISM   Beta vulgaris
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
           Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
           and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
           fingerprinting allows access to 25 000 potential sugar beet genes
           Plant J. 32 (5), 845-857 (2002)

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
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MEDLINE 22362189
PUBMED 12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
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FEATURES
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   Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:
   b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
   orientation:
   SP6-Sali-CCACGCGTCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
   Sequencing granted in the context of the GABI-Beet
   project, local PI: Dr. Katharina Schneider, coordinator:
   Prof. Christian Jung; Sequence submission managed by
   RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. NO. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
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Db      1  AAAAAAAAAA 11

RESULT 369
BQ590590/c
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DEFINITION
cDNA clone 024-019-D02 3-PRIME, mRNA sequence.
ACCESSION   BQ590590
VERSION     BQ590590.1
KEYWORDS    GI:26120173
SOURCE      Beta vulgaris
ORGANISM   Beta vulgaris
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
           Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
           and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
           fingerprinting allows access to 25 000 potential sugar beet genes
           Plant J. 32 (5), 845-857 (2002)

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
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FEATURES
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      line)"
      /db_xref="GABI:189530"
      /db_xref="taxon:161934"
      /clone="024-019-D02"
      /tissue_type="storage root"
      /lab_host="EMDH10B"
      /clone_lib="MP1Z-ADIS-024-storage root"
      /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
      cDNA library from sugar beet, library provided by KWS
      Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
      b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
      orientation:
      SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
      Sequencing granted in the context of the GABI-Beet
      project, local PI: Dr. Katharina Schneider, coordinator:
      Prof. Christian Jung; Sequence submission managed by
      RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 370
BO595827/c
LOCUS
DEFINITION
BO595827 11 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-021-P01 3-PRIME, mRNA sequence.
ACCESSION
BO595827
VERSION
BO595827.1 GI:26125410
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
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FEATURES
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      /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
      cDNA library from sugar beet, library provided by KWS
      Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
      b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
      orientation:
      SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
      Sequencing granted in the context of the GABI-Beet
      project, local PI: Dr. Katharina Schneider, coordinator:
      Prof. Christian Jung; Sequence submission managed by
      RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 371
BO595834/c
LOCUS
DEFINITION
BO595834 11 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-021-B01 3-PRIME, mRNA sequence.
ACCESSION
BO595834
VERSION
BO595834.1 GI:26125417
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 21 row: B column: 01
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      /clone_lib="MP1Z-ADIS-024-developing root"
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      cDNA library from sugar beet, library provided by KWS
      Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
      b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
      orientation:
      SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
      Sequencing granted in the context of the GABI-Beet

```


project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/CABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
|||||
DB 11 AAAAAAAAAA 1

RESULT 372
CF281971/c
LOCUS
DEFINITION 11 bp mRNA linear EST 14-AUG-2003
Oryza sativa cDNA clone 14ETL--09-E07, mRNA sequence.

ACCESSION CF281971 GI:33659358
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 11)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers

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(14ETL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
|||||
DB 11 AAAAAAAAAA 1

RESULT 373
CF290941/c
LOCUS
DEFINITION 11 bp mRNA linear EST 14-AUG-2003
Oryza sativa cDNA clone 14ROOT--01-C22, mRNA sequence.

ACCESSION CF290941 GI:33659974
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 11)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnahm@bio.myongji.ac.kr.

FEATURES
source
1..11
Location/Qualifiers

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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
|||||
DB 11 AAAAAAAAAA 1

RESULT 374
CF290942

LOCUS
DEFINITION 11 bp mRNA linear EST 14-AUG-2003
Oryza sativa cDNA clone 14ROOT--01-C22, mRNA sequence.

ACCESSION CF290942 GI:33659975
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 11)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnahm@bio.myongji.ac.kr.

FEATURES
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1..11
Location/Qualifiers

/organism="Oryza sativa"
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/lab_host="E.coli DH10B"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 1 AAAAAAAAAA 11

RESULT 375
CF291453/c      11 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
14ROOT--01-004.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-004, mRNA sequence.
CF291453
VERSION
CF291453.1 GI:33660486
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..11
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 1 AAAAAAAAAA 11

RESULT 376
CF291454/c      11 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
14ROOT--01-004.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-004, mRNA sequence.
CF291454
VERSION
CF291454.1 GI:33660487
KEYWORDS
SOURCE
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1..11
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/lab_host="E.coli DH10B"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 1 AAAAAAAAAA 11

RESULT 376
CF291454/c      11 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
14ROOT--02-N20.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-N20, mRNA sequence.
CF292150
VERSION
CF292150.1 GI:33661183
KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Db 1 AAAAAAAAAA 11

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LOCUS
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14ROOT--02-N20.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-N20, mRNA sequence.
CF292150
VERSION
CF292150.1 GI:33661183
KEYWORDS
SOURCE
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 1

RESULT 378
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DEFINITION      14ROOT--02-N20.g1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION      CF292151
VERSION      CF292151.1 GI:33661184
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SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 11

RESULT 379
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DEFINITION      14ROOT--02-P21.g1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION      CF292236
VERSION      CF292236.1 GI:33661269
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Query Match      0.7%; Score 11; DB 1; Length 11;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 11

RESULT 379
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LOCUS      11 bp mRNA linear EST 14-AUG-2003
DEFINITION      14ROOT--02-P21.g1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION      CF292236
VERSION      CF292236.1 GI:33661269
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 11

RESULT 380
CF297318/c
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DEFINITION      30DGS--08-B17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
ACCESSION      CF297318
VERSION      CF297318.1 GI:33666351
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 AAAAAAAAAA 1

RESULT 381
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DEFINITION      11 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--01-C03, mRNA sequence.
ACCESSION      CF297948
VERSION        CF297948.1 GI:33669709
KEYWORDS
SOURCE
ORGANISM        Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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Db 11 AAAAAAAAAA 1

RESULT 382
CF298806/c
LOCUS
DEFINITION      11 bp mRNA linear EST 15-AUG-2003
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ACCESSION      CF298806
VERSION        CF298806.1 GI:33670567
KEYWORDS
SOURCE
ORGANISM        Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 1

RESULT 382
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DEFINITION      11 bp mRNA linear EST 15-AUG-2003
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VERSION        CF298806.1 GI:33670567
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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KEYWORDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 1

RESULT 383
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ACCESSION      CF299648
VERSION        CF299648.1 GI:33671409
KEYWORDS
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ORGANISM        Oryza sativa
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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DB 11 AAAAAAAAAA 1

RESULT 384
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CF299849
VERSION    CF299849.1 GI:33671610
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
DB 11 AAAAAAAAAA 1

RESULT 385
CF300174/c
LOCUS      11 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--04-H16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-H16, mRNA sequence.
CF300174
VERSION    CF300174.1 GI:33673049
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
RT-PCR."

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CF300174.1 GI:33671935
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SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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QY 1481 AAAAAAAAAA 1491
DB 11 AAAAAAAAAA 1

RESULT 386
CF301288/c
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sativa cDNA clone 7LEAF--06-B16, mRNA sequence.
CF301288
ACCESSION  CF301288.1 GI:33673049
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 387
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LOCUS      11 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-K21.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-K21, mRNA sequence.
ACCESSION  CF301713
VERSION     CF301713.1 GI:33673474
KEYWORDS   EST.
SOURCE     CF301713.1 GI:33673474
ORGANISM   Oryza sativa
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            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 11)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 1

RESULT 388
CF301744
LOCUS      11 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-L14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-L14, mRNA sequence.
ACCESSION  CF301744
VERSION     CF301744.1 GI:33673505
KEYWORDS   EST.
SOURCE     CF301744.1 GI:33673505
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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REFERENCE   1 (bases 1 to 11)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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                        /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                        RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 389
CF302896
LOCUS      11 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--08-N07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-N07, mRNA sequence.
ACCESSION  CF302896
VERSION     CF302896.1 GI:33674657
KEYWORDS   EST.
SOURCE     CF302896.1 GI:33674657
ORGANISM   Oryza sativa
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REFERENCE   1 (bases 1 to 11)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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                        RT-PCR."

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ACCESSION  CF301744
VERSION     CF301744.1 GI:33673505
KEYWORDS   EST.
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            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Qy 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 389
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LOCUS      11 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--08-N07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-N07, mRNA sequence.
ACCESSION  CF302896
VERSION     CF302896.1 GI:33674657
KEYWORDS   EST.
SOURCE     CF302896.1 GI:33674657
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE   1 (bases 1 to 11)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
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Db 11 AAAAAAAAAA 1

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library (ABF) Oryza sativa cDNA clone ABF--01-G20, mRNA sequence.
ACCESSION
CF307845
VERSION
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KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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line."

Query Match      0.7%; Score 11; DB 1; Length 11;
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Db 11 AAAAAAAAAA 1

RESULT 392
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LOCUS
DEFINITION
ABF--07-G06.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-G06, mRNA sequence.
ACCESSION
CF311911
VERSION
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KEYWORDS
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ORGANISM
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

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CF309987/c
LOCUS
DEFINITION
ABF--04-G14.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--04-G14, mRNA sequence.
ACCESSION
CF309987
VERSION
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KEYWORDS
EST.
SOURCE
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ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
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Db 11 AAAAAAAAAA 1

RESULT 392
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DEFINITION
ABF--07-G06.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-G06, mRNA sequence.
ACCESSION
CF311911
VERSION
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KEYWORDS
EST.
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ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea

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Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

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RESULT 393
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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 11)
 Song, S.I., Kim, J.K., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nam B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

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Query Match 0.7%; Score 11; DB 1; Length 11;
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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Location/Qualifiers

QY 1481 AAAAAAAAAA 1491
 11 AAAAAAAAAA 1

RESULT 395
 CF318741/c
 LOCUS
 DEFINITION
 HD--08-P20.b1 OSHDAC1-overexpressing transgenic rice plasmid
 library (HD) Oryza sativa cDNA clone HD--08-P20, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 11)
 Song, S.I., Kim, J.K., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nam B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

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 line."

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 Location/Qualifiers

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 11 AAAAAAAAAA 1

RESULT 394
 CF314533/c
 LOCUS
 DEFINITION
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 library (HD) Oryza sativa cDNA clone HD--03-B13, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 11)
 Song, S.I., Kim, J.K., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nam B.H.
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

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 line."

Query Match 0.7%; Score 11; DB 1; Length 11;
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 Location/Qualifiers

QY 1481 AAAAAAAAAA 1491
 11 AAAAAAAAAA 1

RESULT 395
 CF318741/c
 LOCUS
 DEFINITION
 HD--08-P20.b1 OSHDAC1-overexpressing transgenic rice plasmid
 library (HD) Oryza sativa cDNA clone HD--08-P20, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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 cDNA library (HD)"
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 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.7%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Location/Qualifiers

QY 1481 AAAAAAAAAA 1491
 11 AAAAAAAAAA 1

RESULT 395
 CF318741/c
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 DEFINITION
 HD--08-P20.b1 OSHDAC1-overexpressing transgenic rice plasmid
 library (HD) Oryza sativa cDNA clone HD--08-P20, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
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 Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
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 for 2hrs. Oligo-capped mRNA was reverse transcribed and
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 element binding transcription factor 3 overexpression
 line."

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REFERENCE
AUTHORS      Ehrhartoideae; Oryzeae; Oryza.
              1 (bases 1 to 11)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"
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/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
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derived from rice Histone Deacetylase overexpression
line."

Query Match      0.7%; Score 11; DB 1; Length 11;
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QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 396
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DEFINITION NACL--01-E20.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-E20, mRNA sequence.
ACCESSION  CF326997
VERSION     CF326997.1 GI:33802249
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
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              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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line."

Query Match      0.7%; Score 11; DB 1; Length 11;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 396
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LOCUS      CF326997      11 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--01-E20.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-E20, mRNA sequence.
ACCESSION  CF326997
VERSION     CF326997.1 GI:33802249
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
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line."

AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
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line."

Query Match      0.7%; Score 11; DB 1; Length 11;
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QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 398
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LOCUS      CF327885      11 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--02-I20.g1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION  CF327885
VERSION     CF327885.1 GI:33804018
KEYWORDS   EST.

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QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 397
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ACCESSION  CF326998
VERSION     CF326998.1 GI:33802251
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
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1 (bases 1 to 11)
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 1

RESULT 398
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DEFINITION NACL--02-I20.g1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION  CF327885
VERSION     CF327885.1 GI:33804018
KEYWORDS   EST.

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SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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RESULT 399
LOCUS
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DEFINITION
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ACCESSION
CF328618
VERSION
CF328618.1 GI:33805485
KEYWORDS
EST.
SOURCE
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
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COMMENT
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 1 AAAAAAAAAA 1

RESULT 399
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DEFINITION
NACL--03-J20.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-J20, mRNA sequence.
ACCESSION
CF328618
VERSION
CF328618.1 GI:33805485
KEYWORDS
EST.
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
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RT-PCR."

Query Match 0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 1 AAAAAAAAAA 1

RESULT 401
LOCUS
CF329242/c 11 bp mRNA linear EST 18-AUG-2003
DEFINITION
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sativa cDNA clone NACL--04-H23, mRNA sequence.
ACCESSION
CF329242
VERSION
CF329242.1 GI:33806721

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KEYWORDS
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ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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QY 1481 AAAAAAAAAA 1491
DB 11 AAAAAAAAAA 1
RESULT 402
CF329344/C
LOCUS
DEFINITION
NACL--04-K06.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-K06, mRNA sequence.
ACCESSION
CF329344
VERSION
CF329344.1 GI:33806925
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION
NACL--04-K06.b1 Rice callus plasmid cDNA library (NACL) Oryza
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EST.
SOURCE
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ORGANISM
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 11 AAAAAAAAAA 1
RESULT 402
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LOCUS
DEFINITION
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CF329344
VERSION
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KEYWORDS
EST.
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Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAA 1491
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LOCUS
DEFINITION
NACL--04-K06.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-K06, mRNA sequence.
ACCESSION
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VERSION
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KEYWORDS
EST.
SOURCE
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ORGANISM
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAA 1491
DB 11 AAAAAAAAAA 1
RESULT 402
CF329344/C
LOCUS
DEFINITION
NACL--04-K06.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-K06, mRNA sequence.
ACCESSION
CF329345
VERSION
CF329345.1 GI:33806926
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 11 AAAAAAAAAA 1
RESULT 404
CF331049/C
LOCUS
DEFINITION
NACL--07-A08.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION
CF331049

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RT-PCR."
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DB 11 AAAAAAAAAA 1
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CF329345
LOCUS
DEFINITION
NACL--04-K06.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-K06, mRNA sequence.
ACCESSION
CF329345
VERSION
CF329345.1 GI:33806926
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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AUTHORS
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FEATURES
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 404
CF331049/C
LOCUS
DEFINITION
NACL--07-A08.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-A08, mRNA sequence.
ACCESSION
CF331049

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VERSION     CF331815.1  GI:33811852
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ORGANISM    Oryza sativa
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AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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Search completed: April 21, 2004, 11:00:02
 Job time : 7 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 09:12:59 ; Search time 252 Seconds
(without alignments)
337.159 Million cell updates/sec

Title: US-10-006-430-76

Perfect score: 20

Sequence: 1 accgagtcagatgttga 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 3185356

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*
1: geneseqn1980s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	9	Adc35604 Human CD8
2	20	100.0	50	6	Abz04679 Human leu
3	14.2	71.0	20	3	Aaa66532 Dog genom
4	14.2	71.0	20	3	Aaa66614 Dog genom
5	13.8	69.0	38	2	Aav04408 Primer us
6	13.8	69.0	38	5	Aaf57868 Murine OP
7	13.4	67.0	25	8	Ack17461 Human mic
8	13.4	67.0	31	4	Aai10957 Human sin
9	13.4	67.0	50	6	Abz01461 Human leu
10	13.4	67.0	50	6	Abz01133 Human leu
11	13.4	67.0	50	6	Abz01467 Human leu
12	13.4	67.0	50	9	Add93328 Ptl1 gene
13	13.2	66.0	50	6	Abz05433 Human leu
14	13	65.0	25	8	Ac135316 Human mic
15	12.8	64.0	17	7	AcD52070 HEV inozoy
16	12.8	64.0	17	7	AcD50650 HEV hammy
17	12.8	64.0	20	2	Aat08244 p204, PCR
18	12.8	64.0	20	2	Aat93430 Primer 2
19	12.8	64.0	20	2	Aax17855 Primer #2
20	12.8	64.0	20	3	Aaa78308 Human Ig
21	12.8	64.0	24	2	Aav30090 DNA seque
22	12.8	64.0	24	9	Adc33472 Gnt-V rel
23	12.8	64.0	25	8	Ac169449 Human mic

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c	25	12.8	64.0	25	8	ACK13687	Human mic
c	26	12.8	64.0	25	8	ACI81271	Human mic
c	27	12.8	64.0	25	8	ACH56433	DNA target
c	28	12.8	64.0	27	2	AAQ26429	Human bet
c	29	12.8	64.0	27	3	AAQ38967	Human G p
c	30	12.8	64.0	29	2	AAx86771	PCR prime
c	31	12.8	64.0	30	2	AAx72887	Primer #2
c	32	12.8	64.0	30	3	AAZ98292	P. vivax
c	33	12.8	64.0	30	3	AAA87029	Mutant ta
c	34	12.8	64.0	30	6	AAD44259	Mutant ta
c	35	12.8	64.0	31	7	ACD43663	Human gen
c	36	12.8	64.0	34	7	ACC69768	Human H-F
c	37	12.8	64.0	36	2	AAQ84796	Spinocere
c	38	12.8	64.0	50	6	ABA95147	P. vivax
c	39	12.8	64.0	50	6	ABZ02100	Human leu
c	40	12.6	63.0	25	8	ACK05147	Human mic
c	41	12.6	63.0	25	8	ACI11455	Human mic
c	42	12.6	63.0	25	8	ACK27387	Human mic
c	43	12.6	63.0	25	8	ACI60529	Human mic
c	44	12.6	63.0	25	8	ACI17517	Human mic
c	45	12.6	63.0	25	8	ACK16092	Human mic

ALIGNMENTS

RESULT 1

ADC35604
ID ADC35604 standard; DNA; 20 BP.

XX

AC ADC35604;

DT 18-DEC-2003 (first entry)

DE Human CD81/TAPA-1 antisense oligonucleotide #64.

XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone and all cytidines are 5'-methyl cytidines"

FT modified_base 1..5

FT /tag= a

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

FT modified_base 16..20

FT /tag= c

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FT /note= "2'-methoxyethyl nucleotide"

US2003113914-A1.

19-JUN-2003.

PF 10-DEC-2001; 2001US-00006430.

XX 10-DEC-2001; 2001US-00006430.

XX (ISIS-) ISIS PHARM INC.

XX Graham MJ, Dobie K;

XX WPI; 2003-810907/76.

PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.

XX Claim 3; SEQ ID NO 76; 55pp; English.

XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGGAGTCAGGATGTTGGA 20
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 DB 1 ACGGAGTCAGGATGTTGGA 20

RESULT 2

ID ABZ04679/c
 ID ABZ04679 standard; DNA; 50 BP.

XX AC ABZ04679;

XX 09-JAN-2003 (first entry)

DE Human leukocyte gene expression profiling probe SEQ ID NO 4670.

XX T7; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KW ss.

XX OS Homo sapiens.

XX PN WO200257414-A2.

XX PD 25-JUL-2002.

XX PF 22-OCT-2001; 2001WO-US047856.

XX PR 20-OCT-2000; 2000US-0241994P.

XX PB 08-JUN-2001; 2001US-0296764P.

XX PA (BIOC-) BIOCARDIA INC.

XX PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 PI Ly N, Woodward R, Quettermous T, Johnson F;

XX WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 477; Opp; English.

XX The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful

CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX Sequence 50 BP; 13 A; 17 C; 5 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 50;

Best Local Similarity 100.0%; Pred. No. 2.9; 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 46 ACGGAGTCAGGATGTTGGA 27

RESULT 3

AAA66532

ID AAA66532 standard; DNA; 20 BP.

XX AC AAA66532;

XX 09-OCT-2000 (first entry)

DE Dog genomic marker oligonucleotide sequence SEQ ID NO:394.

XX Dog; genome; genomic marker; radiation hybrid map; identification;
 KW chromosome location; gene marker; polymorphic microsatellite marker;
 KW phenotype; behaviour; pedigree; ss.

XX OS Canis familiaris.

XX PN WO200029615-A2.

XX PD 25-MAY-2000.

XX PF 15-NOV-1999; 99WO-IB001907.

XX PR 13-NOV-1998; 98US-0108193P.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PI Galibert F, Andre C;

XX WPI; 2000-387821/33.

XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
 PT for e.g. identifying genes implicated in phenotypic and behavioral traits
 PT or in genetic diseases and for studying dog pedigrees.

XX Claim 1; Page 70; 87pp; English.

XX The present invention describes a radiation hybrid map of the dog (Canine
 CC familiaris) genome comprising the genome location of a marker selected
 CC from AAA66139 to AAA66942. The radiation hybrid map is useful for
 CC identifying and localising dog genes, since it covers approximately 80 %
 CC of the dog genome and provides a dense map integrating different types
 CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
 CC (or complementary sequences) are especially useful to identify genes
 CC responsible for phenotypic and behavioural traits in dogs, to identify
 CC morbid genes, to analyse diseases and identify implicated genes in such
 CC diseases and their alleles, and to study dog pedigrees. They may also be
 CC useful for isolating corresponding human gene sequences e.g. genes
 CC involved in genetic diseases

XX Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 3; Length 20;

Best Local Similarity 84.2%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGAGTCAGATGTTGCA 20
 ||||| ||||| |||||
 Db 1 CGGAGACTGATGATGCA 19

RESULT 4
 AA66614 standard; DNA; 20 BP.
 ID AA66614
 XX
 AC AAA66614;
 XX
 DT 09-OCT-2000 (first entry)
 XX
 DE Dog genomic marker oligonucleotide sequence SEQ ID NO:476.
 XX
 KM Dog; genome; genomic marker; radiation hybrid map; identification;
 KM chromosome location; gene marker; polymorphic microsatellite marker;
 KM phenotype; behaviour; pedigree; ss.
 OS
 XX Canis familiaris.
 XX
 PN WO200029615-A2.
 XX
 PD 25-MAY-2000.
 XX
 PF 15-NOV-1999; 99WO-IB001907.
 XX
 PR 13-NOV-1998; 98US-0108193P.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCT.
 XX
 PI Galibert F, Andre C;
 XX
 DR WPI; 2000-387821/33.
 XX
 PT New radiation hybrid map of the dog, Canine familiaris, genome, useful
 PT for e.g. identifying genes implicated in phenotypic and behavioral traits
 PT or in genetic diseases and for studying dog pedigrees.
 XX
 PS Claim 1; Page 73; 87pp; English.
 XX
 CC The present invention describes a radiation hybrid map of the dog (Canine
 CC familiaris) genome comprising the genome location of a marker selected
 CC from AA66613 to AA66942. The radiation hybrid map is useful for
 CC identifying and localising dog genes, since it covers approximately 80 %
 CC of the dog genome and provides a dense map integrating different types
 CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
 CC (or complementary sequences) are especially useful to identify genes
 CC responsible for phenotypic and behavioural traits in dogs, to identify
 CC morbid genes, to analyse diseases and identify implicated genes in such
 CC diseases and their alleles, and to study dog pedigrees. They may also be
 CC useful for isolating corresponding human gene sequences e.g. genes
 CC involved in genetic diseases
 CC
 XX
 SQ Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 3; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGAGTCAGATGTTGCA 20
 ||||| ||||| |||||
 Db 1 CGGAGACTGATGATGCA 19

RESULT 5
 AA664408 standard; DNA; 38 BP.
 ID AA664408
 XX
 AC AA664408;
 XX

DT 20-APR-1998 (first entry)
 DE
 XX Primer used in preparation of osteoprotegerin products.
 XX
 KM Osteoprotegerin; antibody; diagnosis; affinity purification;
 KM recombinant production; transgenic animal; treatment; prevention;
 KM antisense oligonucleotide; probe; detection; screening; bone disease;
 KM osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;
 KM rheumatoid arthritis; osteomyelitis; osteolytic metastasis;
 KM periodontal bone loss; bone necrosis; osteopaenia; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN DE19654610-A1.
 XX
 PD 26-JUN-1997.
 XX
 PF 20-DEC-1996; 96DE-01054610.
 XX
 PR 22-DEC-1995; 95US-00577788.
 PR 03-SEP-1996; 96US-00706945.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Lacey DL, Calzone FU, Chang M;
 XX
 DR WPI; 1997-334271/31.
 XX
 PT Nucleic acid encoding osteoprotegerin - useful for treatment of diseases
 PT involving excessive bone loss, e.g. osteoporosis.
 XX
 PS Example 9; Page 52; 182pp; German.
 XX
 CC The present sequence is a primer, which was used in the preparation of
 CC osteoprotegerin (OPG) products. Anti-OPG antibodies can be used in OPG
 CC diagnostic assays, and as affinity purification materials. The OPG cDNA
 CC can be used to express recombinant OPG and to generate transgenic
 CC animals. It can also be used to regulate the level of OPG in mammals,
 CC specifically to increase OPG levels, however the use of antisense
 CC sequences is also contemplated. Fragments of the cDNA can be used as
 CC probes to detect OPG expressing cells and tissue, and to screen cDNA
 CC libraries for related sequences. OPG can be used to treat or prevent bone
 CC diseases, specifically excessive bone loss, e.g. osteoporosis, Paget's
 CC disease, hypercalcaemia, hyperparathyroidism, rheumatoid arthritis,
 CC osteomyelitis, osteolytic metastases, periodontal bone loss, bone
 CC necrosis and osteopaenia
 CC
 XX
 SQ Sequence 38 BP; 6 A; 9 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 2; Length 38;
 Best Local Similarity 88.2%; Pred. No. 3.5e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGTCAGATGTTGCA 20
 ||||| ||||| |||||
 Db 9 GAGTCAGATGTTTCA 25

RESULT 6
 AA57868 standard; DNA; 38 BP.
 ID AA57868
 XX
 AC AA57868;
 XX
 DT 19-APR-2001 (first entry)
 XX
 DE Murine OPG mutagenic PCR primer #18.
 XX
 KM Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
 KM multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
 KM systemic lupus erythematosus; graft-versus-host disease; septic shock;
 KM acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
 KM coronary condition; myocardial infarction; cancer; diabetes; psoriasis;

KW endometriosiis; fever; glomerulonephritis; inflammatory bowel disease;
KW ischaemia; Parkinson's disease; PCR primer; ss.
XX Mus sp.
XX WO200103719-A2.
XX
XX 18-JAN-2001.
XX
XX 07-JUL-2000; 2000WO-US018667.
XX
XX 09-JUL-1999; 99US-00350670.
XX 09-DEC-1999; 99US-00457647.
XX
XX (AMGE-) AMGEN INC.
XX
XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
XX MPI, 2001-103031/11.
XX
XX Treating conditions leading to bone loss such as rheumatoid arthritis,
PT multiple sclerosis and asthma, comprises administering an osteoprotegerin
PT protein in conjunction with e.g. inhibitors of interleukin and tumor
PT necrosis factor alpha.
XX
XX Example 9; Page 145; 316pp; English.
XX
XX The present invention relates to a method for treating conditions leading
CC to bone loss. The method comprises administering a purified and isolated
CC osteoprotegerin (OPG) protein (AAFS783c-AAFS783b and AAB66974-AAB66976)
CC in conjunction with other substances such as tumor necrosis factor-alpha
CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet
CC activating factor (PAF) antagonists. The method is useful for treating
CC conditions leading to bone loss such as rheumatoid arthritis, multiple
CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
CC graft-versus-host disease (GVHD). Other diseases that can be treated
CC include acute pancreatitis, Alzheimer's disease, anorexia,
CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
CC psoriasis and septic shock. The present sequence is a PCR primer used in
CC the present invention
XX
XX Sequence 38 BP; 6 A; 9 C; 11 G; 12 T; 0 U; 0 Other;
SQ
XX
XX Query Match 69.0%; Score 13.8; DB 5; Length 38;
XX Best Local Similarity 88.2%; Pred. No. 3.5e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GAGTCAGAGTGTGTGA 20
DB 9 GAGTCAGAGTGTGTTC 25

RESULT 7
ACK17461
ID ACK17461 standard; DNA; 25 BP.
XX
XX ACK17461;
XX
XX 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 117442.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
OS
XX
XX US2003104410-A1.
PN

XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
PF
XX
XX 16-MAR-2001; 2001US-0276759P.
PR
XX
XX (AFfy-) AFFYMETRIX INC.
XX
XX Miltmann MP;
XX
XX MPI, 2003-567953/53.
XX
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 117442; 9pp; English.
PS
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
XX Sequence 25 BP; 7 A; 6 C; 7 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 67.0%; Score 13.4; DB 8; Length 25;
XX Best Local Similarity 93.3%; Pred. No. 5.4e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACGGAGTCAGAGTGT 15
DB 1 ACGGAGTCAGAGTGT 15

RESULT 8
AA130957/c
ID AA130957 standard; DNA; 31 BP.
XX
XX AA130957;
XX
XX 18-OCT-2001 (first entry)
XX
XX Human single nucleotide polymorphism (SNP) HIVEP1 6.
XX
XX Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
XX Homo sapiens.
OS
XX
XX Key location/Qualifiers
FT Variation replace(16,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"

XX MO20016680-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-US007268.
 XX
 PR 07-MAR-2000; 2000US-0187510P.
 XX
 PR 22-MAY-2000; 2000US-0206129P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR MPI, 2001-522952/57.
 XX
 PT Nucleic acid molecules from the human genome which include polymorphic
 PT sites, useful in methods for predicting the presence, absence or severity
 PT of a particular phenotype or disorder (e.g. diabetes) associated with a
 PT particular genotype.
 XX
 PS Claim 1; Page 119; 145bp; English.
 XX
 CC The invention relates to the identification of nucleic acid molecules
 CC (AA129513-AA131314) from the human genome which include polymorphic sites
 CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing
 XX
 SQ Sequence 31 BP; 5 A; 12 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 67.0%; Score 13.4; DB 4; Length 31;
 Best Local Similarity 93.3%; Pred. No. 5.5e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GTCAGATGTTGTGA 20
 |||||
 DB 31 GTCAGATGTTGTGA 17

RESULT 9
 AB201461
 ID AB201461 standard; DNA; 50 BP.
 XX
 AC AB201461,
 XX

DT 09-JAN-2003 (first entry)
 XX

DE Human leukocyte gene expression profiling probe SEQ ID NO 1452.
 XX

XX T7; leukocyte; gene expression profiling; allograft rejection;
 KM atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KM rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KM ss.
 XX

OS Homo sapiens.
 XX

PN MO200257414-A2.
 XX

PD 25-JUL-2002.
 XX

PF 22-OCT-2001; 2001WO-US047856.
 XX

PR 20-OCT-2000; 2000US-0241994P.
 PR 08-JUN-2001; 2001US-0296764P.
 XX

PA (BIOC-) BIOCARDIA INC.
 XX

PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;

PI Ly N, Woodward R, Quertermous T, Johnson F;
 XX
 DR MPI; 2002-636525/68.
 XX
 PT New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.
 XX
 PS Claim 1; Page 371; opp; English.

XX The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (AB200010-AB208152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 XX

SQ Sequence 50 BP; 8 A; 11 C; 12 G; 19 T; 0 U; 0 Other;
 Query Match 67.0%; Score 13.4; DB 6; Length 50;
 Best Local Similarity 93.3%; Pred. No. 5.7e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGTCAGATGTTG 17
 |||||
 DB 20 GGAGTCAGATGTTG 34

RESULT 10
 AB201133
 ID AB201133 standard; DNA; 50 BP.
 XX
 AC AB201133,
 XX

DT 09-JAN-2003 (first entry)
 XX

DE Human leukocyte gene expression profiling probe SEQ ID NO 1124.
 XX

XX T7; leukocyte; gene expression profiling; allograft rejection;
 KM atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KM rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KM ss.
 XX

OS Homo sapiens.
 XX

PN MO200257414-A2.
 XX

PD 25-JUL-2002.
 XX

PF 22-OCT-2001; 2001WO-US047856.
 XX

PR 20-OCT-2000; 2000US-0241994P.
 PR 08-JUN-2001; 2001US-0296764P.
 XX

PA (BIOC-) BIOCARDIA INC.
 XX

PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 PI Ly N, Woodward R, Quertermous T, Johnson F;

DR MPI; 2002-636525/68.
 XX

XX New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.
 XX

PS Claim 1; Page 360; opp; English.

CC	The invention relates to a system for detecting gene expression, which
CC	comprises one or two isolated DNA molecules that detect expression of a
CC	gene, where the gene corresponds to any of 8143 oligonucleotides
CC	(ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC	for leukocyte expression profiling. It is particularly useful for
CC	diagnosing a disease, monitoring (rate of) progression of a disease,
CC	predicting therapeutic outcome, determining prognosis for a patient,
CC	predicting disease complications in an individual or monitoring response
CC	to treatment in an individual. The diseases include cardiac allograft
CC	rejection, kidney allograft rejection, liver allograft rejection,
CC	atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC	rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX	
S0	Sequence 50 BP; 8 A; 11 C; 12 G; 19 T; 0 U; 0 Other;
OY	Query Match 67.0%; Score 13.4; DB 6; Length 50;
D6	Best Local Similarity 93.3%; Pred. No. 5.7e+03;
	Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	3 GGAGTCGAGTGTG 17 D6 20 GGAGTCGAGTGTG 34
RESULT 11	
ID	ABZ01467 standard; DNA; 50 BP.
XX	AC
XX	ABZ01467;
DT	09-JAN-2003 (first entry)
DE	Human leukocyte gene expression profiling probe SEQ ID NO 1458.
KW	T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe; ss.
OS	Homo sapiens.
PN	WO200257414-A2.
PD	25-JUL-2002.
PJ	22-OCT-2001; 2001WO-US047856.
PR	20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P.
PA	(BIOC-) BIOCARDIA INC.
PI	Wollgumuth J, Fry K, Matczuk G, Altman P, Prentice J, Phillips J; Ly N, Woodward R, Quertermous T, Johnson F;
DR	WPI; 2002-636525/68.
PT	New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
PS	Claim 1; Page 371; Op; English.
CC	The invention relates to a system for detecting gene expression, which
CC	comprises one or two isolated DNA molecules that detect expression of a
CC	gene, where the gene corresponds to any of 8143 oligonucleotides
CC	(ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC	for leukocyte expression profiling. It is particularly useful for
CC	diagnosing a disease, monitoring (rate of) progression of a disease,
CC	predicting therapeutic outcome, determining prognosis for a patient,
CC	predicting disease complications in an individual or monitoring response
CC	to treatment in an individual. The diseases include cardiac allograft
CC	rejection, kidney allograft rejection, liver allograft rejection,

CC	atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC	rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX	
XX	
SQ	Sequence 50 BP; 8 A; 11 C; 12 G; 19 T; 0 U; 0 Other;
OY	Query Match 67.0%; Score 13.4; DB 6; Length 50; Best Local Similarity 93.3%; Pred. No. 5.7e+03; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB	3 GGAGTCGAGTGTGG 17 20 GGAGTCGAGTGTGG 34
RESULT 12	
ID	ADD933328
XX	ADD933328 standard; DNA; 50 BP.
AC	ADD933328;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Fltl gene fragment, target for antisense phosphoramidate morpholino.
XX	
KM	Zebrafish; fltl; angiogenesis; antisense; ds.
XX	
OS	Danio rerio.
PN	W02003079776-A2.
PD	02-OCT-2003.
XX	
PF	25-MAR-2003; 2003WO-EP003089.
XX	
PR	27-MAR-2002; 2002US-0368616P.
XX	
PA	(ARTE-) ARTEMIS PHARM GMBH.
PI	Habeck HA, Schulte-Merker S;
XX	
DR	WPI, 2003-779157/73.
XX	
PT	New engineered mutant teleost embryo having reduced fltl activity, useful
PT	in forward and reverse screens to identify interacting genes in the fltl
PT	pathway, and screening for pharmaceutical agents capable of altering fltl
PT	phenotype.
XX	
PS	Claim 17; Page 33; 34pp; English.
XX	
CC	The present sequence is a 50-nucleotide fragment of a zebrafish gene,
CC	denoted fltl ADD93335, that is required for sprouting angiogenesis.
CC	Claimed antisense phosphoramidate morpholinos (PMOs) of the invention
CC	specifically inactivate a teleost fltl gene, and comprise a sequence of
CC	10-50 nucleotides that is complementary to contiguous nucleotides within
CC	a sequence selected from a group consisting of the present sequence,
CC	those given in ADD93317-ADD93371 and nucleotides 1-400 of fltl ADD93315.
CC	Claimed engineered mutant zebrafish teleost embryos have reduced fltl
CC	activity, which causes a phenotype of normal assembly of main circulatory
CC	routes and a reduction in sprouted vessels. The fltl phenotype may be
CC	caused by an exogenously added nucleic acid inhibitor that specifically
CC	inhibits fltl, such as one of the claimed PMOs. The mutant teleost
CC	embryos are used in genetic and compound screens to identify members of
CC	the fltl signaling pathway and compounds that affect sprouting
CC	angiogenesis.
SQ	Sequence 50 BP; 15 A; 6 C; 12 G; 17 T; 0 U; 0 Other;
OY	Query Match 67.0%; Score 13.4; DB 9; Length 50; Best Local Similarity 93.3%; Pred. No. 5.7e+03; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 6 GTCAGATGTTGTGA 20

DB 26 GTGAGATGTTGTGA 40

RESULT 13
AB205433
ID AB205433 standard; DNA; 50 BP.
XX
AC AB205433;
XX
DT 09-JUN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 5424.
XX
KM T7; leukocyte; gene expression profiling; allograft rejection;
KM atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KM rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KM ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J,
PI Ly N, Woodward R, Quertermous T, Johnson F;
DR MPI; 2002-636525/68.
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 503; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 17 A; 5 C; 20 G; 8 T; 0 U; 0 Other;
XX
Query Match 66.0%; Score 13.2; DB 6; Length 50;
Best Local Similarity 83.3%; Pred. No. 7.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 3 GGAGTCAGAGTGTGTGA 20
DB 6 GAAGTCAGAGAGTTTGA 23

RESULT 14
AC135316/c
ID AC135316 standard; DNA; 25 BP.
XX
AC AC135316;
XX
DT 13-OCT-2003 (first entry)
XX

XX
DE Human microarray DNA oligonucleotide SEQ ID NO 35307.
XX
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; biallelic marker; polymorphism; human;
KM cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR MPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 35307; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labeled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
XX
Query Match 65.0%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 GTCAAGATCTGT 18
DB 19 GTCAAGATCTGT 7

RESULT 15
ACD52070/c
ID ACD52070 standard; RNA; 17 BP.
XX
AC ACD52070;
XX
DT 24-SEP-2003 (first entry)
XX
DE HBV inozyme substrate sequence #200.

Search completed: April 15, 2004, 12:17:54
 Job time : 256 secs

```

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis B virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLAT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGEN J.
PA (MORR/) MORRISSEY D.
PA (PAYC/) PAYCO P.
PA (LEEP/) LEE P.
PA (DRAE/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blart L, Macejak D, Mcswigen J, Morrissey D, Payco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Example 1; Page 154; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberzyme sequences
CC disclosed in the present invention
XX
SQ Sequence 17 BP; 5 A; 6 C; 2 G; 0 T; 4 U; 0 Other;

```

Query Match 64.0%; Score 12.8; DB 7; Length 17;

Best Local Similarity 87.5%; Pred. No. 1e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGTCAGGATGTTGT 18

DB 16 GGACTCAGAGTGTGT 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 10:46:21 ; Search time 2007 Seconds
(without alignments)
297.580 Million cell updates/sec

Title: US-10-006-430-76

Perfect score: 20

Sequence: 1 acgagatcagatgttga 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 138346

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_ges_hum:*
18: em_ges_inv:*
19: em_ges_pln:*
20: em_ges_vit:*
21: em_ges_fun:*
22: em_ges_mam:*
23: em_ges_mus:*
24: em_ges_pro:*
25: em_ges_rod:*
26: em_ges_pig:*
27: em_ges_vrl:*
28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	72.0	48	28	AZ318461
2	14.2	71.0	33	12	BM398979
3	12.8	64.0	45	28	BH619838
4	12.6	63.0	40	9	AI642028

Result No.	Score	Query Match	Length	DB ID	Description
5	12.6	63.0	50	9	AU103832
6	12.6	63.0	50	28	AZ817361
7	12.2	61.0	36	28	AZ487594
8	12.2	61.0	50	9	AU102676
9	12.2	61.0	43	28	AZ346681
10	12.2	60.0	43	28	AZ807113
11	12.2	60.0	50	9	AU105073
12	12.2	60.0	50	9	AU105086
13	11.8	59.0	30	14	CF333773
14	11.8	59.0	41	29	DR17N10T
15	11.8	59.0	41	12	B052697
16	11.6	58.0	40	9	A1080507
17	11.6	58.0	40	28	AQ072891
18	11.6	58.0	42	12	B039854
19	11.6	58.0	43	9	AA096781
20	11.6	58.0	47	28	AZ341255
21	11.6	58.0	47	28	AZ767804
22	11.4	57.0	37	9	AU256480
23	11.4	57.0	41	28	AZ412439
24	11.2	56.0	42	9	A1833018
25	11.2	56.0	43	9	AA972845
26	11.2	56.0	43	28	AZ464392
27	11.2	56.0	45	28	AZ480635
28	11.2	56.0	48	29	AL765485
29	11.2	56.0	50	9	AU102678
30	11.2	56.0	50	9	AU103858
31	11.2	56.0	50	9	AU103914
32	11.2	56.0	50	28	BZ286230
33	11.2	56.0	32	12	B1818900
34	11.2	56.0	32	12	B1824853
35	11.2	56.0	35	14	U44207
36	11.2	56.0	37	14	R36016
37	11.2	56.0	39	29	CG12794
38	11.2	56.0	41	14	CF312745
39	11.2	56.0	43	9	AA911375
40	11.2	56.0	43	29	AL948959
41	11.2	56.0	44	28	AZ787976
42	11.2	56.0	45	12	B066342
43	11.2	56.0	46	14	T98810
44	11.2	56.0	46	14	T98810
45	11.2	56.0	48	28	BH621788

ALIGNMENTS

RESULT 1
LOCUS AZ318461 48 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0037A17R Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0037A17 R, genomic survey sequence.

ACCESSION AZ318461
VERSION AZ318461.1 GI:10368252

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0037 row: A column: 17
 Seg primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 48.

FEATURES

source

1..48
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U0010037A17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid U0010037 library"
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF12072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 72.0%; Score 14.4; DB 28; Length 48;
 Best Local Similarity 93.8%; Pred. No. 2e+04;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AACTCAGGATGTTGTGA 20
 |||
 14 AGTTAGGATGTTGTGA 29

RESULT 2

LOCUS

BM398979/c 33 bp mRNA linear EST 17-JAN-2002
 5009-0-51-D10.t.1 Chlcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM398979

VERSION BM398979.1 GI:18199032

KEYWORDS EST

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

Hydrothermal: Alveolata; Ciliophora; Oligohymenophorea;

1 (bases 1 to 33)

Turkewitz, A.P., Karier, K.M., Uhm, C., Orlas, E., Kirk, K.E.,

Frankel, J., and Klobutcher, L.

EST from Tetrahymena thermophila, strain CUA28.1, growing cells

Unpublished (2002)

CONTACT: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seg primer: T3

Location/Qualifiers

1..33

/organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CUA28.1"
 /db_xref="taxon:5911"
 /clone_lib="Chlcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 71.0%; Score 14.2; DB 12; Length 33;
 Best Local Similarity 84.2%; Pred. No. 2.2e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGAGTCAGGATGTTGTGA 20
 |||
 25 CGGAGTCAGGATGTTGTGA 7

RESULT 3

LOCUS

BH619838 45 bp DNA linear GSS 30-JAN-2002
 1007063B01.1BL_y1 1007 - Rescuedu Grid H Zea mays genomic, genomic survey sequence.

DEFINITION BH619838

ACCESSION BH619838

VERSION BH619838.1 GI:18431010

KEYWORDS GSS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 45)

Walbot V.

Maize genomic sequences found using engineered Rescuedu transposon

Unpublished (2001)

CONTACT: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1007063 column: 18

Class: transposon-tagged.

Location/Qualifiers

1..45

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A186/B73"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="1007 - Rescuedu Grid H"

/note="Organ: leaf; Vector: Rescuedu (engineered from

Bluescript backbone); Site_1: BamHI; Site_2: BglII;

Rescuedu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on Rescuedu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'Rescuedu'. Grid H was grown at Berkeley in 2001. DNA

was extracted from leaf punches, double digested using

BamHI and BglII, and ligated to form circular plasmids.

DH10B cells were transformed and then screened on LB

plates with ampicillin."

ORIGIN

Query Match 64.0%; Score 12.8; DB 28; Length 45;
 Best Local Similarity 87.5%; Pred. No. 1e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGGAGTCAGGATCTTG 17
 |||||
 3 CGGAGTCAGGATCTTG 18

RESULT 4
 A1642028/c
 LOCUS ub74h04.x1 Soares mammary_gland NMLMG Mus musculus cDNA clone
 DEFINITION IMAGE:183511.3; similar to SW:UCP3_MOUSE P56501 MITOCHONDRIAL UNCOUPLING PROTEIN 3; mRNA sequence.

ACCESSION A1642028
 VERSION A1642028.1 GI:4720503
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE 1 (bases 1 to 40)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.lhml.gov) for further information.
 MGI:905979
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 Possible reversed clone: similarity on wrong strand
 High quality sequence stop: 1.

FEATURES
 source
 1..40
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:183511"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /lab_host="DH10B"
 /clone_lib="Soares mammary gland NMLMG"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptor (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 63.0%; Score 12.6; DB 9; Length 40;
 Best Local Similarity 78.9%; Pred. No. 1.2e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACCGAGTCAGGATCTTG 19
 |||||
 24 AAGGAGTCAGGAGCTTG 6

RESULT 5
 AUI03832
 LOCUS AUI03832 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION HRC10538, mRNA sequence.
 ACCESSION AUI03832
 VERSION AUI03832.1 GI:13553353
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 TITLE 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL
 MEDLINE 21270072
 PUBMED 11375928

COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source
 1..50
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HRC10538"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
 Query Match 63.0%; Score 12.6; DB 9; Length 50;
 Best Local Similarity 78.9%; Pred. No. 1.3e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACCGAGTCAGGATCTTG 19
 |||||
 32 ACGTAGTCAGGCTTG 50

RESULT 6
 A2817361
 LOCUS A2817361 50 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0086K21R Mouse 10kb plasmid UGCGM library Mus musculus genomic clone UGCGM0086K21 R, genomic survey sequence.

ACCESSION A2817361
 VERSION A2817361.1 GI:12987365
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE 1 (bases 1 to 50)
 Dunn, D., Aoyagi, B., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)

JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 1000 Std Error: 0.00
 Plate: 0086 row: K column: 21
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 50.
 Location/Qualifiers
 1..50

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0086K21"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCCIM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

ORIGIN

```
Query Match      63.0%; Score 12.6; DB 28; Length 50;
Best Local Similarity 78.9%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      2  CGAGTCAGATGTTGTGA 20
      |||||
Db      25  CTGAGCGAGATGATGTAA 43
```

RESULT 7
AZ487594/c
LOCUS AZ487594 36 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0317B1F Mouse 10kb plasmid UGCCIM library Mus musculus genomic
clone UGCCIM0317B21 F, genomic survey sequence.
ACCESSION AZ487594
VERSION AZ487594.1 GI:10655481
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 36)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weisss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0317 row: B column: 21
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends

High quality sequence stop: 36.
Location/Qualifiers
1. .36

FEATURES
source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0317B21"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCCIM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

ORIGIN

```
Query Match      61.0%; Score 12.2; DB 28; Length 36;
Best Local Similarity 82.4%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2  CGAGTCAGATGTTGT 18
      |||||
Db      30  CGAGTCATCATGTTGT 14
```

RESULT 8
AUI02676/c
LOCUS AUI02676 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AUI02676 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HS101211, mRNA sequence.
ACCESSION AUI02676
VERSION AUI02676.1 GI:13552197
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 50)

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,T., See,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source

ORIGIN
/clone="HS101211"
/clone_lib="Sugano Homo sapiens cDNA library"

Query Match 61.0%; Score 12.2; DB 9; Length 50;
Best Local Similarity 82.4%; Pred. No. 2e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGAGTCAGATGTTGTG 19
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DB 18 GGAGTCAGCTGTTGTG 2

RESULT 9
AZ346681/c 43 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
1M0082G01F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0082G01 F, genomic survey sequence.
ACCESSION
AZ346681
VERSION
AZ346681.1 GI:10425918
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: G column: 01
Seq primer: CATTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers

FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0082G01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into

ORIGIN
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 60.0%; Score 12; DB 28; Length 43;
Best Local Similarity 75.0%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCGACTCAGATGTTGTGA 20
|||||
DB 25 AAGGACTGAGGAGGGGTGA 6

RESULT 10
AZ807113/c 43 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION
2M0069G09R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCG2M0069G09 R, genomic survey sequence.
ACCESSION
AZ807113
VERSION
AZ807113.1 GI:12971138
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0063 row: G column: 02
Seq primer: CAACAAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers

FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis thaliana Carboxyl methyltransferase overexpression line."

ORIGIN

Query Match 59.0%; Score 11.8; DB 14; Length 30;
Best Local Similarity 86.7%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GTCGAGATGTTGTA 20
DB 13 GTCGATGTTTGTGA 27

RESULT 14
DRI7N10T/c 41 bp DNA linear GSS 21-NOV-2002
LOCUS Dario rerio genomic clone DKEY-17N10, genomic survey sequence.
DEFINITION AL733216
ACCESSION AL733216.1 GI:21342233
VERSION
KEYWORDS
SOURCE
ORGANISM

Dario rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Dario.
1 (bases 1 to 41)
Humphrey, S.J., Huckle, E. and Hunt, S.E.
Direct Submission
Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphrey@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 17N10. 17N10 is part of the Dariokey BAC library created by R. Plaetzer and N.V. Keygene.

COMMENT

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers

1.41
/organism="Dario rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-17N10"
/issue_type="Testis"
/note="Vector pindigobAC-536"

ORIGIN

Query Match 59.0%; Score 11.8; DB 29; Length 41;
Best Local Similarity 86.7%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGGAGTCAGATGTT 16
DB 36 CGAAGTCAGATGTT 22

RESULT 15
BJ052697 43 bp mRNA linear EST 29-SEP-2003
LOCUS BJ052697 NIBB Mochii normalized Xenopus neurula library Xenopus
DEFINITION laevis cDNA clone XL042f11 3', mRNA sequence.
ACCESSION BJ052697
VERSION BJ052697.1 GI:17498743
KEYWORDS
SOURCE
ORGANISM

Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.
1 (bases 1 to 43)
Kitayama, A., Teraoka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara, Y.
Expressed genes in X. laevis embryo

JOURNAL

Unpublished (2001)
Contact: Tadao Shin-i

COMMENT

Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsuhigene@nig.ac.jp
The information of this clone is available through the following URL.
<http://xenopus.nibb.ac.jp/>

FEATURES

1.43
Location/Qualifiers
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL042f11"
/issue_type="whole embryo"
/dev_stage="stage 15"
/clone_1ib="NIBB Mochii normalized Xenopus neurula library"

ORIGIN

Query Match 59.0%; Score 11.8; DB 12; Length 43;
Best Local Similarity 86.7%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGTCAGATGTTGTG 19
DB 22 AGTCGATGTTCTG 36

Search completed: April 15, 2004, 12:51:29
Job time : 2008 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 10:50:39 ; Search time 1731 Seconds
(without alignments)
500.786 Million cell updates/sec

Title: US-10-006-430-76

Perfect score: 20

Sequence: 1 acgagatcagatgtctga 20

Scoring table: IDENTITY NUC
Gap0 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 1603530

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_of:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pin:*
35: em_hcg_rnd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	20	6	BD230525
2	14.2	71.0	20	6	BD230607
3	13.8	69.0	38	6	AX076651
4	13.4	67.0	31	6	AX249366
5	13.4	67.0	50	6	AX923380
6	13.2	66.0	28	6	B05487
7	13	65.0	32	6	I07146
8	12.8	64.0	20	6	E40736
9	12.8	64.0	24	6	E15132
10	12.8	64.0	27	6	I57990
11	12.8	64.0	29	6	E26920
12	12.8	64.0	30	6	AR064721
13	12.8	64.0	30	6	AR089162
14	12.8	64.0	30	6	AR153238
15	12.8	64.0	47	6	AR291326
16	12.8	64.0	50	6	AX377926
17	12.6	63.0	41	6	AX515735
18	12.6	63.0	41	6	AX518330
19	12.6	63.0	47	6	AR288483
20	12.4	62.0	20	6	AR212002
21	12.4	62.0	20	6	AR315163
22	12.4	62.0	21	6	AR049055
23	12.4	62.0	21	6	AX095333
24	12.4	62.0	23	6	E59205
25	12.4	62.0	23	6	E64386
26	12.4	62.0	26	6	BD168169
27	12.2	61.0	18	6	AR295893
28	12.2	61.0	21	6	BD177428
29	12.2	61.0	21	6	BD226172
30	12.2	61.0	25	6	AR242533
31	12.2	61.0	26	6	AX201524
32	12.2	61.0	27	6	AX752019
33	12.2	61.0	28	6	AR283917
34	12.2	61.0	28	6	BD005489
35	12.2	61.0	31	6	AR090075
36	12.2	61.0	31	6	AR197110
37	12.2	61.0	31	6	AR259264
38	12.2	61.0	33	6	AR261271
39	12.2	61.0	33	6	AR400534
40	12.2	61.0	33	6	AR405801
41	12.2	61.0	33	6	AX201048
42	12.2	61.0	33	6	AX267847
43	12.2	61.0	34	6	AR142300
44	12.2	61.0	34	6	I27173
45	12.2	61.0	34	6	I32754

ALIGNMENTS

RESULT 1
BD230525
LOCUS BD230525 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes.
ACCESSION BD230525
VERSION BD230525.1 GI:33040295
KEYWORDS JP 2002530091-A/394.
SOURCE
ORGANISM
Canis familiaris
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 20)
Galibert, F. and Andre, C.
Total genome radiation hybrid map of canine genome and its use for

JOURNAL Identification of interesting genes
Patent: JP 2002530091-A 394 17-SEP-2002;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
OS Canis familiaris (dog)
COMMENT PN JP 2002530091-A/394
PD 17-SEP-2002
PF 15-NOV-1999 JP 2000582596
PR 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT, CATHERINE ANDRE
PC C12N15/09, C12Q1/68, C12N15/00
CC B00237R
FH Key
FT source
FEATURES Location/Qualifiers
source 1..20
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"

ORIGIN
Query Match 71.0%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGAGTCAGATGTTGTA 20
|||||
DB 1 CGGAGACTGATGATGTA 19

RESULT 2
BD230607 20 bp DNA linear PAT 17-JUL-2003
LOCUS BD230607
DEFINITION Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes.
ACCESSION BD230607.1 GI:33040377
KEYWORDS JP 2002530091-A/476.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis;
REFERENCE 1 Ibañez 1 to 20
AUTHORS Galibert, F. and Andre, C.
TITLE Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes
JOURNAL PATENT: JP 2002530091-A 476 17-SEP-2002;
COMMENT CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
OS Canis familiaris (dog)
PN JP 2002530091-A/476
PD 17-SEP-2002
PF 15-NOV-1999 JP 2000582596
PR 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT, CATHERINE ANDRE
PC C12N15/09, C12Q1/68, C12N15/00
CC B00237R
FH Key
FT source
FEATURES Location/Qualifiers
source 1..20
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"

ORIGIN
Query Match 71.0%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGAGTCAGATGTTGTA 20
|||||
DB 1 CGGAGACTGATGATGTA 19

RESULT 3
AX076651 38 bp DNA linear PAT 06-FEB-2001
LOCUS AX076651
DEFINITION Sequence 167 from Patent WO0103719.
ACCESSION AX076651
VERSION AX076651.1 GI:12711188
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boyle, W.J., Lacey, D.L., Calzone, F.J., Chang, M.S. and Senaldi, G.
TITLE Combination therapy for conditions leading to bone loss
JOURNAL Patent: WO 0103719-A 167 18-JAN-2001;
Amgen Inc. (US)
FEATURES Location/Qualifiers
source 1..38
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer for deletion mutant."

ORIGIN
Query Match 69.0%; Score 13.8; DB 6; Length 38;
Best Local Similarity 88.2%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGTCAGATGTTGTA 20
|||||
DB 9 GAGTCAGATGTTTCA 25

RESULT 4
AX249366/c 31 bp DNA linear PAT 28-SEP-2001
LOCUS AX249366
DEFINITION Sequence 1445 from Patent WO0166800.
ACCESSION AX249366
VERSION AX249366.1 GI:15863989
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1445 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
source 1..31
/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN
Query Match 67.0%; Score 13.4; DB 6; Length 31;
Best Local Similarity 93.3%; Pred. No. 2.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GTCAGATGTTGTA 20
|||||
DB 31 GTCAGATGTTGTA 17

RESULT 5
AX923380 50 bp DNA linear PAT 18-DEC-2003
LOCUS AX923380
DEFINITION Sequence 14 from Patent WO03079776.
ACCESSION AX923380
VERSION AX923380.1 GI:40216429
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Haback,H.A. and Schulte-Merker,S.
TITLE Identification of the flt1 gene required for angiogenesis in zebrafish, and uses thereof
JOURNAL Patent: WO 03079776-A 14 02-OCT-2003;
Exelixis Deutschland GmbH (DE)
FEATURES Location/Qualifiers
source 1..50
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: PMO 12"

ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 50;
Best Local Similarity 93.3%; Pred. No. 2.6e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GTGAGATGTGTGA 20
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Db 26 GTGAGATGTGTGA 40

RESULT 6
E05487 28 bp DNA linear PAT 29-SEP-1997
LOCUS PCR primer.
DEFINITION E05487
ACCESSION E05487
VERSION E05487.1 GI:2173676
KEYWORDS JP 1993244982-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 28)
AUTHORS Nakatani,T., Gomi,H., Jiyon,W. and Noguchi,H.
TITLE ANTHROPOMORPHISM B-B10
JOURNAL Patent: JP 1993244982-A 15 24-SEP-1993;
SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD, BIOTEST AG,
INOTERAPII LAB
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
FN JP 1993244982-A/15
PD 24-SEP-1993
PF 06-DEC-1991 JP 1991323319
PI NAKATANI TOMOSUKE, GOMI HIDEYUKI, JIYON WAI DENESU, PI
NOGUCHI HIROSHI
PC C12P21/08,A61K39/395//C12N5/10,C12N15/13,G01N33/577; CC
strandness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
FEATURES Location/Qualifiers
source 1..28
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 28;
Best Local Similarity 83.3%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACCGATCAGATGTGT 18
|||
Db 1 ACTGATCAGAGATGT 18

RESULT 7
I07146/c 32 bp DNA linear PAT 02-DEC-1994
LOCUS 107146

DEFINITION Sequence 5 from Patent EP 0341892.
ACCESSION I07146
VERSION I07146.1 GI:589824
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Ingolia,T.D., Kovacevic,S., Miller,J.R. and Skatrud,P.L.
TITLE Recombinant DNA expression vectors and DNA compounds that encode deacetoxycephalosporin C synthetase
JOURNAL Patent: EP 0341892-A1 5 15-NOV-1989;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 65.0%; Score 13; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ACTCAGATGTGTG 17
|||
Db 18 ACTCAGATGTGTG 6

RESULT 8
E40736 20 bp DNA linear PAT 31-JAN-2002
LOCUS Antihuman Fas humanized antibody-containing antirheumatic.
DEFINITION E40736
ACCESSION E40736
VERSION E40736.1 GI:18627325
KEYWORDS JP 2000154149-A/107.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Serizawa,N., Hanyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.
TITLE Antihuman Fas humanized antibody-containing antirheumatic
JOURNAL Patent: JP 2000154149-A 107 06-JUN-2000;
SANKYO CO LTD
COMMENT OS Artificial Sequence
FN JP 2000154149-A/107
PD 06-JUN-2000
PF 17-SEP-1999 JP 1999263984
PI NOBUKI SERIZAWA,HIDEYUKI HANYAMA,WATARU TAKAHASHI, PI KAORI
NAKAHARA,
PI SHIN YONEHARA
PC A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00
CC
FH Key location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 6.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTCAGATGTGTGA 20
|||
Db 4 AGTGGGATGTGTGA 19

RESULT 9
E16132

LOCUS E16132 24 bp DNA linear PAT 28-JUL-1999
DEFINITION Sequence of Ecs-1-binding motif.
ACCESSION E16132
VERSION E16132.1 GI:5710815
KEYWORDS JP 1998137000-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Taniguchi N.
TITLE SCREENING OF METASTASIS SUPPRESSOR
JOURNAL Patent: JP 198137000-A 1 28-MAR-1998;
SUNTORY LTD, TANIGUCHI NAOYUKI
COMMENT OS None
NC Artificial sequences.
PN JP 1998137000-A/1
PD 26-MAY-1998
PF 01-NOV-1998 JP 1996305486
PI TANIGUCHI NAOYUKI
PC C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566//C12N15/09;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
FH key Location/Qualifiers
FT source 1..24
LOCATION/Qualifiers
1..24
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
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Best Local Similarity 87.5%; Pred. No. 6e+04; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2;

Qy 3 GGAGTCAGATGTTGT 18
Db 2 GGAGTCAGATGTTGT 17

RESULT 10
LOCUS 157990 27 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5610137.
ACCESSION 157990
VERSION 157990.1 GI:2483054
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Townes, T.M. and McCune, S.L.
TITLE Transgenic, cross-linked hemoglobin
JOURNAL Patent: US 5610137-A 6 11-MAR-1997;
FEATURES Location/Qualifiers
1..27
source /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 64.0%; Score 12.8; DB 6; Length 27;
Best Local Similarity 87.5%; Pred. No. 6e+04; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2;

Qy 3 GGAGTCAGATGTTGT 18
Db 23 GGAGTCAGATGTTGT 8

RESULT 11

LOCUS E26920 29 bp DNA linear PAT 18-JUN-2001
DEFINITION Mutant secretory device enzyme capable of efficiently secreting
ACCESSION E26920
VERSION E26920.1 GI:13026340
KEYWORDS JP 199169182-A/11.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Takashi, K., Yoko, A. and Hideaki, Y.
TITLE Mutant secretory device enzyme capable of efficiently secreting
JOURNAL protein into medium in coryneform bacterium
Patent: JP 199169182-A 11 29-JUN-1999;
MITSUBISHI CHEM CORP
COMMENT OS Unidentified
PN JP 199169182-A/11
PD 29-JUN-1999
PF 10-DEC-1997 JP 1997361768
PI TAKASHI KOBAYASHI, YOKO ASAI, HIDEAKI YUKAWA
PC C12N15/09, C12N1/21, C12P21/02//C12N15/09, C12R1:13, (C12N1/21,
PC C12R1:19),
PC (C12N1/21, C12R1:13), (C12P21/02, C12R1:19), C12N15/00, (C12N15/00,
PC C12R1:13)
CC Strandedness: Single;
CC Topology: linear;
FH key Location/Qualifiers
FT source 1..29
LOCATION/Qualifiers
1..29
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 64.0%; Score 12.8; DB 6; Length 29;
Best Local Similarity 87.5%; Pred. No. 6e+04; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2;

Qy 1 ACCGAGTCAGATGTT 16
Db 14 ACCGAGTCAGATGTT 29

RESULT 12
LOCUS AR064721 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 37 from patent US 5849306.
ACCESSION AR064721
VERSION AR064721.1 GI:5994937
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Sim, K.lee., Chitnis, C., Miller, L.H., Peterson, D.S., Su, X.-Z. and
TITLE Binding domains from Plasmodium vivax and Plasmodium falciparum
JOURNAL erythrocyte binding proteins
Patent: US 5849306-A 37 15-DEC-1998;
FEATURES Location/Qualifiers
1..30
source /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 64.0%; Score 12.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 6e+04; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2;


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QY      5 AGTCAGAGATGTTGTA 20
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      30 ACTCAGAGAGTGTGTA 15

RESULT 13
LOCUS   AR089162
DEFINITION
Sequence 20 from patent US 5993827.
ACCESSION AR089162
VERSION   AR089162.1 GI:10015919
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS  Sim,K.Lee., Chitins,C., Miller,L.H., Peterson,D.S., Su,X.-Z. and
          Wellem's,T.E.
TITLE     Binding domains from plasmodium vivax and plasmodium falciparum
          erythrocyte binding proteins
JOURNAL   Patent: US 5993827-A 20 30-NOV-1999;
FEATURES
SOURCE    Location/Qualifiers
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          /mol_type="unassigned DNA"

ORIGIN
Query Match      64.0%; Score 12.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AGTCAGAGATGTTGTA 20
      1 ||||| |||||
      30 ACTCAGAGAGTGTGTA 15

RESULT 14
LOCUS   AR153238
DEFINITION
Sequence 240 from patent US 6235480.
ACCESSION AR153238
VERSION   AR153238.1 GI:15120770
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS  Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,
          Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,
          Olson,R.J., Wood,K.V. and Welch,R.
TITLE     Detection of nucleic acid hybrids
JOURNAL   Patent: US 6235480-A 240 22-MAY-2001;
FEATURES
SOURCE    Location/Qualifiers
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          /mol_type="unassigned DNA"

ORIGIN
Query Match      64.0%; Score 12.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AGTCAGAGATGTTGTA 20
      1 ||||| |||||
      2 AGTCAGAGAGTGTGTA 17

RESULT 15
LOCUS   AR291326/C
DEFINITION
Sequence 3061 from patent US 6537751.
ACCESSION AR291326
VERSION   AR291326.1 GI:31678610

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KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 47)
AUTHORS  Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE     Biallelic markers for use in constructing a high density
          disequilibrium map of the human genome
JOURNAL   Patent: US 6537751-A 3061 25-MAR-2003;
FEATURES
SOURCE    Location/Qualifiers
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          /organism="unknown"
          /mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 77.8%; Pred. No. 5.9e+04;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 ACCGACTCAGATGTTGT 18
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      37 ACCGGGTGAGATGTTGT 20
      1 ||||| |||||

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Job time : 1735 secs

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 12:18:05 ; Search time 234 Seconds

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Title: US-10-006-430-76

Perfect score: 20
Sequence: 1 acggagtcagatgtgtga 20

Scoring table:

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Searched: 2890132 seqs, 2237290429 residues

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Listing first 45 summaries

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- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	14	US-10-006-430-76
2	20	100.0	50	15	US-10-131-827-4670
3	15.4	77.0	47	15	US-10-170-097-1178
4	13.8	69.0	38	11	US-09-405-032-167
5	13.4	67.0	25	14	US-10-098-263B-117442
6	13.4	67.0	31	9	US-09-801-274-1445
7	13.4	67.0	50	15	US-10-402-365-14
8	13.4	67.0	50	15	US-10-131-827-1124
9	13.4	67.0	50	15	US-10-131-827-1452
10	13.4	67.0	50	15	US-10-131-827-1458
11	13.2	66.0	50	15	US-10-131-827-3424
12	13	65.0	25	14	US-10-098-263B-35307
13	12.8	64.0	25	14	US-09-877-478-901
14	12.8	64.0	17	10	US-09-877-478-901
15	12.8	64.0	17	12	US-10-342-902-200

c 16	12.8	64.0	17	12	US-10-342-902-901	Sequence 901, App
c 17	12.8	64.0	18	9	US-09-969-373-1732	Sequence 1732, App
c 18	12.8	64.0	25	14	US-10-215-112-5569	Sequence 5569, App
c 19	12.8	64.0	25	14	US-10-098-263B-27690	Sequence 27690, App
c 20	12.8	64.0	25	14	US-10-098-263B-69440	Sequence 69440, App
c 21	12.8	64.0	25	14	US-10-098-263B-81262	Sequence 81262, App
c 22	12.8	64.0	25	14	US-10-098-263B-113668	Sequence 113668, App
c 23	12.8	64.0	30	9	US-09-790-417-240	Sequence 240, App
c 24	12.8	64.0	30	13	US-10-153-273-37	Sequence 37, App1
c 25	12.8	64.0	31	10	US-09-912-263-97	Sequence 97, App1
c 26	12.8	64.0	47	15	US-10-345-143-3061	Sequence 3061, App
c 27	12.8	64.0	50	15	US-10-131-827-2091	Sequence 2091, App
c 28	12.6	63.0	25	14	US-10-098-263B-11446	Sequence 11446, App
c 29	12.6	63.0	25	14	US-10-098-263B-17508	Sequence 17508, App
c 30	12.6	63.0	25	14	US-10-098-263B-60520	Sequence 60520, App
c 31	12.6	63.0	25	14	US-10-098-263B-105128	Sequence 105128, App
c 32	12.6	63.0	25	14	US-10-098-263B-116073	Sequence 116073, App
c 33	12.6	63.0	47	15	US-10-098-263B-127368	Sequence 127368, App
c 34	12.6	63.0	47	15	US-10-349-143-218	Sequence 218, App
c 35	12.6	63.0	50	15	US-10-131-827-1177	Sequence 1177, App
c 36	12.4	62.0	20	15	US-10-289-762-5700	Sequence 5700, App
c 37	12.4	62.0	21	9	US-09-753-143-44	Sequence 44, App1
c 38	12.4	62.0	25	14	US-10-098-263B-44418	Sequence 44418, App
c 39	12.4	62.0	26	12	US-10-398-877-76	Sequence 76, App1
c 40	12.4	62.0	29	12	US-10-231-079-58	Sequence 58, App1
c 41	12.4	62.0	50	15	US-10-131-827-1177	Sequence 1177, App
c 42	12.4	62.0	50	15	US-10-131-827-1178	Sequence 1178, App
c 43	12.4	61.0	17	10	US-09-877-478-201	Sequence 201, App
c 44	12.2	61.0	17	12	US-10-342-902-201	Sequence 201, App
c 45	12.2	61.0	18	15	US-10-349-143-7628	Sequence 7628, App

ALIGNMENTS

RESULT 1
US-10-006-430-76
Sequence 76, Application US/10006430
Publication No. US20030113914A1
GENERAL INFORMATION:
APPLICANT: Mark J. Graham
TITLE OF INVENTION: KENNETH DOBLE
FILE REFERENCE: RTS-0341
CURRENT APPLICATION NUMBER: US/10/006,430
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 76
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-430-76

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGGATCAGATGTTGTGA 20
DB 1 ACAGGATCAGATGTTGTGA 20

RESULT 2
US-10-131-827-4670/c
Sequence 4670, Application US/10131827
Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc

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/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
/ FILE REFERENCE: 506612000120
/ CURRENT APPLICATION NUMBER: US/10/131,827
/ CURRENT FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: US 10/006,290
/ PRIOR FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: US 60/296,764
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 9090
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4670
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-131-827-4670

Query Match          100.0%; Score 20; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGGAGTCAGATGTTGTA 20
DB 46 ACGGAGTCAGATGTTGTA 27

RESULT 3
US-10-170-097-1178/c
/ Sequence 1178, Application US/10170097
/ Publication No. US20030228582A1
/ GENERAL INFORMATION:
/ APPLICANT: Blumenfeld, Marta
/ APPLICANT: Bouquelere, Lydie
/ APPLICANT: Chumakov, Ilya
/ APPLICANT: Cohen, Amick
/ TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
/ TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
/ FILE REFERENCE: GEN-114XC2D1
/ CURRENT APPLICATION NUMBER: US/10/170,097
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: US 09/641,638
/ PRIOR FILING DATE: 2000-08-16
/ PRIOR APPLICATION NUMBER: US 09/502,330
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: US 60/133,200
/ PRIOR FILING DATE: 1999-05-07
/ PRIOR APPLICATION NUMBER: US 09/275,267
/ PRIOR FILING DATE: 1999-03-23
/ PRIOR APPLICATION NUMBER: US 60/119,917
/ PRIOR FILING DATE: 1999-02-12
/ NUMBER OF SEQ ID NOS: 1304
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1178
/ LENGTH: 47
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 24
/ OTHER INFORMATION: 10-298-122 : polymorphic base C or T
US-10-170-097-1178

Query Match          77.0%; Score 15.4; DB 15; Length 47;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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/ Sequence 167, Application US/09405032
/ Publication No. US20030207827A1
/ GENERAL INFORMATION:
/ APPLICANT: Amgen Inc.
/ TITLE OF INVENTION: OSTEOPROTEGERIN
/ NUMBER OF SEQUENCES: 168
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Amgen Inc.
/ STREET: 1840 Dehavenland Drive
/ CITY: Thousand Oaks
/ STATE: California
/ COUNTRY: United States
/ ZIP: 91320
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ APPLICATION DATA:
/ FILING DATE: 24-Sep-1999
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Winter, Robert B.
/ REFERENCE/DOCKET NUMBER: A-378-CIP2
/ INFORMATION FOR SEQ ID NO: 167:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 38 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-09-405-032-167

Query Match          69.0%; Score 13.8; DB 11; Length 38;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGTCAGATGTTGCA 20
DB 9 GAGTCAGATGTTGCA 25

RESULT 5
US-10-098-263B-117442
/ Sequence 117442, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 117442
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-117442

Query Match          67.0%; Score 13.4; DB 14; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 6
US-09-801-274-1445/C
; Sequence 1445, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Carcilli, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1445
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1445

Query Match      67.0%; Score 13.4; DB 9; Length 31;
Best Local Similarity 93.3%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  GTGAGATGTTGTGA 20
Db      31  GTGAGATGTTGTGA 17

RESULT 7
US-10-402-365-14
; Sequence 14, Application US/10402365
; Publication No. US20030229913A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS DEUTSCHLAND GMBH
; TITLE OF INVENTION: Identification of the FLT1 Gene Required for Angiogenesis in
; FILE REFERENCE: AR03-003C
; CURRENT APPLICATION NUMBER: US/10/402,365
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/368,616
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Synthetic
US-10-402-365-14

Query Match      67.0%; Score 13.4; DB 15; Length 50;
Best Local Similarity 93.3%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  GTGAGATGTTGTGA 20
Db      26  GTGAGATGTTGTGA 40

RESULT 8
US-10-131-827-1124
; Sequence 1124, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
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; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1124
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1124

Query Match      67.0%; Score 13.4; DB 15; Length 50;
Best Local Similarity 93.3%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  GGAGTCAGATGTTG 17
Db      20  GGAGTCAGATGTTG 34

RESULT 9
US-10-131-827-1452
; Sequence 1452, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1452
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1452

Query Match      67.0%; Score 13.4; DB 15; Length 50;
Best Local Similarity 93.3%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  GGAGTCAGATGTTG 17
Db      20  GGAGTCAGATGTTG 34

RESULT 10
US-10-131-827-1458
; Sequence 1458, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
```

```
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1458
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1458
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```
Query Match          67.0%; Score 13.4; DB 15; Length 50;
Best Local Similarity 93.3%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 GGAGTCAGAGTGTG 17
        |||||
Db      20 GGAGTCAGAGTGTG 34
```

```
RESULT 11
US-10-131-827-5424
; Sequence 5424, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5424
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-5424
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```
Query Match          66.0%; Score 13.2; DB 15; Length 50;
Best Local Similarity 83.3%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 GGAGTCAGAGTGTGCA 20
        |||||
Db      6 GAAGTCAGAGAGTTTGA 23
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```
RESULT 12
US-10-098-263B-35307/C
; Sequence 35307, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 35307
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-35307
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```
Query Match          65.0%; Score 13; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GTCCAGATGTTGT 18
        |||||
Db      19 GTCCAGATGTTGT 7
```

```
RESULT 13
US-09-877-478-200/C
; Sequence 200, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1993-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 200
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-200
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```
Query Match          64.0%; Score 12.8; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 8.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GGAGTCAGAGTGTGT 18
        |||||
Db      17 GGAGTCAGAGTGTGT 2
```

```
RESULT 14
US-09-877-478-901/C
; Sequence 901, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
```

```

; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 901
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-901
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```

Query Match      64.0%; Score 12.8; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 8.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      3 GGAGTCAGAGTGTGT 18
        ||| ||| ||| ||| |||
Db      16 GGACTCAAGATGTGT 1
```

```

RESULT 15
US-10-342-902-200/C
; Sequence 200, Application US/10342902
; Publication No. US2004054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBHB00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-200
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```

Query Match      64.0%; Score 12.8; DB 12; Length 17;
Best Local Similarity 87.5%; Pred. No. 8.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

QY      3 GGAGTCAGAGTGTGT 18
        ||| ||| ||| ||| |||
Db      17 GGACTCAAGATGTGT 2
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Search completed: April 15, 2004, 13:24:37
Job time : 235 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 12:23:31 ; Search time 51 Seconds

(without alignments)
217.628 Million cell updates/sec

Title: US-10-006-430-76

Perfect score: 20

Sequence: 1 acgagtcagatgtgtga 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 839752

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile61.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.4	77.0	47	4	US-09-641-638-1178 Sequence 1178, Ap
C 2	13.2	66.0	28	2	US-08-232-081B-25 Sequence 25, Appl
C 3	12.8	64.0	20	2	US-08-623-906A-55 Sequence 55, Appl
C 4	12.8	64.0	27	1	US-08-100-465-6 Sequence 6, Appl
C 5	12.8	64.0	30	2	US-08-568-459A-37 Sequence 37, Appl
C 6	12.8	64.0	30	2	US-08-487-826B-20 Sequence 20, Appl
C 7	12.8	64.0	30	3	US-09-358-972-240 Sequence 240, Appl
C 8	12.8	64.0	30	3	US-09-430-615-9 Sequence 9, Appl
C 9	12.8	64.0	30	4	US-09-210-288-37 Sequence 37, Appl
C 10	12.8	64.0	47	4	US-09-422-978-3061 Sequence 3061, Ap
C 11	12.6	63.0	47	4	US-09-422-978-218 Sequence 218, Appl
C 12	12.4	62.0	20	4	US-09-198-452A-5700 Sequence 5700, Ap
C 13	12.4	62.0	20	4	US-09-198-452A-5700 Sequence 5700, Ap
C 14	12.4	62.0	21	1	US-08-559-303B-44 Sequence 44, Appl
C 15	12.4	62.0	21	3	US-09-175-828-44 Sequence 44, Appl
C 16	12.2	61.0	18	4	US-09-422-978-7628 Sequence 7628, Ap
C 17	12.2	61.0	20	4	US-09-422-978-7628 Sequence 7628, Ap
C 18	12.2	61.0	25	4	US-09-645-629-6 Sequence 6, Appl
C 19	12.2	61.0	28	4	US-09-603-613-1 Sequence 1, Appl
C 20	12.2	61.0	31	2	US-08-859-998-195 Sequence 195, App
C 21	12.2	61.0	31	4	US-09-225-928-195 Sequence 195, App
C 22	12.2	61.0	31	4	US-09-225-928-195 Sequence 195, App
C 23	12.2	61.0	33	4	US-09-636-215-821 Sequence 821, Appl
C 24	12.2	61.0	33	4	US-09-636-215-821 Sequence 821, Appl
C 25	12.2	61.0	34	1	US-08-437-841-28 Sequence 28, Appl
C 26	12.2	61.0	34	1	US-08-286-521-28 Sequence 28, Appl
C 27	12.2	61.0	34	1	US-08-436-175-28 Sequence 28, Appl

C 28	12.2	61.0	34	3	US-08-943-682-28 Sequence 28, Appl
C 29	12.2	61.0	34	5	PCT-US95-09464-28 Sequence 28, Appl
C 30	12.2	61.0	36	1	US-08-437-841-29 Sequence 29, Appl
C 31	12.2	61.0	36	1	US-08-286-521-29 Sequence 29, Appl
C 32	12.2	61.0	36	1	US-08-436-175-29 Sequence 29, Appl
C 33	12.2	61.0	36	3	US-08-943-682-29 Sequence 29, Appl
C 34	12.2	61.0	36	5	PCT-US95-09464-29 Sequence 29, Appl
C 35	12.2	61.0	47	4	US-09-671-317-576 Sequence 576, App
C 36	12.2	61.0	47	4	US-09-422-978-3049 Sequence 3049, Ap
C 37	12	60.0	20	4	US-09-601-144-16 Sequence 16, Appl
C 38	12	60.0	22	1	US-08-388-779A-6 Sequence 6, Appl
C 39	12	60.0	22	1	US-08-591-070A-6 Sequence 6, Appl
C 40	12	60.0	22	2	US-08-927-855-6 Sequence 6, Appl
C 41	12	60.0	25	3	US-09-173-914-34 Sequence 34, Appl
C 42	12	60.0	28	4	US-08-997-685A-21 Sequence 21, Appl
C 43	12	60.0	38	4	US-09-371-772B-8016 Sequence 8016, Ap
C 44	11.8	59.0	20	2	US-08-117-952-693 Sequence 693, App
C 45	11.8	59.0	20	3	US-09-487-445-87 Sequence 87, Appl

ALIGNMENTS

```
RESULT 1
US-09-641-638-1178/C
; Sequence 1178, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumefeld, Marta
; APPLICANT: Bouguetelert, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Anatck
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641, 638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 1178
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-298-122 : polymorphic base C or T
US-09-641-638-1178

Query Match      77.0% Score 15.4; DB 4; Length 47;
Best Local Similarity 84.2% Pred. No. 43;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 ACCGAGTCAGATGTGTG 19
Db      37 ACCGAGTCAGATGTGTG 19

RESULT 2
US-08-232-081B-25
; Sequence 25, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
```

APPLICANT: WIJENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-232-081B-25

Query Match 66.0%; Score 13.2; DB 2; Length 28;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGAGTCAGATGTTGT 18
DB 1 ACTGAGTCAGAGAGATGT 18

RESULT 3
US-08-623-906A-55
Sequence 55, Application US/08623906A
GENERAL INFORMATION:
APPLICANT: Stevenson, Tamara
APPLICANT: Dvorak, Jan
APPLICANT: Halverson, Joy
TITLE OF INVENTION: Microsatellite Sequences for Canine
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBRACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,906A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-62282/B1R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-623-906A-55

Query Match 64.0%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 8.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGTCAGATGTTGTG 19
DB 1 GACTCATGATGTTGTG 16

RESULT 4
US-08-100-465-6/c
Sequence 6, Application US/08100465
Patent No. 5610137
GENERAL INFORMATION:
APPLICANT: TOWNES, TIM M., ET AL.
TITLE OF INVENTION: TRANSGENIC, CROSS-LINKED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,465
FILING DATE: 30-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/630,825
FILING DATE: DECEMBER 20, 1990
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 004005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 27
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-100-465-6

Query Match 64.0%; Score 12.8; DB 1; Length 27;
Best Local Similarity 87.5%; Pred. No. 8.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGTCAGATGTTGT 18

DB 23 GGAGTCAGCATGCTGT 8

RESULT 5

US-08-459A-37/C
Sequence 37, Application US/08568459A

Patent No. 5849306

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan

APPLICANT: Miller, Louis H.

APPLICANT: Peterson, David S.

APPLICANT: Su, Xin-zhaun

APPLICANT: Wellens, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe Martens Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: California

COUNTRY: US

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/568,459A

FILING DATE: 07-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Israelisen, Ned

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH121.001CP1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-568-459A-37

Query Match Best Local Similarity 64.0%; Score 12.8; DB 2; Length 30;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGTCAGGATGTTGTGA 20
DB 30 ACTCAGGAAGTTGTGA 15

US-08-487-826B-20/C
Sequence 20, Application US/08487826B

Patent No. 5993827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan

APPLICANT: Miller, Louis H.

APPLICANT: Peterson, David S.

APPLICANT: Su, Xin-zhaun

APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe Martens Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: California

COUNTRY: US

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,826B

FILING DATE: 10-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Israelisen, Ned

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH121.001CP1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-487-826B-20

Query Match Best Local Similarity 64.0%; Score 12.8; DB 2; Length 30;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGTCAGGATGTTGTGA 20
DB 30 ACTCAGGAAGTTGTGA 15

US-09-358-972-240
Sequence 240, Application US/09358972

Patent No. 6235480

GENERAL INFORMATION:

APPLICANT: Shultz, John W.

APPLICANT: Lewis, Martin K.

APPLICANT: Ileppe, Donna

APPLICANT: Mandrekar, Michelle

APPLICANT: Kephart, Daniel

APPLICANT: Rhodes, Richard B.

APPLICANT: Andrews, Christine A.

APPLICANT: Hartnett, James R.

APPLICANT: Gu, Trent

APPLICANT: Olson, Ryan J.

APPLICANT: Wood, Keith W.

APPLICANT: Welch, Roy

TITLE OF INVENTION: Nucleic Acid Detection

FILE REFERENCE: Pro-103 6868/75528

CURRENT APPLICATION NUMBER: US/09/358,972

CURRENT FILING DATE: 1999-07-22

EARLIER APPLICATION NUMBER: 09/252,436

EARLIER FILING DATE: 1999-02-18

EARLIER APPLICATION NUMBER: 09/042,287

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; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 240
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mutant target
US-09-358-972-240

Query Match      64.0%; Score 12.8; DB 3; Length 30;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AGTCAGGATGTTGTA 20
DB      2 AGTCAGCAGCTTGTGA 17

RESULT 8
US-09-430-615-9
; Sequence 9, Application US/09430615
; Patent No. 6277578
; GENERAL INFORMATION:
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leippe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Andrews, Christine Ann
; APPLICANT: Hartnett, James Robert
; APPLICANT: Welch, Roy
; APPLICANT: Shultz, John William
; TITLE OF INVENTION: Method for Amplified Nucleic Acid Detection
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/430,615
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/252,436
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mutant target
US-09-430-615-9

Query Match      64.0%; Score 12.8; DB 3; Length 30;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AGTCAGGATGTTGTA 20
DB      2 AGTCAGCAGCTTGTGA 17

RESULT 9
US-09-210-288-37/c
; Sequence 37, Application US/09210288
; Patent No. 6392026
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
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; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FMDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-0176
; TELEFAX: (619) 235-8550
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-09-210-288-37

Query Match      64.0%; Score 12.8; DB 4; Length 30;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AGTCAGGATGTTGTA 20
DB      30 ACTCAGGAAGTTGTGA 15

RESULT 10
US-09-422-978-3061/c
; Sequence 3061, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3061
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
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OTHER INFORMATION: 99-21921-338 : polymorphic base T or C
US-09-422-978-3061

Query Match 64.0%; Score 12.8; DB 4; Length 47;
Best Local Similarity 77.8%; Pred. No. 9.6e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACGAGTCAGGATGTTGT 18
DB 37 ACGAGTCAGGATGTTGT 20

RESULT 11
US-09-422-978-218
Sequence 218, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marla
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
EARLIER FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 218
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-13589-362 : polymorphic base A or G
US-09-422-978-218

Query Match 63.0%; Score 12.6; DB 4; Length 47;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGAGTCAGGATGTTGT 19
DB 3 ACGAGTCAGGATGTTGT 21

RESULT 12
US-09-798-096-58
Sequence 58, Application US/09798096
Patent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Walt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 58
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-798-096-58

Query Match 62.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAGTCAGGATGT 15
DB 6 CTGAGTCAGGATGT 19

RESULT 13
US-09-198-452A-5700/C
Sequence 5700, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 5700
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5700

Query Match 62.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTCAGGATGTTGT 18
DB 17 ACTCAGGATGTTGT 4

RESULT 14
US-08-559-303B-44/C
Sequence 44, Application US/08559303B
Patent No. 5824501
GENERAL INFORMATION:
APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
APPLICANT: GRODEN
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BLOOM'S SYNDROME
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESS: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,303B
FILING DATE: NOVEMBER 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR

MOLECULE TYPE:
DESCRIPTION: OTHER NUCLEIC ACID
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-559-303B-44

Query Match 62.0%; Score 12.4; DB 1; Length 21;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAGTCAGGATGT 15
DB 15 CTGAGTCAGGATGT 2

RESULT 15

US-09-175-828-44/C
Sequence 44, Application US/09175828
Patent No. 6221643
GENERAL INFORMATION:
APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
APPLICANT: GRODEN
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT
NUMBER OF INVENTIONS: OF BLOOM'S SYNDROME
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/175,828
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/559,303
FILING DATE: NOVEMBER 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ. ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: OTHER NUCLEIC ACID
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-175-828-44

Query Match 62.0%; Score 12.4; DB 3; Length 21;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAGTCAGGATGT 15
DB 15 CTGAGTCAGGATGT 2

Search completed: April 15, 2004, 13:25:40
Job time : 53 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2004, 10:38:24 ; Search time 5 Seconds
(without alignments)
3.541 Million cell updates/sec

Title: us-10-006-430-3
Perfect score: 1496
Sequence: 1 ccattgtctggaagcgc.....tgcataaaaaaaaaaaaaa 1496

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 368 seqs, 5918 residues

Total number of hits satisfying chosen parameters: 736

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 363 summaries

Database : rge3.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	26	1.7	26	1	BD097225
2	24	1.6	24	1	BD097226
3	21	1.4	21	1	AX763858
4	20	1.3	20	1	AX763859
5	20	1.3	21	1	AX145918
6	20	1.3	21	1	AX145919
7	19	1.3	20	1	AR030917
8	19	1.3	20	1	I28309
9	19	1.3	20	1	I47310
10	19	1.3	21	1	AX825109
11	18.4	1.2	21	1	AX825127
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13	18	1.2	20	1	AR140280
14	18	1.2	20	1	AR140558
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18	18	1.2	21	1	AX825152
19	17.4	1.2	20	1	E12411
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21	17	1.1	18	1	A67588
22	17	1.1	18	1	AR089726
23	17	1.1	18	1	E32450
24	17	1.1	18	1	AX028843
25	16.6	1.1	19	1	A79657
26	16.6	1.1	19	1	AR147331
27	16.4	1.1	18	1	AI4689
28	16.4	1.1	18	1	AR208425
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30	16.4	1.1	18	1	AX085251
31	16.4	1.1	18	1	AX361600
32	16.4	1.1	18	1	AX814932
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C 111	1.1	18	1	AX268883	ACCESSION:AX268883	C 184	15	1.0	15	1	BD084687	ACCESSION:BD084687
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BD097225

LOCUS

BD097225

DEFINITION

A therapeutic agent for hepatitis type C.

ACCESSION

BD097225

VERSION

BD097225.1

GI:22642799

KEYWORDS

WO 0158459-A/12.

SOURCE

synthetic construct

ORGANISM

synthetic construct

REFERENCE

1 (bases 1 to 26)

AUTHORS

Itamura,S., Shibui,T., Seki,M., Yotsumoto,Y., Matsuura,Y. and Miyamura,T.

TITLE

A therapeutic agent for hepatitis type C

JOURNAL

Patent: WO 0158459-A 12 16-AUG-2001;

COMMENT

MITSUBISHI TOKYO PHARMACEUTICALS INC,SEIMA ITAMI,TATSURO SHIBUI, MAKOTO SEKI,YOSHIHISA YOTSUMOTO,YOSHIHARU MATSUURA,TATSUO MIYAMURA

OS

Artificial Sequence

PN

WO 0158459-A/12

PD

16-AUG-2001

PF

13-FEB-2001

PR

14-FEB-2000

PI

SEIMA ITAMI,TATSURO SHIBUI,MAKOTO SEKI,YOSHIHISA YOTSUMOTO, PI YOSHIHARU MATSUURA,TATSUO MIYAMURA

PC

A61K31/737,A61K38/17,A61K39/395,A61K45/00,A61P31/20,C07K16/10, PC: C12N15/09,

CC

G01N33/50,G01N33/53,G01N33/576

FT

Primer

Location/Qualifiers

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source

ALIGNMENTS

BD097225 26 bp DNA linear PAT 27-AUG-2002

A therapeutic agent for hepatitis type C.

BD097225

BD097225.1

GI:22642799

synthetic construct

synthetic construct

artificial sequences.

1 (bases 1 to 26)

Itamura,S., Shibui,T., Seki,M., Yotsumoto,Y., Matsuura,Y. and

Miyamura,T.

A therapeutic agent for hepatitis type C

Patent: WO 0158459-A 12 16-AUG-2001;

MITSUBISHI TOKYO PHARMACEUTICALS INC,SEIMA ITAMI,TATSURO SHIBUI,

MAKOTO SEKI,YOSHIHISA YOTSUMOTO,YOSHIHARU MATSUURA,TATSUO MIYAMURA

OS Artificial Sequence

PN WO 0158459-A/12

PD 16-AUG-2001

PF 13-FEB-2001

PR 14-FEB-2000

PI SEIMA ITAMI,TATSURO SHIBUI,MAKOTO SEKI,YOSHIHISA YOTSUMOTO, PI

YOSHIHARU MATSUURA,TATSUO MIYAMURA

PC A61K31/737,A61K38/17,A61K39/395,A61K45/00,A61P31/20,C07K16/10,

PC: C12N15/09,

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FT Primer

Location/Qualifiers

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source

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ACCESSION BD097226
VERSION WO 0158459-A/13.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Itami,S., Shibui,T., Seki,M., Yotsumoto,Y., Matsuura,Y. and Miyamura,T.
TITLE A therapeutic agent for hepatitis type C
JOURNAL Patent: WO 0158459-A/13 16-AUG-2001;
MITSUBISHI TOKYO PHARMACEUTICALS INC,SEIMA ITAMI,TATSURO SHIBUI,
MAKOTO SEKI,YOSHIHISA YOTSUMOTO,YOSHIHARU MATSUURA,TATSUO MIYAMURA
OS Artificial Sequence
PN WO 0158459-A/13
PD 16-AUG-2001
PF 13-FEB-2001 WO 2001JP000967
PR 14-FEB-2000 JP ODP 034906
PI SEIMA ITAMI,TATSURO SHIBUI,MAKOTO SEKI,YOSHIHISA YOTSUMOTO,PI
YOSHIHARU MATSUURA,TATSUO MIYAMURA
PC A61K31/737,A61K38/17,A61K39/395,A61K45/00,A61P31/20,C07K16/10,
PC C12N15/09.
PC G01N33/50,G01N33/53,G01N33/576
CC Primer
FH Key
FT source
FT Location/Qualifiers
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LOCUS AX763858 21 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 13 from Patent WO03040407.
ACCESSION AX763858
VERSION AX763858.1 GI:32258220
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ORGANISM artificial sequences.
REFERENCE 1
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Db 1 AAGGCTGTGGTGAACACCTTC 21

RESULT 4
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LOCUS AX763859 20 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 14 from Patent WO03040407.
ACCESSION AX763859
VERSION AX763859.1 GI:32258221
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ruiz,P., Grzeskowiak,R., Drungowski,M., Witt,H., Osterziel,K., Perrot,A. and Saleh,A.
TITLE Novel markers for cardiopathies
JOURNAL Patent: WO 03040407-A 14 15-MAY-2003;
MAX-PLANCK-GESELLSCHAFT (DE)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer CD81_R"

Query Match
  Best Local Similarity 1.3%; Score 20; DB 1; Length 20;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 931 GAACAGCTCCGTGTACTGAG 950
      |||||
Db 20 GAACAGCTCCGTGTACTGAG 1

RESULT 5
AX145918
LOCUS AX145918 21 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 109 from Patent WO0134840.
ACCESSION AX145918
VERSION AX145918.1 GI:14284436
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Au,K.G., Chen,J.G., Patil,N. and Thomas,D.
TITLE Genetic compositions and methods
JOURNAL Patent: WO 0134840-A 109 17-MAY-2001;
GLAXO GROUP LIMITED (GB); Affymetrix, Inc. (US)
FEATURES
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        /mol_type="unassigned DNA"

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/db_xref="taxon:9606"
1..21
/notes="n' represents a polymorphic base"

variation
Query Match
  1.3%; Score 20; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 979 TGCAGTGCCTTAAAGTACC 999
|||||
Db 1 TGCAGTGCCTTAAAGTACC 21

RESULT 6
AX145919
LOCUS AX145919 21 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 110 from Patent WO0134840.
ACCESSION AX145919
VERSION AX145919.1 GI:14284437
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Au,K.G., Chen,J.G., Patil,N. and Thomas,D.
TITLE Genetic compositions and methods
JOURNAL Patent: WO 0134840-A 110 17-MAY-2001;
GLAXO GROUP LIMITED (GB) ; Affymetrix, Inc. (US)
FEATURES
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      /mol_type="unassigned DNA"
variation
  1..21
    /notes="n' represents a polymorphic base"

Query Match
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Best Local Similarity 95.2%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1036 ATACGTTTCGGTATATCTC 1056
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Db 1 ATACGTTTCGGTATATCTC 21

RESULT 7
AR030917/c
LOCUS AR030917 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5861487.
ACCESSION AR030917
VERSION AR030917.1 GI:5944131
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 20)
AUTHORS Holton,T.A., Cornish,E.Cecily., Kovacic,F., Tanaka,Y. and
Lester,D.Ruth.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: US 5861487-A 20 19-JAN-1999;
FEATURES
  source
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      /mol_type="unassigned DNA"

Query Match
  1.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 GCTAAAAA 1496
|||||
Db 1478 GCTAAAAA 1496

RESULT 8
AX825109/c
LOCUS AX825109 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 7 from Patent WO03072818.
ACCESSION AX825109
VERSION AX825109.1 GI:39750838
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
  1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
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Db 20 CTAACAAAAA 1496

RESULT 14
LOCUS AX825107/c 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 33 from patent US 6207802.
ACCESSION AX825107
VERSION AX825107.1 GI:14483054
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo,K.M., Bosseman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 33 27-MAR-2001;
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1496
Db 20 CTAACAAAAA 1496

RESULT 15
LOCUS AX825107/c 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 5 from Patent WO03072818.
ACCESSION AX825107
VERSION AX825107.1 GI:39750836
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 5 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 21 /note="LNA-T (Locked Nucleic Acid)"

Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1496
Db 20 CTAACAAAAA 1496

RESULT 16
LOCUS AX825108/c 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 6 from Patent WO03072818.
ACCESSION AX825108
VERSION AX825108.1 GI:39750837
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 6 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 21 /note="LNA-T (Locked Nucleic Acid)"

Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1496
Db 20 CTAACAAAAA 1496

RESULT 17
LOCUS AX825110/c 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 8 from Patent WO03072818.
ACCESSION AX825110
VERSION AX825110.1 GI:39750839
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1

AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 8 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES

source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
modified_base 6
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
modified_base 12
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
modified_base 18
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"

Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
|||||
Db 20 CTAAGAAAAA 3

RESULT 18
AX825152/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 50 from Patent WO03072818.
DEFINITION AX825152
ACCESSION AX825152
VERSION AX825152.1 GI:39750881
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 50 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
modified_base 6
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
modified_base 9
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"

modified_base 12
/mod_base=OTHER
modified_base 15
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
modified_base 18
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"

Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
|||||
Db 21 CTAAGAAAAA 4

RESULT 19
E12411/c 20 bp DNA linear PAT 27-APR-1998
LOCUS Oligonucleotide.
DEFINITION E12411
ACCESSION E12411
VERSION E12411.1 GI:3251244
KEYWORDS JP 1996332100-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Okano,K. and Kanbara,H.
TITLE PRIMER FOR DNA POLYMERASE REACTION AND DETERMINATION OF
POLYNUCLEOTIDE SEQUENCE USING THE SAME
JOURNAL Patent: JP 1996332100-A 1 17-DEC-1996;
HITACHI LTD

COMMENT OS None
OC Artificial sequences.
FN JP 1996332100-A/1
PD 17-DEC-1996
PF 06-JUN-1995 JP 1995139051
PI OKANO KAZUNOBU, KANBARA HIDEKI
PC C1201/68,C07H21/04//C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH Key
FT Location/Qualifiers
FT source 1. .20
FT /organism='Artificial sequences'.

FEATURES source 1. .20
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1475 CATGCTAAAAA 1493
|||||
Db 19 CAGCTAAAAA 1

RESULT 20
AX040984/c 20 bp DNA linear PAT 23-NOV-2000
LOCUS Sequence 31 from Patent WO0065040.
DEFINITION AX040984
ACCESSION AX040984
VERSION AX040984.1 GI:11340580
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.									
REFERENCE	1								
AUTHORS	Helentjaris, T.G., Habben, J.E. and Sun, Y.								
TITLE	Cell cycle genes and methods of use								
JOURNAL	Patent: WO 0065040-A 31 02-NOV-2000;								
FEATURES	PIONEER HI-BRED INTERNATIONAL, INC. (US)								
source	Location/Qualifiers								
	1..20								
	/organism="Zea mays"								
	/mol_type="unassigned DNA"								
	/db_xref="taxon:4577"								
Query Match	1.2%;	Score 17.4;	DB 1;	Length 20;					
Best Local Similarity	94.7%;	Pred. No. 58;							
Matches	18;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;				
QY	222	CGCGCGCCCGCGCGCCCAT 240							
Db	19	CAGCCGCCCGCGCGCCCAT 1							
RESULT 21									
A67588									
LOCUS	A67588	18 bp	DNA	linear	PAT 05-MAY-1999				
DEFINITION	Sequence 8 from Patent WO9744485.								
ACCESSION	A67588								
VERSION	A67588.1	GI:4756451							
KEYWORDS	unidentified								
SOURCE	unidentified								
ORGANISM	unclassified.								
REFERENCE	1	(bases 1 to 18)							
AUTHORS	Goodfellow, P.N.								
TITLE	METHODS FOR IDENTIFYING A MUTATION IN A GENE OF INTEREST								
JOURNAL	Patent: WO 9744485-A 8 27-NOV-1997;								
FEATURES	HEXAGEN TECHNOLOGY LIMITED (GB)								
source	Location/Qualifiers								
	1..18								
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	/mol_type="unassigned DNA"								
	/db_xref="taxon:32644"								
Query Match	1.1%;	Score 17;	DB 1;	Length 18;					
Best Local Similarity	100.0%;	Pred. No. 54;							
Matches	17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
QY	25	CGCGCGCGCGCGCGCG 41							
Db	2	CGCGCGCGCGCGCGCG 18							
RESULT 22									
AR089726									
LOCUS	AR089726	18 bp	DNA	linear	PAT 07-SEP-2000				
DEFINITION	Sequence 8 from patent US 5994075.								
ACCESSION	AR089726								
VERSION	AR089726.1	GI:10016481							
KEYWORDS	Unknwn.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1	(bases 1 to 18)							
AUTHORS	Goodfellow, P.N.								
TITLE	Methods for identifying a mutation in a gene of interest without a phenotypic guide								
JOURNAL	Patent: US 5994075-A 8 30-NOV-1999;								
FEATURES	Location/Qualifiers								
source	1..18								
	/organism="unknown"								
	/mol_type="unassigned DNA"								

LOCUS		Al4689		18 bp		DNA	linear	PAT 28-MAR-1999
DEFINITION		Nucleotide sequence 9 from patent number WO8303623.						
ACCESSION		Al4689						
VERSION		Al4689.1						GI:513760
KEYWORDS		unidentified						
SOURCE		unidentified						
ORGANISM		unclassified.						
REFERENCE		1 (bases 1 to 18)						
AUTHORS		CODING DNA FRAGMENTS FOR POLYPEPTIDES CONTAINING AT LEAST ONE						
TITLE		ANTIGENIC DETERMINANT OF THE PAPILLOMAVIRUS PARTICULARLY OF THE 1a						
JOURNAL		HPV TYPE AND CORRESPONDING POLYPEPTIDES						
JOURNAL		Patent: WO 8303623-A 9 27-OCT-1983;						
JOURNAL		Location/Qualifiers						
source		1. .18						
Query Match		1.1%; Score 16.4; DB 1; Length 18;						
Best Local Similarity		94.4%; Pred. No. 71;						
Matches		17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;						
QY		1478 GCTAAAAAAAAAAAAAAAAA 1495						
Db		1 GCATAAAAAAAAAAAAAAAAAA 18						
RESULT 28								
AR208425/c		AR208425						
LOCUS		Sequence 5 from patent US 6383754.						
DEFINITION		Sequence 5 from patent US 6383754.						
ACCESSION		AR208425						
VERSION		AR208425.1						GI:21509576
KEYWORDS		Unknown.						
SOURCE		Unknown.						
ORGANISM		Unclassified.						
REFERENCE		1 (bases 1 to 18)						
AUTHORS		Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.						
TITLE		Binary encoded sequence tags						
JOURNAL		Patent: US 6383754-A 5 07-MAY-2002;						
JOURNAL		Location/Qualifiers						
source		1...18						
Query Match		1.1%; Score 16.4; DB 1; Length 18;						
Best Local Similarity		94.4%; Pred. No. 71;						
Matches		17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;						
QY		1478 GCTAAAAAAAAAAAAAAAAA 1495						
Db		18 GCATAAAAAAAAAAAAAAAAAA 1						
RESULT 29								
AX028845/c		AX028845						
LOCUS		Sequence 29 from Patent WO9732023.						
DEFINITION		Sequence 29 from Patent WO9732023.						
ACCESSION		AX028845						
VERSION		AX028845.1						GI:10189948
KEYWORDS		synthetic construct						
SOURCE		synthetic construct						
ORGANISM		artificial sequences.						
REFERENCE		1						
AUTHORS		Brugliera,F., Holton,T.A. and Michael,M.Z.						
TITLE		Genetic sequences encoding flavonoid pathway enzymes and uses						
JOURNAL		Patent: WO 9732023-A 29 04-SEP-1997;						
JOURNAL		FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY						


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FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Oligonucleotide"

Query Match
  Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA 1496
Db 18 CGAAAAA 1

RESULT 30
AX085251/c
LOCUS
  DEFINITION
    Sequence 5 from Patent W00112855.
  ACCESSION
    AX085251
  VERSION
    AX085251.1 GI:13275309
  KEYWORDS
    .
  SOURCE
    synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Kaufman,J.C., Roth,M.E., Lizardi,P.M., Peng,L. and Latimer,D.R.
  TITLE
    Binary encoded sequence tags
  JOURNAL
    Patent: WO 0112855-A 5 22-FEB-2001;
    YALE UNIVERSITY (US)
  FEATURES
    source
      1. .18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"

Query Match
  Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAA 1495
Db 18 GCAAAAAA 1

RESULT 31
AX361600/c
LOCUS
  DEFINITION
    Sequence 18 from Patent W0208461.
  ACCESSION
    AX361600
  VERSION
    AX361600.1 GI:18694219
  KEYWORDS
    .
  SOURCE
    synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Linnarsson,S.G., Ernfor,P.G. and Bauren,G.G.
  TITLE
    A method and an algorithm for mrna expression analysis
  JOURNAL
    Patent: WO 0208461-A 18 31-JAN-2002;
    Global Genomics AB (SE)
  FEATURES
    source
      1. .18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Double-stranded product DNA"

Query Match
  Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Double-stranded product DNA"

Query Match
  Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA 1496
Db 18 CGAAAAA 1

RESULT 32
AX814932/c
LOCUS
  DEFINITION
    Sequence 18 from Patent W03064691.
  ACCESSION
    AX814932
  VERSION
    AX814932.1 GI:39104070
  KEYWORDS
    .
  SOURCE
    synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Linnarsson,S., Ernfor,P., Bauren,G., Metsis,A., Pihlak,A. and
    Montellius,A.
  TITLE
    Methods and means for manipulating nucleic acid
  JOURNAL
    Patent: WO 03064691-A 18 07-AUG-2003;
    Global Genomics AB (SE)
  FEATURES
    source
      1. .18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Description of Artificial Sequence: Double-stranded
        product DNA"

Query Match
  Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA 1496
Db 18 CGAAAAA 1

RESULT 33
AR102020/c
LOCUS
  DEFINITION
    Sequence 18 from patent US 6083731.
  ACCESSION
    AR102020
  VERSION
    AR102020.1 GI:12812818
  KEYWORDS
    .
  SOURCE
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 19)
  AUTHORS
    Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.
  TITLE
    Recombinant materials and methods for the production of limonene
    hydroxylases
  JOURNAL
    Patent: US 6083731-A 18 04-JUL-2000;
  FEATURES
    source
      1. .19
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 1.1%; Score 16.2; DB 1; Length 19;
  Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1496
Db 19 DAAAAA 3

RESULT 34
AR134802/c
LOCUS
  DEFINITION
    Sequence 18 from patent US 6194185.
  ACCESSION
    AR134802

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VERSION AR134802.1 GI:14123707
SOURCE   .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS  Croteau,R.Bruce., Lupien,S.Lee, and Karp,F.
TITLE     Recombinant materials and methods for production of limonene
          hydroxylases
JOURNAL   Patent: US 6194185-A 18 27-FEB-2001;
FEATURES  Location/Qualifiers
          source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 89;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
Db 19 DAAAAAAAAAAAAAAAAA 3

RESULT 35
AR163080
LOCUS AR163080 19 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6270966.
ACCESSION AR163080
VERSION AR163080.1 GI:16233563
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Weinstein,J.N. and Buolamwini,J.
TITLE Restriction display (RD-PCR) of differentially expressed mRNAs
JOURNAL Patent: US 6270966-A 1 07-AUG-2001;
FEATURES Location/Qualifiers
          source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 89;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
Db 19 DAAAAAAAAAAAAAAAAA 3

RESULT 36
E08331/c
LOCUS E08331 19 bp DNA linear PAT 29-SEP-1997
DEFINITION Reverse transcription primer.
ACCESSION E08331
VERSION E08331.1 GI:2176448
KEYWORDS JP 1994303997-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Takagi,S. and Kamloka,S.
TITLE DETERMINATION OF CDNA
JOURNAL Patent: JP 1994303997-A 2 01-NOV-1994;
          NIPPON TELEGR & TELEPH CORP <NTT>
COMMENT OS None
          OC Artificial sequences.
          EN JP 1994303997-A/2
          FD 01-NOV-1994
          PF 16-APR-1993 JP 1993112515
          PI TAKAGI SHIGERU, KAMIOKA SUKEYUKI

VERSION AR134802.1 GI:14123707
SOURCE   .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS  Croteau,R.Bruce., Lupien,S.Lee, and Karp,F.
TITLE     Recombinant materials and methods for production of limonene
          hydroxylases
JOURNAL   Patent: US 6194185-A 18 27-FEB-2001;
FEATURES  Location/Qualifiers
          source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 89;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
Db 19 DAAAAAAAAAAAAAAAAA 3

RESULT 37
AR027678/c
LOCUS AR027678 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5856435.
ACCESSION AR027678
VERSION AR027678.1 GI:5938498
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Bazile,D., Emile,C., Helene,C. and Spenlehauser,G.
TITLE Nucleic acid-containing composition, its preparation and use
JOURNAL Patent: US 5856435-A 15 05-JAN-1999;
FEATURES Location/Qualifiers
          source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 38
AR037355/c
LOCUS AR037355 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5801155.
ACCESSION AR037355
VERSION AR037355.1 GI:5955211
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 5801155-A 2 01-SEP-1998;
FEATURES Location/Qualifiers
          source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAAA 1

RESULT 39
LOCUS AR104584 PAT 14-FEB-2001
DEFINITION Sequence 131 from patent US 6093809.
ACCESSION AR104584
VERSION AR104584.1 GI:12817292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 16)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 131 25-JUL-2000;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 1 AAAAAAAAAAAAAAA 16

RESULT 40
LOCUS AR175845 PAT 17-DEC-2001
DEFINITION Sequence 131 from patent US 6309867.
ACCESSION AR175845
VERSION AR175845.1 GI:17917144
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 16)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 131 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 1 AAAAAAAAAAAAAAA 16

RESULT 41
LOCUS I38676 PAT 13-MAY-1997
DEFINITION Sequence 36 from patent US 5614617.
ACCESSION I38676
VERSION I38676.1 GI:2084730
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 36 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAAA 1

RESULT 42
LOCUS I38682/c PAT 13-MAY-1997
DEFINITION Sequence 42 from patent US 5614617.
ACCESSION I38682
VERSION I38682.1 GI:2084736
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 42 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAAA 1

RESULT 43
LOCUS I38700 PAT 13-MAY-1997
DEFINITION Sequence 60 from patent US 5614617.
ACCESSION I38700
VERSION I38700.1 GI:2084754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 60 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAAA 1

Db 16 AAAAAAAAAAAAAAAAAA 1
|||||
RESULT 44
AR221692/c
LOCUS AR221692 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 2 from patent US 6426408.
ACCESSION AR221692
VERSION AR221692.1 GI:23328764
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutayavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 2 30-JUL-2002;
FEATURES
source Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAAAAAA 1
|||||
RESULT 45
AR222462
LOCUS AR222462 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 22 from patent US 6429300.
ACCESSION AR222462
VERSION AR222462.1 GI:23329993
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 22 06-AUG-2002;
FEATURES
source Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16
|||||
RESULT 46
AR257437/c
LOCUS AR257437 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6486308.
ACCESSION AR257437
VERSION AR257437.1 GI:27307448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutayavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates

JOURNAL Patent: US 6486308-A 2 26-NOV-2002;
FEATURES
source Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAAAAAA 1
|||||
RESULT 47
LOCUS AX039049 16 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 2 from Patent WO0061594.
ACCESSION AX039049
VERSION AX039049.1 GI:11228345
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Beier,M. and Hoheisel,J.
TITLE Nucleoside derivatives with photo-unstable protective groups
JOURNAL Patent: WO 0061594-A 2 19-OCT-2000;
DEUTSCHES KREBSFORSCH (DE); BEIER MARKUS (DE); HOHEISEL JOERG (DE)
FEATURES
source Location/Qualifiers
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16
|||||
RESULT 48
AX235176/c
LOCUS AX235176 16 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 9 from Patent WO0163282.
ACCESSION AX235176
VERSION AX235176.1 GI:15593767
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
TITLE Analysis of biological targets using a biochip comprising a fluorescent marker
JOURNAL Patent: WO 0163282-A 9 30-AUG-2001;
COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES
source Location/Qualifiers
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="sequence synthetic"
Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 49
BD167413
LOCUS
DEFINITION Surface-roughened slide glass and method of analyzing biological
substance using the same.
ACCESSION BD167413
VERSION BD167413.1 GI:27873225
KEYWORDS JP 2002211954-A/1.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 16)
AUTHORS Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE Surface-roughened slide glass and method of analyzing biological
substance using the same
JOURNAL Patent: JP 2002211954-A 1 31-JUL-2002;
TOYO KOHAN CO LTD
COMMENT OS Artificial Sequence
PN JP 2002211954-A/1
PD 31-JUL-2002
PF 30-OCT-2001 JP 2001332778
PI HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
PC C12Q1/68,
PC GOIN33/53,GOIN33/53,GOIN37/00,C12N15/00,C12N15/00 CC
Surface-roughened slide glass and method of analyzing CC
biological substance
CC using the same
FH Key Location/Qualifiers
FT source 1..16
/organism="Artificial Sequence".

FEATURES
source
1..16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No.64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 51
A28997/c
LOCUS
DEFINITION primer sequence 4 from patent EP0522880.
ACCESSION A28997
VERSION A28997.1 GI:1248848
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial constructs.
REFERENCE 1 (bases 1 to 17)
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: EP 0522880-A 16 13-JAN-1993;
INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
FEATURES
source
1..17
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No.74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 52
AR104585/c
LOCUS
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION AR104585
VERSION AR104585.1 GI:12817293
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 132 25-JUL-2000;
FEATURES
Location/Qualifiers

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source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 53
LOCUS AR141074 17 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 5 from patent US 6207819.
ACCESSION AR141074
VERSION AR141074.1 GI:14483570
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed
backbone oligomeric compounds
JOURNAL Patent: US 6207819-A 5 27-MAR-2001;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 54
LOCUS AR172076/c 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 30 from patent US 6297425.
ACCESSION AR172076
VERSION AR172076.1 GI:17911026
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Scelonge,C.J. and Bidney,D.L.
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices
JOURNAL Patent: US 6297425-A 30 02-OCT-2001;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 55
LOCUS AR173367/c 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 30 from patent US 6303846.
ACCESSION AR173367
VERSION AR173367.1 GI:17912858
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Scelonge,C.J. and Bidney,D.L.
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices
JOURNAL Patent: US 6303846-A 30 16-OCT-2001;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 56
LOCUS AR175846/c 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 132 from patent US 6309867.
ACCESSION AR175846
VERSION AR175846.1 GI:17917145
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 132 30-OCT-2001;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 57
LOCUS E34258/c 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION E34258
VERSION E34258.1 GI:18624263
KEYWORDS JP 2000106879-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No.N. and Ogawa,K.
TITLE Pollinosis-associated gene
JOURNAL Patent: JP 2000106879-A 2 18-APR-2000;
COMMENT GENOX RESEARCH INC
OS Artificial Sequence
PN JP 2000106879-A/2
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
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Db          20 CTGACTCCGTCATTAAATAA 1
|||||
RESULT 42
ADC35554/c
ID ADC35554 standard; DNA; 20 BP.
XX
AC ADC35554;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #14.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraepanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 26; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 471 TGGGCTGCTACGGGGCCATC 490
|||||
Db 20 TGGGCTGCTACGGGGCCATC 1
|||||
RESULT 43
ADC35566/c
ID ADC35566 standard; DNA; 20 BP.
XX
AC ADC35566;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #26.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraepanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 38; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
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Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 753 ACAATTGTGCTCCCTCGGC 772
   |||||
Db 20 ACAATTGTGCTCCCTCGGC 1

RESULT 44
ID ADC35579/c
XX
AC ADC35579;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #39.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 51; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC

CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 8 C; 5 G; 1 T; 0 U; 0 Other;
Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 912 TGCTGTGCTGTGGCATCCGG 931
   |||||
Db 20 TGCTGTGCTGTGGCATCCGG 1

RESULT 45
ID ADC35587/c
XX
AC ADC35587;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #47.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 59; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC
```


CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.

XX
SQ Sequence 20 BP; 9 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1060 TACACGTAGCCTTTTACTT 1079
Db 20 TACACGTAGCCTTTTACTT 1

RESULT 46
ADC35589/c
ID ADC35589 standard; DNA; 20 BP.
XX
AC ADC35589;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #49.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 61; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The

CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.

XX
SQ Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 TTACCTTTTCAGGGCTGATG 1131
Db 20 TTACCTTTTCAGGGCTGATG 1

RESULT 47
ADC35581/c
ID ADC35581 standard; DNA; 20 BP.
XX
AC ADC35581;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #41.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 53; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a

CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 922 TGGCATCCGGACAGCTCCG 941
 |||||
 Db 20 TGGCATCCGGACAGCTCCG 1

RESULT 48
 ADC35582/c
 ID ADC35582 standard; DNA; 20 BP.

XX ADC35582;
 XX
 DT 18-DEC-2003 (first entry)
 XX Human CD81/TAPA-1 antisense oligonucleotide #42.

XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX Homo sapiens.

Key	Location/Qualifiers
modified_base	1..20
	/*tag= b
	/mod_base= OTHER
	/note= "Phosphorothioate backbone and all cytidines are 5
	-methyl cytidines"
modified_base	1..5
	/*tag= a
	/mod_base= OTHER
	/note= "2'-methoxyethyl nucleotide"
modified_base	16..20
	/*tag= c
	/mod_base= OTHER
	/note= "2'-methoxyethyl nucleotide"

US2003113914-A1.

19-JUN-2003.

10-DEC-2001; 2001US-00006430.

10-DEC-2001; 2001US-00006430.

(ISIS-) ISIS PHARM INC.

Graham MJ, Dobie K;

WPI; 2003-810907/76.

XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX Claim 3; SEQ ID NO 54; 55pp; English.

XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TCCGGAACAGCTCCGTGTAC 946
 |||||
 Db 20 TCCGGAACAGCTCCGTGTAC 1

RESULT 49
 ADC35598/c
 ID ADC35598 standard; DNA; 20 BP.

XX ADC35598;
 XX
 DT 18-DEC-2003 (first entry)
 XX Human CD81/TAPA-1 antisense oligonucleotide #58.

XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.

XX Homo sapiens.

Key	Location/Qualifiers
modified_base	1..20
	/*tag= b
	/mod_base= OTHER
	/note= "Phosphorothioate backbone and all cytidines are 5
	-methyl cytidines"
modified_base	1..5
	/*tag= a
	/mod_base= OTHER
	/note= "2'-methoxyethyl nucleotide"
modified_base	16..20
	/*tag= c
	/mod_base= OTHER
	/note= "2'-methoxyethyl nucleotide"

US2003113914-A1.

19-JUN-2003.

10-DEC-2001; 2001US-00006430.

10-DEC-2001; 2001US-00006430.

(ISIS-) ISIS PHARM INC.

Graham MJ, Dobie K;

WPI; 2003-810907/76.

XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and

PT disease associated with expression of CD81 such as inflammation disorder.

PS Example 15; SEQ ID NO 70; 55pp; English.

XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 5 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1355 GTTCGAGACCGAGTCTGTG 1374

DB 20 GTTCGAGACCGAGTCTGTG 1

RESULT 50

ADC35550/c
 ID ADC35550 standard; DNA; 20 BP.

XX AC ADC35550;

XX 18-DEC-2003 (first entry)

DE Human CD81/TAPA-1 antisense oligonucleotide #10.

XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone and all cytidines are 5

FT -methyl cytidines"

FT modified_base 1..5

FT /tag= a

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

XX US2003113914-A1.

PN 19-JUN-2003.

XX 10-DEC-2001; 2001US-00006430.

XX 10-DEC-2001; 2001US-00006430.

XX (ISIS-) ISIS PHARM INC.

XX Graham MJ, Dobie K;

PI WPI; 2003-810907/76.

DR

XX

PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.

XX Claim 3; SEQ ID NO 22; 55pp; English.

XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 6 A; 8 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 ATCCTGGGTGTGCGCCCTGTG 339

DB 20 ATCCTGGGTGTGCGCCCTGTG 1

RESULT 51

ADC35552/c

ID ADC35552 standard; DNA; 20 BP.

XX AC ADC35552;

XX 18-DEC-2003 (first entry)

DE Human CD81/TAPA-1 antisense oligonucleotide #12.

XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone and all cytidines are 5

FT -methyl cytidines"

FT modified_base 1..5

FT /tag= a

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

XX US2003113914-A1.

PN 19-JUN-2003.

XX 10-DEC-2001; 2001US-00006430.

XX 10-DEC-2001; 2001US-00006430.

XX (ISIS-) ISIS PHARM INC.

PA WPI; 2003-810907/76.

```
PI Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX Claim 3; SEQ ID NO 24; 55pp; English.
XX The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 402 CCAACACCTTCTATGTAGGC 421
Db 20 CCAACACCTTCTATGTAGGC 1
RESULT 52
ADC35555/c
ID ADC35555 standard; DNA; 20 BP.
XX ADC35555;
XX 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #15.
DE Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX Homo sapiens.
OS Homo sapiens.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
US2003113914-A1.
XX 19-JUN-2003.
PD 10-DEC-2001; 2001US-00006430.
XX 10-DEC-2001; 2001US-00006430.
PR 10-DEC-2001; 2001US-00006430.
```

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XX (ISIS-) ISIS PHARM INC.
PA Graham MJ, Dobie K;
PI WPI; 2003-810907/76.
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX Claim 3; SEQ ID NO 27; 55pp; English.
XX The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 497 TCCAGTGCCTCTCGGGAC 516
Db 20 TCCAGTGCCTCTCGGGAC 1
RESULT 53
ADC35569/c
ID ADC35569 standard; DNA; 20 BP.
XX ADC35569;
XX 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #29.
DE Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX Homo sapiens.
OS Homo sapiens.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
US2003113914-A1.
XX 19-JUN-2003.
PD 10-DEC-2001; 2001US-00006430.
XX 10-DEC-2001; 2001US-00006430.
PR 10-DEC-2001; 2001US-00006430.
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PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 41; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 830 TTCTCCGGGAGGTGTACCT 849
DB 20 TTCTCCGGGAGGTGTACCT 1
RESULT 54
ADC35593/C
ID ADC35593 standard; DNA; 20 BP.
XX
AC ADC35593;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #53.
XX
KW Antisense; ss; human; CD81; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.

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XX 19-JUN-2003.
PD
XX 10-DEC-2001; 2001US-00006430.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 65; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 5 A; 7 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1210 GGTCCAGGGTGTCTGCCT 1229
DB 20 GGTCCAGGGTGTCTGCCT 1
RESULT 55
ADC35560/C
ID ADC35560 standard; DNA; 20 BP.
XX
AC ADC35560;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #20.
XX
KW Antisense; ss; human; CD81; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER

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FT XX /note= "2'-methoxyethyl nucleotide"
PN US2003113914-A1.
XX PD 19-JUN-2003.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX DR WPI; 2003-810907/76.
XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 32; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 597 CCAAGGATGTGAAGCAGTTC 616
Db 20 CCAAGGATGTGAAGCAGTTC 1
RESULT 56
ADC35588/c
ID ADC35588 standard; DNA; 20 BP.
XX AC ADC35588;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 antisense oligonucleotide #48.
XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"

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FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX PN US2003113914-A1.
XX PD 19-JUN-2003.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX DR WPI; 2003-810907/76.
XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 60; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1098 TCTGAACCTTCCTGTACCT 1117
Db 20 TCTGAACCTTCCTGTACCT 1
RESULT 57
ADC35594/c
ID ADC35594 standard; DNA; 20 BP.
XX AC ADC35594;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 antisense oligonucleotide #54.
XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5

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FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl nucleotide"
FT      modified_base
FT      16..20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl nucleotide"
XX
XX      US2003113914-A1.
XX
XX      19-JUN-2003.
XX
XX      10-DEC-2001; 2001US-00006430.
XX
XX      10-DEC-2001; 2001US-00006430.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Graham MJ, Dobie K;
XX
XX      WPI; 2003-810907/76.
XX
XX      Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX      inhibiting the expression of CD81, useful for treating infections and
XX      disease associated with expression of CD81 such as inflammation disorder.
XX
XX      Claim 3; SEQ ID NO 66; 55pp; English.
XX
XX      The invention relates to a compound (antisense oligonucleotide)
XX      hybridizing with the eighth nucleobase portion of an active site on a
XX      nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX      and inhibiting the expression of CD81. Also included is a composition
XX      comprising the antisense oligonucleotide and a carrier or a diluent. The
XX      antisense oligonucleotide is useful for inhibiting the expression of CD81
XX      in cells or tissues. The antisense oligonucleotide is also useful for
XX      treating infections preferably viral, bacterial and parasitic and
XX      diseases such as inflammatory disorders and autoimmune disorders. The
XX      disease or condition is characterised by chemical dependency (e.g.
XX      cocaine addiction). The present sequence is a CD81 antisense
XX      oligonucleotide of the invention.
XX
XX      Sequence 20 BP; 4 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
XX
XX      Query Match      1.3%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 33;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1242 CTCTCTGGGAGCCACTGCG 1261
XX      Db      20 CTCTCTGGGAGCCACTGCG 1
XX
XX      RESULT 58
XX      ADC35602/c
XX      ID ADC35602 standard; DNA; 20 BP.
XX
XX      AC      ADC35602;
XX
XX      DT      18-DEC-2003 (first entry)
XX
XX      DE      Human CD81/TAPA-1 antisense oligonucleotide #62.
XX
XX      Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX      cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX      virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX      bacterial infection.
XX
XX      OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1..20
XX      /*tag= b
XX      /mod_base= OTHER
XX

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FT      /note= "Phosphorothioate backbone and all cytidines are 5
FT      -methyl cytidines"
FT      modified_base
FT      1..5
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl nucleotide"
FT      modified_base
FT      16..20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl nucleotide"
XX
XX      US2003113914-A1.
XX
XX      19-JUN-2003.
XX
XX      10-DEC-2001; 2001US-00006430.
XX
XX      10-DEC-2001; 2001US-00006430.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Graham MJ, Dobie K;
XX
XX      WPI; 2003-810907/76.
XX
XX      Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX      inhibiting the expression of CD81, useful for treating infections and
XX      disease associated with expression of CD81 such as inflammation disorder.
XX
XX      Claim 3; SEQ ID NO 74; 55pp; English.
XX
XX      The invention relates to a compound (antisense oligonucleotide)
XX      hybridizing with the eighth nucleobase portion of an active site on a
XX      nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX      and inhibiting the expression of CD81. Also included is a composition
XX      comprising the antisense oligonucleotide and a carrier or a diluent. The
XX      antisense oligonucleotide is useful for inhibiting the expression of CD81
XX      in cells or tissues. The antisense oligonucleotide is also useful for
XX      treating infections preferably viral, bacterial and parasitic and
XX      diseases such as inflammatory disorders and autoimmune disorders. The
XX      disease or condition is characterised by chemical dependency (e.g.
XX      cocaine addiction). The present sequence is a CD81 antisense
XX      oligonucleotide of the invention.
XX
XX      Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX      Query Match      1.3%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 33;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1409 ACACGTCGCGCTTCACTGTA 1428
XX      Db      20 ACACGTCGCGCTTCACTGTA 1
XX
XX      RESULT 59
XX      ADC35542/c
XX      ID ADC35542 standard; DNA; 20 BP.
XX
XX      AC      ADC35542;
XX
XX      DT      18-DEC-2003 (first entry)
XX
XX      DE      Human CD81/TAPA-1 antisense oligonucleotide #2.
XX
XX      Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX      cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX      virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX      bacterial infection.
XX
XX      OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1..20
XX      /*tag= b
XX      /mod_base= OTHER
XX

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FT modified_base 1..20
FT /mod_base= b
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /mod_base= a
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /mod_base= OTHER
FT /tag= c
FT /note= "2'-methoxyethyl nucleotide"
XX
XX US2003113914-A1.
XX 19-JUN-2003.
XX 10-DEC-2001; 2001US-00006430.
XX 10-DEC-2001; 2001US-00006430.
XX (ISIS-) ISIS PHARM INC.
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 14; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 9 A; 5 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 33;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 291 ATTTCGTCCTTCGCTGGCT 310
XX |||||
XX 20 ATTTCGTCCTTCGCTGGCT 1
XX
XX RESULT 60
XX ADC35553/c
XX ID ADC35553 standard; DNA; 20 BP.
XX
XX AC ADC35553;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #13.
XX
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX

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```

OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone and all cytidines are 5
XX -methyl cytidines"
XX modified_base 1..5
XX /mod_base= a
XX /note= "2'-methoxyethyl nucleotide"
XX modified_base 16..20
XX /mod_base= OTHER
XX /tag= c
XX /note= "2'-methoxyethyl nucleotide"
XX
XX US2003113914-A1.
XX 19-JUN-2003.
XX 10-DEC-2001; 2001US-00006430.
XX 10-DEC-2001; 2001US-00006430.
XX (ISIS-) ISIS PHARM INC.
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Example 15; SEQ ID NO 25; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 8 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 33;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 410 TTCTATGTAGGCATCTACAT 429
XX |||||
XX 20 TTCTATGTAGGCATCTACAT 1
XX
XX Db
XX
XX RESULT 61
XX ADC35576/c
XX ID ADC35576 standard; DNA; 20 BP.
XX
XX AC ADC35576;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #36.
XX
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX

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KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Graham MJ, Dobie K;
 XX
 DR WPI; 2003-810907/76.
 XX
 PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX
 PS Claim 3; SEQ ID NO 48; 55pp; English.
 XX
 CC The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 896 ATGATCTGACATGGTGCT 915
 Db 20 ATGATCTGACATGGTGCT 1
 RESULT 62
 ADC35596/c
 ID ADC35596 standard; DNA; 20 BP.
 XX
 AC ADC35596;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #56.

XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Graham MJ, Dobie K;
 XX
 DR WPI; 2003-810907/76.
 XX
 PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX
 PS Claim 3; SEQ ID NO 68; 55pp; English.
 XX
 CC The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1309 GCCCGTCCTGTGGGTGCAC 1328
 Db 20 GCCCGTCCTGTGGGTGCAC 1
 RESULT 63
 ADC35541/c
 ID ADC35541 standard; DNA; 20 BP.
 XX
 AC ADC35541;
 XX

```
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #1.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addition; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
PI Graham MJ, Dobie K;
PI WPI; 2003-810907/76.
XX
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 15; SEQ ID NO 13; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATTGCTGGAAGCGC 20
DB 20 CCATTGCTGGAAGCGC 1
RESULT 64
ADC35546/c
ID ADC35546 standard; DNA; 20 BP.
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XX ADC35546;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #6.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addition; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
PI Graham MJ, Dobie K;
PI WPI; 2003-810907/76.
XX
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 15; SEQ ID NO 18; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 9 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 277 GCTCTGCTCTCAATTTCG 296
DB 20 GCTCTGCTCTCAATTTCG 1
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RESULT 65
ADC35559/c
ID ADC35559 standard; DNA; 20 BP.
XX
AC ADC35559;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #19.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PS Claim 3; SEQ ID NO 31; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 592 GATGCCAAGGATGTGAAGC 611
|||||

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Db 20 GATGCCAAGGATGTGAAGC 1
RESULT 66
ADC35601/c
ID ADC35601 standard; DNA; 20 BP.
XX
AC ADC35601;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #61.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PS Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PS inhibiting the expression of CD81, useful for treating infections and
PS disease associated with expression of CD81 such as inflammation disorder.
XX
SQ Example 15; SEQ ID NO 73; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1393 GCACCTGTCTTCTTAACAC 1412
DB 20 GCACCTGTCTTCTTAACAC 1

RESULT 67
ADC35604/c
ID ADC35604 standard; DNA; 20 BP.
XX
AC ADC35604;
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #64.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 76; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1430 TCACAACATCTCTGACTCCGT 1449
DB 20 TCACAACATCTCTGACTCCGT 1

RESULT 68
ADC35532
ID ADC35532 standard; DNA; 20 BP.
XX
AC ADC35532;
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 RT-PCR primer #1.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection; PCR; primer; RT-PCR; reverse transcriptase PCR;
KW GAPDH; glyceraldehyde-3-phosphate dehydrogenase.
XX
OS Homo sapiens.
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 13; SEQ ID NO 4; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a reverse transcriptase (RT)-
CC PCR primer (either for CD81 or glyceraldehyde-3-phosphate dehydrogenase,
CC GAPDH) used to assay the level of mRNA pre and post treatment with the
CC antisense oligonucleotides.
XX
SQ Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 590 CAGATCGCCCAAGGATGTGAA 609
DB 1 CAGATCGCCCAAGGATGTGAA 20

```
RESULT 69
ADC35573/c
ID ADC35573 standard; DNA; 20 BP.
XX
AC ADC35573;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #33.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PS Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 45; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 857 ATGCTGCCATCGTGTGCG 876

|||||||

```
Db 20 ATGCTGCCATCGTGTGCG 1
RESULT 70
ADC35562/c
ID ADC35562 standard; DNA; 20 BP.
XX
AC ADC35562;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #22.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PS Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 34; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 607 GAAGCAGTCTATGACCAGG 626
|||||
Db 20 GAAGCAGTCTATGACCAGG 1

RESULT 71
ADC35565/c
ID ADC35565 standard; DNA; 20 BP.
XX
AC ADC35565;
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #25.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 37; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 747 TCAAGACAATTGTGTCCC 766
|||||
Db 20 TCAAGACAATTGTGTCCC 1

RESULT 72
ADC35578/c
ID ADC35578 standard; DNA; 20 BP.
XX
AC ADC35578;
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #38.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 15; SEQ ID NO 50; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.

```
XX SQ Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 907 CATGGTCTGCTGTGGCA 926
Db 20 CATGGTCTGCTGTGGCA 1

RESULT 73
ADC35580/c
ID ADC35580-standard; DNA; 20 BP.
XX AC ADC35580;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 antisense oligonucleotide #40.
XX KW Antisense; ss; human; CD81; TAPA-1; tetraepanin; viral infection;
XX KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX KW bacterial infection.
XX OS Homo sapiens.
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5 /*tag= a
FT /mod_base= OTHER
FT modified_base 16..20 /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX PN 19-JUN-2003.
XX PD 10-DEC-2001; 2001US-00006430.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX PI WPI; 2003-810907/76.
XX DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 52; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridizing with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
```

```
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 917 TGCTGTGCATCCGGAACAG 936
Db 20 TGCTGTGCATCCGGAACAG 1

RESULT 74
ADC35603/c
ID ADC35603 standard; DNA; 20 BP.
XX AC ADC35603;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 antisense oligonucleotide #63.
XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX KW bacterial infection.
XX OS Homo sapiens.
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5 /*tag= a
FT /mod_base= OTHER
FT modified_base 16..20 /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX PN 19-JUN-2003.
XX PD 10-DEC-2001; 2001US-00006430.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX PI WPI; 2003-810907/76.
XX DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 75; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridizing with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
```

CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1415 CGCCTTCAACTGTAATCACA 1434
 |||||
 DB 20 CGCCTTCAACTGTAATCACA 1

RESULT 75
 ADC35606/c
 ID ADC35606 standard; DNA; 20 BP.
 XX
 AC ADC35606;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #66.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Graham MJ, Dobie K;
 XX
 DR WPI; 2003-810907/76.
 XX
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX
 PS Claim 3; SEQ ID NO 78; 55pp; English.
 XX
 CC The invention relates to a compound (antisense oligonucleotide)
 CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)

CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 4 C; 2 G; 9 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1447 CGTCATTTAATAAAGAAGA 1466
 |||||
 DB 20 CGTCATTTAATAAAGAAGA 1

RESULT 76
 ADC35547/c
 ID ADC35547 standard; DNA; 20 BP.
 XX
 AC ADC35547;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #7.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Graham MJ, Dobie K;
 XX
 DR WPI; 2003-810907/76.
 XX
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX
 PS Example 15; SEQ ID NO 19; 55pp; English.
 XX

CC The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 9 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 286 CTTCAATTGCTTCTGGC 305
 DB 20 CTTCAATTGCTTCTGGC 1

RESULT 77
 ADC35549/C
 ID ADC35549 standard; DNA; 20 BP.
 AC ADC35549;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #9.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PP 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Graham MJ, Dobie K;
 PI WPI; 2003-810907/76.
 XX
 DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 XX inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.

XX
 PS Claim 3; SEQ ID NO 21; 55pp; English.
 XX
 CC The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 304 GCTGGCTGGAGCGTGATCC 323
 DB 20 GCTGGCTGGAGCGTGATCC 1

RESULT 78
 ADC35561/C
 ID ADC35561 standard; DNA; 20 BP.
 AC ADC35561;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #21.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PP 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Graham MJ, Dobie K;
 PI WPI; 2003-810907/76.
 XX
 DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 XX inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.

PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 PS Example 15; SEQ ID NO 33; 55pp; English.

XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 602 GATGTGAGCAGTCTCTATCA 621

Db 20 GATGTGAGCAGTCTCTATCA 1

RESULT 79

ADC35563/c
 ID ADC35563 standard; DNA; 20 BP.

XX ADC35563;

XX 18-DEC-2003 (first entry)

XX Human CD81/TAPA-1 antisense oligonucleotide #23.

KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone and all cytidines are 5

FT -methyl cytidines"

FT modified_base 1..5

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

XX US2003113914-A1.

XX 19-JUN-2003.

XX 10-DEC-2001; 2001US-00006430.

XX 10-DEC-2001; 2001US-00006430.

XX (ISIS-) ISIS PHARM INC.

XX Graham MJ, Dobie K;

XX

XX WPI; 2003-810907/76.

XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.

XX Claim 3; SEQ ID NO 35; 55pp; English.

XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 33;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 665 GCCAAGGCTGTGTTGAAGAC 684

Db 20 GCCAAGGCTGTGTTGAAGAC 1

RESULT 80

ADC35570/c

ID ADC35570 standard; DNA; 20 BP.

XX ADC35570;

XX 18-DEC-2003 (first entry)

XX Human CD81/TAPA-1 antisense oligonucleotide #30.

KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone and all cytidines are 5

FT -methyl cytidines"

FT modified_base 1..5

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

XX US2003113914-A1.

XX 19-JUN-2003.

XX 10-DEC-2001; 2001US-00006430.

XX 10-DEC-2001; 2001US-00006430.

XX

```
PA (ISIS-) ISIS PHARM INC.
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX Claim 3; SEQ ID NO 42; 55pp; English.
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridizing with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 836 GGGAGCTGTACCTCATCGG 855
DB 20 GGGAGCTGTACCTCATCGG 1
RESULT 81
ADC35575/c
ID ADC35575 standard; DNA; 20 BP.
AC ADC35575;
XX 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #35.
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX Homo sapiens.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone and all cytidines are 5
XX modified_base 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotide"
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX 19-JUN-2003.
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX Example 15; SEQ ID NO 47; 55pp; English.
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridizing with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 884 ATGATCTTCGAGATGATCCT 903
DB 20 ATGATCTTCGAGATGATCCT 1
RESULT 82
ADC35583/c
ID ADC35583 standard; DNA; 20 BP.
AC ADC35583;
XX 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #43.
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX Homo sapiens.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone and all cytidines are 5
XX modified_base 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotide"
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX
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PD 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 55; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 33;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 935 AGCTCGGTACTGAGGCC 954
Db 20 AGCTCGGTACTGAGGCC 1

RESULT 83
ADC35592/c
AC ADC35592;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #52.
XX
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"

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XX US2003113914-A1.
XX
XX 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 64; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 8 C; 7 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 33;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1205 CCTGGGGTCCCAGGTGCTC 1224
Db 20 CCTGGGGTCCCAGGTGCTC 1

RESULT 84
ADC35600/c
ID ADC35600 standard; DNA; 20 BP.
XX
XX ADC35600;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #60.
XX
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"

```

```
FT FT      /*tag= c
FT FT      /mod_base= OTHER
XX XX      /note= "2'-methoxyethyl nucleotide"
PN PN      US2003113914-A1.
XX XX      19-JUN-2003.
XX XX      10-DEC-2001; 2001US-00006430.
XX XX      10-DEC-2001; 2001US-00006430.
PA (ISIS-) ISIS PHARM INC.
XX Graham MJ, Dobie K;
PI WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
PS Claim 3; SEQ ID NO 72; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridizing with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1375 GGCACCTCTGCTTCATGC 1394
DB 20 GGCACCTCTGCTTCATGC 1
RESULT 85
AAQ75716/c
XX AAQ75716 standard; DNA; 21 BP.
XX AAQ75716;
XX
XX 04-AUG-1995 (first entry)
Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1477 TGCTAAAAA 1496
DB 21 TGCTAAAAA 2
RESULT 86
AAQ75661/c
XX AAQ75661 standard; DNA; 21 BP.
XX AAQ75661;
XX
XX 04-AUG-1995 (first entry)
Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.3%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1476 ATGCTAATAAAAAAAAAAAAAA 1496
 ||||| ||||| ||||| ||||| |||||
 Db 21 ATGCAAAAAAAAAAAAAAAAAA 1

RESULT 87
 AAQ49436/c
 ID AAQ49436 standard; cDNA; 20 BP.
 XX
 AC AAQ49436;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-APR-1994 (first entry)
 XX
 XX Cytochrome P450 sequence amplification PCR primer polyT.
 DE Transgenic plants; altered petal colour; polymerase chain reaction; ss.
 KW Synthetic.
 OS
 XX WO9320206-A1.
 PN 14-OCT-1993.
 PD
 XX 25-MAR-1993; 93WO-AU000127.
 PF
 XX 27-MAR-1992; 92AU-00001538.
 PR 07-JAN-1993; 93AU-00006698.
 XX
 PA (ITFL-) INT FLOWER DEV PTY LTD.
 XX
 PI Holton TA, Cornish BC, Tanaka Y;
 XX
 DR WPI; 1993-336914/42.
 XX
 PT Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to
 PT create transgenic plants with altered petal colour.
 XX
 PS Disclosure; Page 25; 86pp; English.
 XX
 CC The sequence is that of a PCR primer which was used in polymerase chain
 CC reactions for the amplification of cloned cytochrome P450 sequences.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 GCTAATAAAAAAAAAAAAAA 1496
 ||||| ||||| ||||| ||||| |||||
 Db 20 GCTAATAAAAAAAAAAAAAA 2

RESULT 88
 AAQ75578/c
 ID AAQ75578 standard; DNA; 20 BP.
 XX
 AC AAQ75578;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX

PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 GCTAATAAAAAAAAAAAAAA 1496
 ||||| ||||| ||||| ||||| |||||
 Db 20 GCTAATAAAAAAAAAAAAAA 2

RESULT 89
 ABZ88266
 ID ABZ88266 standard; DNA; 20 BP.
 XX
 AC ABZ88266;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIC-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

```
XX PS Disclosure; SEQ ID NO 3508; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
    Query Match      1.3%; Score 19; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 52;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1478 GCTAAAAA1496
DB 1 GCTAAAAA1496
RESULT 90
AAQ7518/c
ID AAQ7518 standard; DNA; 21 BP.
AC AAQ7518;
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
    Query Match      1.3%; Score 19; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 57;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1478 GCTAAAAA1496
DB 20 GCTAAAAA1496
RESULT 92
AAQ7517/c
ID AAQ7517 standard; DNA; 21 BP.
XX AAQ7517;
XX 04-AUG-1995 (first entry)
```

```
XX PS Disclosure; SEQ ID NO 3508; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
    Query Match      1.3%; Score 19; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 52;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1478 GCTAAAAA1496
DB 1 GCTAAAAA1496
RESULT 90
AAQ7518/c
ID AAQ7518 standard; DNA; 21 BP.
AC AAQ7518;
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
```

XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
PN
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1478 GCTAATAAAAAAAAAAAAAA 1496
DB 20 GCTAATAAAAAAAAAAAAAA 2
XX
RESULT 93
ABZ00175/c
ID ABZ00175 standard; DNA; 50 BP.
XX
XX ABZ00175;
AC
XX 09-JAN-2003 (first entry)
DT
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 166.
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
XX Homo sapiens.
OS
XX
XX WO200257414-A2.
PN
XX 25-JUL-2002.
PD
XX
XX 22-OCT-2001; 2001WO-US047856.
PF
XX 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
PA
XX

PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quettermous T, Johnson F;
XX
DR WPI; 2002-636525/68.
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 332; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 11 A; 18 C; 6 G; 15 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 19; DB 1; Length 50;
Best Local Similarity 65.1%; Pred. No. 2.4e+02;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1127 TGATGTCACTAGTGGCGGTGTATGATGAGTGAGACGGGCGCTG 1169
DB 48 TGATTACAGTTGAAGGCGACGGTGTAGAAAGACAGGTGCATG 6
XX
RESULT 94
AAQ75572/c
ID AAQ75572 standard; DNA; 20 BP.
XX
XX AAQ75572;
AC
XX 04-AUG-1995 (first entry)
DT
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1478 GCTAATAAAAAAAAAAAAAA 1496
DB 20 GCTAATAAAAAAAAAAAAAA 2
XX
RESULT 93
ABZ00175/c
ID ABZ00175 standard; DNA; 50 BP.
XX
XX ABZ00175;
AC
XX 09-JAN-2003 (first entry)
DT
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 166.
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
XX Homo sapiens.
OS
XX
XX WO200257414-A2.
PN
XX 25-JUL-2002.
PD
XX
XX 22-OCT-2001; 2001WO-US047856.
PF
XX 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
PA
XX

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 68;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 TGCCTAAAAA 1496
 ||| |||
 DB 20 TGCCTAAAAA 1496
 ||| |||

RESULT 95
 AAQ75748/c
 ID AAQ75748 standard; DNA; 21 BP.
 XX
 AC AAQ75748;
 XX
 DT
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; Gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.2%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 75;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 TGCCTAAAAA 1496
 ||| |||
 DB 21 TGCCTAAAAA 2
 ||| |||

RESULT 96
 AAQ75620/c
 ID AAQ75620 standard; DNA; 21 BP.
 XX
 AC AAQ75620;
 XX
 DT 04-AUG-1995 (first entry)
 XX

PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 TGCTAAAAA 1496
||| |||||
DB 21 TGTAAAAA 2

RESULT 98
AAQ75660/c
ID AAQ75660 standard; DNA; 21 BP.
XX
AC AAQ75660;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 TGCTAAAAA 1496
||| |||||
DB 21 TGTAAAAA 2

RESULT 98
AAQ75660/c
ID AAQ75660 standard; DNA; 21 BP.
XX
AC AAQ75660;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 TGCTAAAAA 1496
||| |||||
DB 21 TGTAAAAA 2

RESULT 98
AAQ75660/c
ID AAQ75660 standard; DNA; 21 BP.
XX
AC AAQ75660;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.

DB 20 TGCAAAAAAAAAAAAAAAAA 1

RESULT 99
AAQ75684/c
ID AAQ75684 standard; DNA; 21 BP.
XX
AC AAQ75684;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
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XX
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XX
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CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 TGCTAAAAA 1496
||| |||||
DB 21 TGATAAAAAAAAAAAAAAAAA 2

RESULT 100
AAQ75700/c
ID AAQ75700 standard; DNA; 21 BP.
XX
AC AAQ75700;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.

```

XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PS WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
      Query Match 1.2%; Score 18.4; DB 1; Length 21;
      Best Local Similarity 95.0%; Pred. No. 75;
      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1477 TCGTAAAAAATAAAAAAAAAA 1496
DB 21 TCGTAAAAAATAAAAAAAAAA 2
      RESULT 101
      AAQ75659/c
      ID AAQ75659 standard; DNA; 21 BP.
      AC AAQ75659;
      DT 04-AUG-1995 (first entry)
      XX Reverse transcription primer used in cDNA analysis technique.
      XX Analysis; gene expression; reverse transcription; primer; cDNA;
      KW aggregate; restriction enzyme; ss.
      XX Synthetic.
      OS JP06303997-A.
      PN 01-NOV-1994.
      PD 16-APR-1993; 93JP-00112515.
      XX 16-APR-1993; 93JP-00112515.
      PR 16-APR-1993; 93JP-00112515.
      XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
      PA WPI; 1995-018287/03.
      XX Analysis of cDNA and gene expression - by amplification of mRNA followed
      XX PT by digestion with restriction enzymes.
      XX PS Disclosure; Page 6; 11pp; Japanese.
      XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
      XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
      XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
      XX CC and using the aggregate of mRNAs as the template for each reverse
      XX CC transcription primer; (b) digesting each of the prepared aggregates of
      XX CC the double-stranded cDNAs with restriction enzyme and; (c)
      XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
      XX CC method can be used to analyse gene expression rapidly and easily

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XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
      Query Match 1.2%; Score 18.4; DB 1; Length 21;
      Best Local Similarity 95.0%; Pred. No. 75;
      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1477 TCGTAAAAAATAAAAAAAAAA 1496
DB 20 TCGTAAAAAATAAAAAAAAAA 1
      RESULT 102
      AAQ75712/c
      ID AAQ75712 standard; DNA; 21 BP.
      XX AAQ75712;
      AC AAQ75712;
      XX 04-AUG-1995 (first entry)
      XX Reverse transcription primer used in cDNA analysis technique.
      XX Analysis; gene expression; reverse transcription; primer; cDNA;
      KW aggregate; restriction enzyme; ss.
      XX Synthetic.
      OS JP06303997-A.
      PN 01-NOV-1994.
      PD 16-APR-1993; 93JP-00112515.
      XX 16-APR-1993; 93JP-00112515.
      PR 16-APR-1993; 93JP-00112515.
      XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
      PA WPI; 1995-018287/03.
      XX Analysis of cDNA and gene expression - by amplification of mRNA followed
      XX PT by digestion with restriction enzymes.
      XX PS Disclosure; Page 7; 11pp; Japanese.
      XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
      XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
      XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
      XX CC and using the aggregate of mRNAs as the template for each reverse
      XX CC transcription primer; (b) digesting each of the prepared aggregates of
      XX CC the double-stranded cDNAs with restriction enzyme and; (c)
      XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
      XX CC method can be used to analyse gene expression rapidly and easily
      XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
      Query Match 1.2%; Score 18.4; DB 1; Length 21;
      Best Local Similarity 95.0%; Pred. No. 75;
      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1477 TCGTAAAAAATAAAAAAAAAA 1496
DB 21 TACTAAAAAATAAAAAAAAAA 2
      RESULT 103
      AAQ75704/c
      ID AAQ75704 standard; DNA; 21 BP.
      XX AAQ75704;
      AC AAQ75704;
      XX 04-AUG-1995 (first entry)
      XX

```

```
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 1lpp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
    Query Match 1.2%; Score 18.4; DB 1; Length 21;
    Best Local Similarity 95.0%; Pred. No. 75;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    OY 1477 TCGTAAAAA 1496
    Db 21 TCCTAAAAA 1
RESULT 104
AAQ75708/c
ID AAQ75708 standard; DNA; 21 BP.
XX
AC AAQ75708;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 1lpp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
    Query Match 1.2%; Score 18.4; DB 1; Length 21;
    Best Local Similarity 95.0%; Pred. No. 75;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    OY 1477 TCGTAAAAA 1496
    Db 21 TCCTAAAAA 2
RESULT 105
AAQ75662/c
ID AAQ75662 standard; DNA; 21 BP.
XX
AC AAQ75662;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 1lpp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
    Query Match 1.2%; Score 18.4; DB 1; Length 21;
    Best Local Similarity 95.0%; Pred. No. 75;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    OY 1477 TCGTAAAAA 1496
    Db 20 TCGAAAAA 1
Query Match 1.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1477 TCGTAAAAA 1496
Db 20 TCGAAAAA 1
```

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XX DE RESULT 106
XX ID ADC35533/C
XX KW ADC35533 standard; DNA; 18 BP.
XX AC ADC35533;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 RT-PCR primer #2.
XX DE Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
XX KW bacterial infection; PCR; primer; RT-PCR; reverse transcriptase PCR;
XX KW GAPDH; glyceraldehyde-3-phosphate dehydrogenase.
XX OS Homo sapiens.
XX US2003113914-A1.
XX PN 19-JUN-2003.
XX PD 10-DEC-2001; 2001US-00006430.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PS (ISIS-) ISIS PHARM INC.
XX PA Graham MJ, Dobie K;
XX PI WPI; 2003-810907/76.
XX DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Example 13; SEQ ID NO 5; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridizing with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX CC disease or condition is characterised by chemical dependency (e.g.
XX CC cocaine addiction). The present sequence is a reverse transcriptase (RT)-
XX CC PCR primer (either for CD81 or glyceraldehyde-3-phosphate dehydrogenase,
XX CC GAPDH) used to assay the level of mRNA pre and post treatment with the
XX CC antisense oligonucleotides.
XX SQ Sequence 18 BP; 2 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 TGATGACGCCCAACGCG 666
DB 18 TGATGACGCCCAACGCG 1

RESULT 107
AAQ75551/C
ID AAQ75551 standard; DNA; 19 BP.
AC AAQ75551;
XX DT 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.
Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
Synthetic.
JP06303997-A.
01-NOV-1994.
16-APR-1993; 93JP-00112515.
16-APR-1993; 93JP-00112515.
(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
WPI; 1995-018287/03.
Analysis of cDNA and gene expression - by amplification of mRNA followed

XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX WPI; 1995-018287/03.
XX DR Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAA 1496
DB 19 CTAAAAAATAAAAAA 2

RESULT 108
AAQ75575/C
ID AAQ75575 standard; DNA; 20 BP.
AC AAQ75575;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX WPI; 1995-018287/03.
XX DR Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.

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PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
    Query Match      1.2%; Score 18; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 81;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
    |||||
DB 19 CTAAGAAAAA 2

RESULT 109
AAQ75577/c
ID AAQ75577 standard; DNA; 20 BP.
XX
XX
AC AAQ75577;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match      1.2%; Score 18; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 81;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
    |||||
DB 19 CTAAGAAAAA 2

RESULT 111
AAQ75577/c
ID AAQ75577 standard; DNA; 20 BP.
XX
XX
AC AAQ75577;
XX
XX 25-MAR-2003 (revised)
XX
DT 15-MAY-1996 (first entry)
XX
DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.
XX
XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS Synthetic.
XX
XX EP676470-A1.

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XX PD 11-OCT-1995.
XX PF 04-OCT-1990; 95EP-00105391.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 28-SEP-1990; 90MO-US005548.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 01-OCT-1990; 90US-00589701.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX PI WPI; 1995-346090/45.
XX DR WPI; 1995-346090/45.
XX PT New stem cell factor polypeptide(s) - for stimulating the growth of
XX PT primitive progenitor cells, esp. for treating disorders involving blood
XX PT cells.
XX PS Example 3; Fig 12C; 127pp; English.
XX CC AAT04915-T04922 are oligonucleotide primers and probes used for the
XX CC amplification and sequencing of mammalian stem cell factor (SCF). Non-
XX CC naturally occurring SCF and C-terminally truncated polypeptides, having
XX CC amino acid sequences sufficiently duplicative of naturally occurring SCF,
XX CC stimulate growth of primitive progenitors such as haematopoietic
XX CC progenitor cells, neural stem cells and primordial germ stem cells. The
XX CC peptides can be used in a composition for treating leucopenia, anaemia or
XX CC thrombocytopenia, for enhancing engraftment of bone marrow during
XX CC transplantation or for bone marrow recovery after chemotherapy or
XX CC radiation-induced bone marrow aplasia or myelosuppression. They can also
XX CC be used for treating neoplasia, nerve damage, infertility, intestinal
XX CC damage or myeloproliferative disorders. Antibodies may be raised against
XX CC the peptides for use in detection or neutralisation of SCF in serum. SCF
XX CC may be useful for the treatment of AIDS and severe combined
XX CC immunodeficiency (SCID) states alone or in combination with other factors
XX CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX CC Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX SQ Query Match 1.2%; Score 18; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 81;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1479 CTAATAAAAAAAAAAAAAA 1496
XX DB 20 CTAATAAAAAAAAAAAAAA 3
XX RESULT 112
XX AAAL3753/C
XX ID AAAL3753 standard; DNA; 20 BP.
XX AC AAAL3753;
XX XX 27-JUL-2000 (first entry)
XX DT Stem cell factor universal oligonucleotide 220-7.
XX DE Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
XX KW primitive progenitor cell; haematopoietic disorder; syngeneic;
XX KW allogeneic; autologous bone marrow transplant; gene therapy;
XX KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
XX KW cancer; ss.
XX OS Synthetic.
XX OS EP992579-A1.
XX PN EP992579-A1.
XX XX 12-APR-2000.
XX PD 12-APR-2000.
XX PF 31-DEC-1998; 98US-00224681.

PF 04-OCT-1990; 99EP-00122861.
XX 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 28-SEP-1990; 90MO-US005548.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 04-OCT-1990; 90EP-00310899.
XX XX (AMGE-) AMGEN INC.
XX XX Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
XX XX WPI; 2000-259135/23.
XX DR WPI; 2000-259135/23.
XX PT Production of hematopoietic cells suitable for administration to a
XX PT subject using progenitor cells and expanding the cells using stem cell
XX PT factor.
XX PS Example 3; Fig 12C; 123pp; English.
XX CC A method has been developed of making haematopoietic cells suitable for
XX CC administration to a subject. The method comprises: (a) obtaining the cells
XX CC haematopoietic progenitor cells from a donor; and (b) expanding the cells
XX CC by adding to the cells a haematopoietically effective dose of a
XX CC polypeptide product having at least part of the primary structural
XX CC confirmation and one or more of the biological properties of naturally
XX CC occurring stem cell factor (SCF). The method is useful for stimulating
XX CC primitive progenitor cells including early haematopoietic progenitor
XX CC cells which are capable of maturing to erythroid, megakaryocyte,
XX CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
XX CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
XX CC SCF is useful for treating haematopoietic disorders. The method is useful
XX CC for expanding early haematopoietic progenitors in syngeneic, allogeneic
XX CC or autologous bone marrow transplant. SCF is useful for enhancing the
XX CC efficiency of gene therapy based on transfecting haematopoietic stem
XX CC cells. SCF is also useful for combating the myelosuppressive effects of
XX CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
XX CC after acute blood loss and as a boost to the immune system for fighting
XX CC neoplasia (cancer). The present sequence represents a universal
XX CC oligonucleotide which is used in an example from the present invention
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX Query Match 1.2%; Score 18; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 81;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1479 CTAATAAAAAAAAAAAAAA 1496
XX DB 20 CTAATAAAAAAAAAAAAAA 3
XX RESULT 113
XX AAH41332/C
XX ID AAH41332 standard; DNA; 20 BP.
XX AC AAH41332;
XX XX 21-AUG-2001 (first entry)
XX DT Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.
XX DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.
XX KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
XX KW gene therapy; PCR primer; mutagenesis; probe; ss.
XX OS Synthetic.
XX OS US6207454-B1.
XX PN US6207454-B1.
XX XX 27-MAR-2001.
XX PD 27-MAR-2001.
XX PF 31-DEC-1998; 98US-00224681.

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XX 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
PR 24-MAY-1995; 95US-00449653.
PR 12-JAN-1998; 98US-00005893.
XX (AMGE-) AMGEN INC.
PA
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI WPI; 2001-366062/38.
XX
XX Enhancing efficiency of polynucleotide into a target
PT mammalian cell in vitro, involves exposing cell that expresses a stem
PT cell factor receptor to stem cell factor, and introducing polynucleotide
PT into cell in vitro.
XX
XX Example 3; Fig 12C; 210pp; English.
PS
XX The present invention describes a method for enhancing (E) the efficiency
CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC receptor to a biologically active SCF, its analogue or fragment, which
CC induces cell proliferation, and introducing (I) to (II) in vitro.
CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC The method is useful for enhancing the efficiency of the transfer of a
CC polynucleotide into a target mammalian cell in vitro. The method is
CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC AAB98390 represent sequences used in the exemplification of the present
CC invention
XX
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
DB 20 CTAAAAAATAAAAAAAAAA 3

RESULT 114
AA04112/c
ID AA04112 standard; DNA; 20 BP.
XX
XX AA04112;
AC
XX
XX 29-AUG-2001 (first entry)
DT
XX
XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
DE
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX US6207417-B1.
PN
XX
XX 27-MAR-2001.
PD
XX
XX 07-JUN-1995; 95US-00482918.
PF
XX
XX 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.

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PR 21-DEC-1993; 93US-00172329.
XX
XX (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
XX (MART/) MARTIN F H.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI WPI; 2001-298941/31.
XX
XX Novel nucleic acids encoding stem cell factor useful for treating
PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
PT disease, Kala azar, anemia and septicemia.
XX
XX Example 3; Fig 12C; 209pp; English.
PS
XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal
CC oligonucleotides (AA04110-AA04117) used in the isolation of the human
CC SCF (stem cell factor) cDNA sequence. The present invention relates to
CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC including early haematopoietic progenitor cells. The invention also
CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
CC (AA04081-AA04117) used in the isolation of human and rat SCF sequences.
CC The polynucleotide encoding SCF is useful for producing SCF and useful in
CC gene therapy. It is useful for treating disorders involving blood cells
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC disorders such as piebaldism and vitiligo
XX
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
DB 20 CTAAAAAATAAAAAAAAAA 3

RESULT 115
AAF89092/c
ID AAF89092 standard; DNA; 20 BP.
XX
XX AAF89092;
AC
XX
XX 13-JUL-2001 (first entry)
DT
XX
XX Mammalian stem cell factor PCR primer SEQ ID NO: 33.
DE
XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW neurological damage; intestinal damage; infertility; AIDS; SCID;
KW severe combined immunodeficiency; PCR primer; ss.
XX
XX Mammalia.
OS
XX
XX US6207802-B1.
PN
XX
XX 27-MAR-2001.
PD
XX
XX 09-NOV-1994; 94US-00336728.
PF
XX
XX 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 25-NOV-1992; 92US-00982255.

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XX PA (AMGE-) AMGEN INC.
XX PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX XX WPI; 2001-353108/37.
XX DR
XX PT Novel isolated non-human mammalian stem cell factor polypeptide
XX PT stimulating growth of early hematopoietic progenitor cells, useful for
XX PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
XX PT sarcoidosis.
XX XX Example 3; Fig 12C; 209pp; English.
XX XX The present invention provides the protein and coding sequences of
XX CC mammalian stem cell factors (SCFs). These are capable of stimulating the
XX CC growth of early hematopoietic progenitor cells, neural stem cells and
XX CC primordial germ stem cells. The sequences are useful in the treatment of
XX CC leukemias, hematopoietic disorders, aplastic anaemia, paroxysmal
XX CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
XX CC and intestinal damage, infertility, AIDS and severe combined
XX CC immunodeficiency (SCID). The present sequence is primer used to amplify
XX CC an SCF in the exemplification of the invention
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1496
DB 20 CTAAAAAATAAAAAAAAAA 3
RESULT 116
AAH23890/c
ID AAH23890 standard; DNA; 20 BP.
AC AAH23890;
DT 07-AUG-2001 (first entry)
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
XX PCR primer; ss.
XX Homo sapiens.
XX OS
XX US6204363-B1.
XX PN
XX PD 20-MAR-2001.
XX PF 25-NOV-1992; 92US-00982255.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 10-APR-1991; 91US-00684535.
XX PA (AMGE-) AMGEN INC.
XX PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX DR WPI; 2001-256683/26.
XX PT New stem cell factor polypeptides and their analogs which stimulate
XX PT growth of early hematopoietic progenitors, useful for treating aplastic
XX PT anemia, carcinoma, multiple myeloma, vitiligo, Kala azar, Hodgkin's

```

```

PT XX disease.
PS XX Example 3; Fig 12C; 166pp; English.
XX XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal
XX CC oligonucleotides (AAH23898-AAH23895) used in the isolation of the human
XX CC SCF (stem cell factor) cDNA sequence. The present invention relates to
XX CC novel stem cell factors (AAH73561-AAH73568, AAB73571-AAH73576) and the
XX CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX CC including early hematopoietic progenitor cells. The invention also
XX CC describes SCF peptides (AAB73578-AAH73597) and the oligonucleotides
XX CC (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
XX CC The polynucleotide encoding SCF is useful for producing SCF and useful in
XX CC gene therapy. It is useful for treating disorders involving blood cells
XX CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
XX CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
XX CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
XX CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin
XX CC B12 and folic acid deficiency, pyridoxine deficiency, and
XX CC hypopigmentation disorders such as piebaldism and vitiligo
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1496
DB 20 CTAAAAAATAAAAAAAAAA 3
RESULT 117
AAS04213/c
ID AAS04213 standard; DNA; 20 BP.
AC AAS04213;
DT 29-AUG-2001 (first entry)
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
XX PCR primer; ss.
XX Homo sapiens.
XX OS
XX US6218148-B1.
XX PN
XX PD 17-APR-2001.
XX PF 21-DEC-1993; 93US-00172329.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 25-NOV-1992; 92US-00982255.
XX PA (AMGE-) AMGEN INC.
XX PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX DR WPI; 2001-281051/29.
XX PT Isolated DNA sequence, encoding polypeptide product useful for
XX PT stimulating growth of early hematopoietic progenitor cells.
XX PS Example 3; Fig 12C; 167pp; English.
XX XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal

```

CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
 CC and the polynucleotides encoding them. SCF stimulate primitive progenitor
 CC cells including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as piebaldism and vitiligo
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
 Query Match 1.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1479 CTAAAAAATAAAAAAAAAA 1496
 DB 20 CTAAAAAATAAAAAAAAAA 3
 RESULT 118
 AAS10448/c
 ID AAS10448 standard; DNA; 20 BP.
 XX
 AC AAS10448;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human stem cell factor (SCF) cDNA universal PCR primer 220-7.
 XX
 KW Human; stem cell factor; SCF; haematopoietic progenitor cell;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6248319-B1.
 XX
 PD 19-JUN-2001.
 XX
 PF 24-MAY-1995; 95US-00449653.
 XX
 PR 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 10-APR-1991; 91US-00684535.
 PR 25-NOV-1992; 92US-00982255.
 PR 21-DEC-1993; 93US-00172329.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2001-407312/43.
 XX
 XX Increasing the number of early hematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell factor.
 XX
 PS Example 3; Fig 12C; 210pp; English.
 XX
 CC The present sequence for universal PCR primer 220-7 is 1 of 19 PCR

CC primers (AAS10435-AAS10453) used to amplify various portions of the human
 CC SCF cDNA sequence. The sequence is described in an invention relating to
 CC novel stem cell factors, the polynucleotides encoding them and methods
 CC for producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral blood
 CC by administering a haematopoietically effective human stem cell factor
 CC polypeptide. The methods are useful for the treatment of blood disorders,
 CC including myelofibrosis, myeloclerosis, osteopetrosis, metastatic
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
 CC lymphoma, Gaucher's disease, Niemann-pick disease, refractory anaemia,
 CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation
 CC disorders i.e. piebaldism and viral induced disorders, including AIDS
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
 Query Match 1.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1479 CTAAAAAATAAAAAAAAAA 1496
 DB 20 CTAAAAAATAAAAAAAAAA 3
 RESULT 119
 AAD35465/c
 ID AAD35465 standard; DNA; 20 BP.
 XX
 AC AAD35465;
 XX
 DT 25-JUL-2002 (first entry)
 XX
 DE Rat SCF 5' cDNA amplifying PCR primer, 220-7.
 XX
 KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
 KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
 KW infertility; neoplasia; myelofibrosis; myeloclerosis; osteopetrosis;
 KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
 KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-pick disease;
 KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
 KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
 KW disseminated fungus disease; Fulminating septicemia; piebaldism; AIDS;
 KW acquired immune deficiency syndrome; malaria; military tuberculosis;
 KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
 KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
 KW primer; ss.
 XX
 OS Rattus sp.
 XX
 PN US2002018763-A1.
 XX
 PD 14-FEB-2002.
 XX
 PF 12-JAN-1998; 98US-00005243.
 XX
 PR 24-MAY-1995; 95US-00449653.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2002-350789/38.
 XX
 XX Novel non-naturally-occurring stem cell factor polypeptide, useful for
 PT treating leucopenia, thrombocytopenia, anemia and for enhancing
 PT engraftment of bone marrow during transplantation in a mammal.
 XX
 PS Example 3; Fig 12C; 217pp; English.
 XX
 CC The present invention relates to novel non-naturally-occurring stem cell

CC factor (SCF) polypeptides having an amino acid sequence sufficiently
 CC duplicative of that of naturally-occurring SCF to allow possession of
 CC haematopoietic biological activity of naturally occurring SCF. Sequences
 CC of the invention are useful for treating leucopenia, thrombocytopaenia,
 CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
 CC engraftment of bone marrow during transplantation in mammals and chemical
 CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
 CC are also useful for treating acquired immune deficiency in a human, nerve
 CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
 CC damage in a mammal. SCF sequences are useful for preparing biologically
 CC active polymer polypeptide adduct, for enhancing transfection of early
 CC haematopoietic progenitor cells with a gene, and transfer of a gene into
 CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,
 CC osteoporosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
 CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
 CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
 CC splenic pancytopenia, disseminated fungus disease, malaria, military
 CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
 CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
 CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
 CC and vitiligo. The present sequence is a PCR primer which is used for
 CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
 CC exemplification of the invention

XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
 DB 20 CTAAGAAAAA 3

RESULT 120

AB573849/c

ID ABS73849 standard; DNA; 20 BP.

AC ABS73849;

DT 05-DEC-2002 (first entry)

DE SCF universal oligonucleotide 220-7.

XX Stem cell factor; SCF; blood-forming system; blood cell disorder;

XX haematopoietic system; metastatic carcinoma; acute leukaemia;

XX multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;

XX refractory erythroblastic anaemia; military tuberculosis; cytostatic;

XX disseminated fungus disease; haematopoietic; tuberculous;

XX antianaemic; antifungal; antimarial; dermatological; ss.

XX Synthetic.

XX EP1241258-A2.

PN 18-SEP-2002.

XX 04-OCT-1990; 2002EP-00008587.

XX 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 28-SEP-1990; 90NO-US005548.

PR 01-OCT-1990; 90US-00589701.

PR 04-OCT-1990; 90EP-00310899.

PR 04-OCT-1990; 95EP-00105391.

XX (AMGE-) AMGEN INC.

XX Zeebo KM, Suggs SV, Bosselman RA, Martin FH;

PI

XX

DR WPI; 2002-684093/74.

XX Production of a human stem cell factor (SCF) polypeptide for treating
 PT disorders involving blood cells, such as leukemia, comprises culturing
 PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
 PT encoding the human SCF.

XX Example 3; Fig 12C; 120pp; English.

XX The present invention relates to novel stem cell factors (SCFs),
 CC polynucleotide sequences encoding the SCFs, and methods of producing
 CC them. SCFs are involved in the blood-forming (haematopoietic) system in
 CC mammals, particularly humans. The method of the invention is useful for
 CC the production of human SCF. The stem cell factors are useful to treat
 CC disorders involving blood cells e.g. metastatic carcinoma, acute
 CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
 CC erythroblastic anaemia, military tuberculosis, disseminated fungus
 CC disease, malaria, and vitiligo. The present sequence representing a
 CC universal oligonucleotide for SCF DNA is used in the examples of the
 CC present invention

XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496

DB 20 CTAAGAAAAA 3

RESULT 121

ABA05917/c

ID ABA05917 standard; DNA; 20 BP.

AC ABA05917;

DT 05-MAR-2002 (first entry)

DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 7.

XX Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;

XX PCR primer; ss.

XX Hepatitis B virus.

XX EP1152063-A1.

XX 07-NOV-2001.

XX 03-MAY-2000; 2000EP-00109436.

XX 03-MAY-2000; 2000EP-00109436.

XX (DEKF-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Schroeder KH, Koike K;

XX WPI; 2002-068256/10.

XX Diagnosing hepatitis B virus (HBV) infection stages and determining the

PT risk for hepatocellular carcinoma, comprises identifying full length HBV

PT transcripts and truncated HBV transcripts in a serum sample.

XX Example 1; Page 6; 25pp; English.

XX The invention relates to diagnosis of hepatitis B virus (HBV) infection

CC stages comprising identification of full length HBV transcripts (I) and

CC truncated HBV transcripts (II) in a serum sample, where the ratio of I:II

CC is indicative of a particular infection stage. The method is useful for

CC diagnosing HBV infection stages and determining the risk for developing

CC hepatocellular carcinoma. The present sequence is that of a HBV

```
CC diagnostic PCR primer, useful for the invention
XX
SQ Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;

Query Match      1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 GCTAATAAAAAAAAAAAAAA 1495
DB 18 GCTAATAAAAAAAAAAAAAA 1

RESULT 122
ABZ89240
ID ABZ89240 standard; DNA; 20 BP.
XX
AC ABZ89240;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
WPI; 2003-229219/22.
XX
Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
Disclosure; SEQ ID NO 4482; 872pp; English.
XX
The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
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CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

Query Match      1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAAAAAA 1496
DB 1 CTAATAAAAAAAAAAAAAA 18

RESULT 123
ADE52461/C
ID ADE52461 standard; DNA; 20 BP.
XX
AC ADE52461;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stem cell factor (SCF) related DNA #32.
XX
KW Stem cell factor; SCF; haematopoietic activity; infertility;
KW intestinal damage; myeloproliferative disorder; leucopenia;
KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW milary tuberculosis; haematopoietic progenitor cell; ss.
XX
OS Synthetic.
XX
PN US2002031491-A1.
XX
PD 14-MAR-2002.
XX
PF 31-DEC-1998; 98US-00224683.
XX
PR 16-OCT-1989; 89US-00422383.
XX
PR 11-JUN-1990; 90US-00537198.
XX
PR 24-AUG-1990; 90US-00573616.
XX
PR 01-OCT-1990; 90US-00589701.
XX
PR 10-APR-1991; 91US-00684535.
XX
PR 25-NOV-1992; 92US-00982255.
XX
PR 21-DEC-1993; 93US-00172329.
XX
PR 24-MAY-1995; 95US-00449653.
XX
PR 12-JAN-1998; 98US-00005893.
XX
(ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;
XX
WPI; 2003-851459/79.
XX
New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT immune deficiency, also related nucleic acid and antibodies.
XX
Disclosure; SEQ ID NO 33; 217pp; English.
XX
The invention relates to stem cell factor (SCF) polypeptides with
CC haematopoietic activity and the polynucleotides encoding them. The
CC polypeptides are used for treating infertility, intestinal damage,
CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC for improving engraftment of bone marrow transplants, for enhancing bone
CC marrow recovery after radiotherapy or chemotherapy and in treatment of
CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC carcinoma, leukaemia and milary tuberculosis. The SCF polypeptides are
CC also used to expand haematopoietic progenitor cells for transplantation
CC and to prepare such cells for transfection with a gene. The SCF
CC polynucleotides can be used for recombinant expression of the
CC polypeptides and also as probes for mapping of the SCF gene, for
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CC identifying SCF-related diseases and as a marker for neighbouring genes.
CC Antibodies raised against the polypeptides are useful in diagnosis and to
CC remove SCF from blood. This sequence represents SCF related DNA of the
CC invention.
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
      1.2%; Score 18; DB 1; Length 20;
Query Match 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 20 CTAAAAAATAAAAAAAAAA 3
RESULT 124
AAQ75713/c
ID AAQ75713 standard; DNA; 21 BP.
XX
AC AAQ75713;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
      1.2%; Score 18; DB 1; Length 21;
Query Match 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2
RESULT 125
AAQ75703/c
ID AAQ75703 standard; DNA; 21 BP.
XX
AC AAQ75703;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
      1.2%; Score 18; DB 1; Length 21;
Query Match 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2
RESULT 126
AAQ75714/c
ID AAQ75714 standard; DNA; 21 BP.
XX
AC AAQ75714;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
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XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;
      1.2%; Score 18; DB 1; Length 21;
Query Match 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2
RESULT 126
AAQ75714/c
ID AAQ75714 standard; DNA; 21 BP.
XX
AC AAQ75714;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
```

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XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match          1.2%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 89;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2

RESULT 127
AAQ75705/c
ID AAQ75705 standard; DNA; 21 BP.
XX
XX AAQ75705;
AC
DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
    Query Match          1.2%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 89;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2

RESULT 128
AAQ75706/c
ID AAQ75706 standard; DNA; 21 BP.
XX
XX AAQ75706;
AC
DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
    Query Match          1.2%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 89;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2

RESULT 129
AAQ75707/c
ID AAQ75707 standard; DNA; 21 BP.
XX
XX AAQ75707;
AC
DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
XX JP06303997-A.
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XX 01-NOV-1994.
XX
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 89;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAAAAAATAAAAAA 1496
XX |||||||
XX DB 19 CTAAAAAATAAAAAA 2
XX
XX RESULT 130
XX AAQ75710/c
XX ID AAQ75710 standard; DNA; 21 BP.
XX
XX AC AAQ75710;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 89;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAAAAAATAAAAAA 1496
XX |||||||
XX DB 19 CTAAAAAATAAAAAA 2
XX
XX RESULT 130
XX AAQ75710/c
XX ID AAQ75710 standard; DNA; 21 BP.
XX
XX AC AAQ75710;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
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CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 89;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAAAAAATAAAAAA 1496
XX |||||||
XX DB 19 CTAAAAAATAAAAAA 2
XX
XX RESULT 131
XX AAQ75709/c
XX ID AAQ75709 standard; DNA; 21 BP.
XX
XX AC AAQ75709;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 89;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAAAAAATAAAAAA 1496
XX |||||||
XX DB 19 CTAAAAAATAAAAAA 2
XX
XX RESULT 132
XX AAQ75711/c
XX ID AAQ75711 standard; DNA; 21 BP.
XX
XX AC AAQ75711;
XX
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DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1479 CTAAAAA1496
DB 19 CTAAAAA1496

RESULT 133
AAQ75550/c
ID AAQ75550 standard; DNA; 19 BP.
XX
XX AAQ75550;
AC
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1479 CTAAAAA1496
DB 19 CTAAAAA1496

RESULT 133
AAQ75550/c
ID AAQ75550 standard; DNA; 19 BP.
XX
XX AAQ75550;
AC
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1478 GCTAAAAA1496
DB 19 GCTAAAAA1496

RESULT 134
AAQ75574/c
ID AAQ75574 standard; DNA; 20 BP.
XX
XX AAQ75574;
AC
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1478 GCTAAAAA1496
DB 19 GCTAAAAA1496

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Db      19 GCAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 135
AAQ75586/c
ID AAQ75586 standard; DNA; 20 BP.
XX
AC AAQ75586;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAAAAAAAAAAAAAAAAA 1496
Db 20 GATAAAAAAAAAAAAAAAAAAAAA 2

RESULT 137
AAQ75562/c
ID AAQ75562 standard; DNA; 20 BP.
XX
AC AAQ75562;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAAAAAAAAAAAAAAAAA 1496
Db 20 GATAAAAAAAAAAAAAAAAAAAAA 2

RESULT 136
AAQ75594/c
ID AAQ75594 standard; DNA; 20 BP.
XX
AC AAQ75594;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX

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PT by digestion with restriction enzymes.
PS Disclosure; Page 5; 1lpp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
    Query Match 1.2%; Score 17.4; DB 1; Length 20;
    Best Local Similarity 94.7%; Pred. No. 1.1e+02;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAATAAAAAAAAAA 1496
DB 20 GTTAAAAAATAAAAAAAAAA 2

RESULT 141
AAQ75571/c
ID AAQ75571 standard; DNA; 20 BP.
XX
XX AC AAQ75571;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; Gene expression; Reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 5; 1lpp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
    Query Match 1.2%; Score 17.4; DB 1; Length 20;
    Best Local Similarity 94.7%; Pred. No. 1.1e+02;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAATAAAAAAAAAA 1496
DB 20 GTTAAAAAATAAAAAAAAAA 2

RESULT 142
AAC83128/c
ID AAC83128 standard; DNA; 20 BP.
XX
XX AC AAC83128;
XX
XX DT 23-FEB-2001 (first entry)
XX
XX DE Cell cycle regulatory gene related oligonucleotide SEQ ID 31.
XX
XX KW Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
XX cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
XX cotton; rice; barley; millet; ss.
XX
XX OS Zea mays.
XX
XX PN WO200065040-A2.
XX
XX PD 02-NOV-2000.
XX
XX PF 13-APR-2000; 2000WO-US009975.
XX
XX PR 22-APR-1999; 99US-0130849P.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Helentjaris TG, Habben JE, Sun Y;
XX
XX DR WPI; 2000-687333/67.
XX
XX PT Nucleic acids useful for producing transgenic plants, preferably maize,
XX with increased cell cycle gene activity, preferably activity of cyclin
XX and/or cyclin-dependent kinase.
XX
XX PS Disclosure; Page 107; 122pp; English.
XX
XX CC Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
XX AAB35806 which are involved in regulating the cell cycle. The protein and
XX DNA sequences have been isolated from Zea mays (corn), and the invention
XX also includes oligonucleotides AAC83114 - AAC83139 which are related to
XX the cell cycle polynucleotides. The cell cycle polynucleotide sequences
XX are useful for producing transgenic plants such as maize, soybean,
XX sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
XX millet with increased levels of cell cycle gene activity, such as
XX activity of cyclin and cyclin-dependent kinases. The DNA sequences are
XX also useful as probes for detecting deficiencies in the level of mRNA in
XX screening for desired transgenic plants, for detecting mutations in the
XX gene, for monitoring upregulation of expression or changes in enzyme
XX activity in screening assays of compounds, for detecting any number of
XX allelic variants, orthologs or paralogues of the gene, and site-directed
XX mutagenesis in eukaryotic cells. The DNA sequences are also useful for
XX recombinant expression of the encoded polypeptides and as immunogens for
XX preparing and screening antibodies. A transgenic plant comprising an
XX expression cassette including a cell cycle regulatory gene is useful for
XX assaying enzyme agonists and antagonists, and as immunogens or antigens
XX to obtain antibodies. The antibodies are useful in assaying expression
XX levels of cell cycle regulatory proteins, for identifying and isolating
XX nucleic acids from expression libraries, for identifying homologues of
XX polypeptides from other species, and for purification of the proteins
XX
XX SQ Sequence 20 BP; 2 A; 5 C; 11 G; 2 T; 0 U; 0 Other;
    Query Match 1.2%; Score 17.4; DB 1; Length 20;
    Best Local Similarity 94.7%; Pred. No. 1.1e+02;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 222 CCGCCGCCCGCGCGCCCAT 240
DB 19 CAGCCGCCCGCGCGCCCAT 1

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AAI69679/c	Wang Y, Zhang H, Li H;	1.2%; Score 17.4; DB 1; Length 20;	0
AAI69679	WPI; 2001-550442/62.	Best Local Similarity 94.7%; Pred. No. 1.1e+02;	0
AAI69679	Hepatitis E virus gene sequence and its application.	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	0
AAI69679	Hepatitis E virus gene sequence and its application.		0
AAI69679	Example 1; Page 15(Disclosure); 34pp; Chinese.		0
AAI69679	The present invention relates to a novel nucleotide sequence and protein		0
AAI69679	of a new hepatitis E virus HEV-T1 and the application of the nucleotide		0
AAI69679	sequence and protein in diagnosing, preventing and treating hepatitis.		0
AAI69679	The present sequence is a PCR primer described in the exemplification of		0
AAI69679	the invention		0
AAI69679	Sequence 20 BP; 7 A; 6 C; 6 G; 1 T; 0 U; 0 Other;		0
AAI69679	Query Match 1.2%; Score 17.4; DB 1; Length 20;		0
AAI69679	Best Local Similarity 94.7%; Pred. No. 1.1e+02;		0
AAI69679	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		0
AAI69679	700 TGACTGCTGGCTCCAGC 718		0
AAI69679	20 TGACTGCTGGCTCCTGC 2		0
AAI69679	RESULT 145		0
AAI69679	ABZ85532		0
AAI69679	ID ABZ85532 standard; DNA; 20 BP.		0
AAI69679	XX ABZ85532;		0
AAI69679	AC ABZ85532;		0
AAI69679	XX 17-OCT-2003 (first entry)		0
AAI69679	Human oligonucleotide sequence.		0
AAI69679	Human; antisense; lung dysfunction; nasal airway dysfunction;		0
AAI69679	antiflammatory steroid; ubiquinone; antiinflammatory; antiallergic;		0
AAI69679	antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;		0
AAI69679	antisense gene therapy; respiratory; lung; adenosine sensitivity;		0
AAI69679	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;		0
AAI69679	lung inflammation; respiratory disease; ds.		0
AAI69679	Homo sapiens.		0
AAI69679	WO200285308-A2.		0
AAI69679	31-OCT-2002.		0
AAI69679	23-APR-2002; 2002WO-US013135.		0
AAI69679	24-APR-2001; 2001US-0286137P.		0
AAI69679	(EPIG-) EPIGENESIS PHARM INC.		0
AAI69679	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;		0
AAI69679	Miller S, Tang L, Shahabuddin S;		0
AAI69679	WPI; 2003-229219/22.		0
AAI69679	Pharmaceutical composition for treating ailments associated with impaired		0
AAI69679	respiration, has oligo(s) antisense to specific gene(s) or its		0
AAI69679	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or		0
AAI69679	ubiquinone.		0
AAI69679	Claim 15; SEQ ID NO 774; 872pp; English.		0
AAI69679	The invention relates to a novel pharmaceutical composition, which has a		0
AAI69679	first active agent comprising an oligonucleotide antisense to the		0
AAI69679	initiation codon, coding region, 5' or 3' end genomic flanking regions,		0
AAI69679	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of		0
AAI69679	junctions of genes encoding a polypeptide associated with lung and/or		0
AAI69679	nasal airway dysfunction and a second active agent comprising an		0
AAI69679	(CHME-) CHINESE MEDICINE & BIOLOGIC PROD APPRAIS.		0


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XX OS Synthetic.
XX OS Mus sp.
XX PN WO9744485-A1.
XX PD 27-NOV-1997.
XX PF 16-MAY-1997; 97WO-GB001354.
XX PR 17-MAY-1996; 96GB-00010355.
XX PA (HEXA-) HEXAGEN TECHNOLOGY LTD.
XX PI Goodfellow PN;
XX XX WPI; 1998-018536/02.
XX DR Identification of mutation(s) in genes of interest - without prior
XX PT observation of phenotypic alteration in the mutated organism or cell.
XX PS Example 4; Page 41; 56pp; English.
XX CC PCR primers AAV16001-18 were used to identify mutations in Sox-3 using
XX CC the method of the invention. The primers are located throughout the gene
XX CC and are unique to Sox-3. The method comprises testing a nucleic acid
XX CC sample from a mutated organism for a mutation in a gene of interest
XX CC without the prior observation of a phenotypic alteration in the mutated
XX CC organism resulting from the mutation. Sox-3 is a member of the Sox gene
XX CC family, a family of about 20 genes which all encode a "HMG" box, which is
XX CC a DNA-binding domain. Mice were mutagenised using ENU mutagenesis. The
XX CC mutagenised mice were tested by PCR with each primer set and fluorescent
XX CC single strand conformation polymorphism (SSCP), which identifies mice
XX CC carrying mutations in Sox-3. The method provides mutational screening
XX CC based on genomic and genetic techniques rather than on phenotypic
XX CC observation. The method identifies and characterises genes via
XX CC mutagenesis to identify genes encoding products which may have
XX CC therapeutic benefit. The method also identifies the presence of mutations
XX CC in a gene which do not rely solely upon prior matching of a gene with a
XX CC disease. Heterozygotic organisms can also be screened to identify those
XX CC carrying a mutation in a copy of a gene of interest even though the gene
XX CC may be recessive and therefore causes no phenotypic alteration
XX CC
XX CC Sequence 18 BP; 1 A; 6 C; 11 G; 0 T; 0 U; 0 Other;
XX CC
XX CC Query Match 1.1%; Score 17; DB 1; Length 18;
XX CC Best Local Similarity 100.0%; Pred. No. 1e+02;
XX CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX QY 25 CGCGCGCGACGCGCG 41
XX DB 2 CGCGCGCGACGCGCG 18
XX
XX RESULT 149
XX AAX18373/c
XX ID AAX18373 standard; DNA; 18 BP.
XX XX
XX AC AAX18373;
XX XX
XX DT 11-MAY-1999 (first entry)
XX DE RT-PCR primer of the invention SEQ ID 14.
XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX XX
XX OS Synthetic.
XX PN JP11032765-A.
XX XX
XX PD 09-FEB-1999.
XX PF 18-JUL-1997; 97JP-00208312.
XX
XX PR 18-JUL-1997; 97JP-00208312.
XX PA (TAKI ) TAKARA SHUZO CO LTD.
XX XX
XX DR WPI; 1999-183822/16.
XX XX
XX PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX PS Disclosure; Page 11; 19pp; Japanese.
XX CC This sequence represents a primer of the invention. The invention relates
XX CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
XX CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
XX CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
XX CC natural number indicating the repetition of alpha; beta, delta = V or N;
XX CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
XX CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
XX CC repetition of gamma, in which thymine expressed by gamma is composed of
XX CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
XX CC useful as primers for RT-PCR and determination of base sequences. The new
XX CC sequences allow for reproductive and highly efficient analysis of gene
XX CC sequences
XX CC
XX SQ Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX CC
XX CC Query Match 1.1%; Score 17; DB 1; Length 18;
XX CC Best Local Similarity 100.0%; Pred. No. 1e+02;
XX CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX QY 1480 TAAAAAATAAAAA 1496
XX DB 17 TAAAAAATAAAAA 1
XX
XX RESULT 150
XX AAX18372/c
XX ID AAX18372 standard; DNA; 18 BP.
XX XX
XX AC AAX18372;
XX XX
XX DT 11-MAY-1999 (first entry)
XX DE RT-PCR primer of the invention SEQ ID 13.
XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX XX
XX OS Synthetic.
XX PN JP11032765-A.
XX XX
XX PD 09-FEB-1999.
XX PF 18-JUL-1997; 97JP-00208312.
XX PR 18-JUL-1997; 97JP-00208312.
XX PA (TAKI ) TAKARA SHUZO CO LTD.
XX XX
XX DR WPI; 1999-183822/16.
XX XX
XX PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX PS Disclosure; Page 11; 19pp; Japanese.
XX CC This sequence represents a primer of the invention. The invention relates
XX CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
XX CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
XX CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
XX CC natural number indicating the repetition of alpha; beta, delta = V or N;
XX CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
XX CC thymine

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CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX
 SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
 DB 17 TAAAAAAAAAAAAAAAAA 1

RESULT 151
 AAZ90640/C
 ID AAZ90640 standard; DNA; 18 BP.
 XX
 AC AAZ90640;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE Human adipose tissue gene amplifying primer #1.
 XX
 KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 OS Homo sapiens.
 XX
 PN JP2000037190-A.
 XX
 PD 08-FEB-2000.
 XX
 PF 23-JUL-1998; 98JP-00225228.
 XX
 PR 23-JUL-1998; 98JP-00225228.
 XX
 PA (NIPPON) JAPAN TOBACCO INC.
 XX
 DR WPI; 2000-306578/27.
 XX
 PT A physiologically active protein specifically derived from mammal tissue.
 PS
 PS Example 2; Page 18; 50pp; Japanese.
 XX
 CC The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 CC proteins (AAZ90631-633) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAAAAAAAAAAAAA 1495
 DB 18 CTAAAAAAAAAAAAAAAAA 2

RESULT 152
 AAZ43267
 ID AAZ43267 standard; DNA; 18 BP.
 XX
 AC AAZ43267;

XX
 DT 11-FEB-2000 (first entry)
 XX
 DE Murine Sox3 gene PCR primer 8.
 XX
 KW Screening; mutation; treatment; disease; drug discovery; PCR primer; ss.
 XX
 OS Mus musculus.
 XX
 PN US5994075-A.
 XX
 PD 30-NOV-1999.
 XX
 PF 16-MAY-1997; 97US-00857946.
 XX
 PR 17-MAY-1996; 96US-0017824P.
 XX
 PA (HEXA-) HEXAGEN TECHNOLOGY LTD.
 XX
 PI Goodfellow PN;
 XX
 DR WPI; 2000-038255/03.
 XX
 PT Identifying a mutation in a gene of interest in an organism useful for
 PT identifying genes encoding products which may have therapeutic benefits.
 XX
 PS Example 5; Col 63-64; 70pp; English.
 XX
 CC This invention describes a novel mutational screening method based on
 CC genomic and genetic techniques to identify and characterize a mutation in
 CC a gene of interest without first selecting a phenotypic characteristic.
 CC The screening methods are useful for identifying genes encoding products
 CC which may have therapeutic benefit for treating human or animal diseases.
 CC The method can be used for the DNA mutation screening of a class or a
 CC family of genes providing a rapid assay for identifying mutant genes. The
 CC methods produce organisms which can be used for drug discovery e.g.
 CC providing a model for the study and treatment of a disease state, allow
 CC in vitro assessment of drug activity and interbreeding of mutants which
 CC allow investigation of gene interactions in the overall phenotype. A
 CC range of phenotypes associated with different mutations, and specified
 CC mutations in a gene of interest can be determined. The method can be
 CC adapted to screen for a mutation in two or more genes of interest in an
 CC organism. The methods allow mutations in a gene of interest to be
 CC identified without having to rely on matching a gene with a disease.
 CC AAZ43260-243421 represent PCR primers used in the method of the invention
 XX
 SQ Sequence 18 BP; 1 A; 6 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CGCGCGCGCGCGCGCG 41
 DB 2 CGCGCGCGCGCGCGCG 18

RESULT 153
 AA05252
 ID AA05252 standard; DNA; 18 BP.
 XX
 AC AA05252;
 XX
 DT 19-MAY-2000 (first entry)
 XX
 DE PCR primer D-R used in Sox-3 amplimer generation.
 XX
 KW PCR primer; Sox-2; Sox-3; T gene; Tyrosinase; MGF; Sry; C-kit; Tryp-1;
 KW Pax-6; mutation detection; therapeutic target identification; mouse;
 XX
 XX mast cell growth factor; ss.
 OS
 OS Mus sp.
 XX

PN US6015670-A.
 XX 18-JAN-2000.
 XX 14-NOV-1997; 97US-00970740.
 PF 17-MAY-1996; 96US-0017824P.
 PR 16-MAY-1997; 97US-00857946.
 XX (HEXA-) HEXAGEN TECHNOLOGY LTD.
 XX Goodfellow PN;
 XX WPI; 2000-181139/16.
 XX Detecting mutations in selected genes, useful e.g. for identifying
 PT therapeutic targets or products, by analyzing DNA in mutated embryonic
 PT stem cells without phenotypic characterization.
 XX
 XX Example 5; Col 31; 66pp; English.
 XX
 CC PCR primers AAA05245-A05406 are used to generate amplicons from the mouse
 CC Sox-3 gene, Sox-2 gene, T gene, tyrosinase gene, Tryp-1 gene, Sry gene,
 CC MGF (mast cell growth factor) gene, c-kit gene, and the Pax-6 gene. The
 CC primers are used in a method for the identification of a mutation in a
 CC selected gene in a tissue without the prior observation of a phenotypic
 CC alteration in the mutated organism or cell. The method is used to
 CC identify mutations in a selected gene that encode products of potential
 CC therapeutic activity or that are potential targets, particularly where
 CC the gene of interest has been identified as a candidate gene by
 CC positional cloning. Other applications are determining functions of genes
 CC in a particular gene and identification of particular mutations. Animals
 CC containing an identified mutation are used as models for studying
 CC diseases or their treatment, and cells from them for in vitro assessment
 CC of drug action. Interbreeding of mutant mice is used to investigate
 CC genetic interaction in the overall phenotype
 XX
 XX Sequence 18 BP; 1 A; 6 C; 11 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 CGCGCGCGACGCGGCG 41
 DB 2 CGCGCGCGACGCGGCG 18
 RESULT 154
 AAQ75552/c
 ID AAQ75552 standard; DNA; 19 BP.
 XX
 AC AAQ75552;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 19 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAATAAAAAA 1496
 DB 18 TAAAAAATAAAAAA 2
 RESULT 155
 AAQ75553/c
 ID AAQ75553 standard; DNA; 19 BP.
 XX
 AC AAQ75553;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

XX WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAATAAAAAA 1496
 DB 18 TAAAAAATAAAAAA 2
 RESULT 155
 AAQ75553/c
 ID AAQ75553 standard; DNA; 19 BP.
 XX
 AC AAQ75553;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 156
 AAQ75584/c
 ID AAQ75584 standard; DNA; 19 BP.
 XX
 AC AAQ75584;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX JP06303997-A.
 PN
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 157
 AAQ75584/c
 ID AAQ75584 standard; DNA; 20 BP.
 XX
 AC AAQ75584;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 OS Synthetic.

XX JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 158
 AAQ75585/c
 ID AAQ75585 standard; DNA; 20 BP.
 XX
 AC AAQ75585;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX JP06303997-A.
 PN
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 159
 AAQ75579/c
 ID AAQ75579 standard; DNA; 20 BP.

XX AC AAQ75579;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 160
 AAQ75589/c
 ID AAQ75589 standard; DNA; 20 BP.

XX AC AAQ75589;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 160
 AAQ75589/c
 ID AAQ75589 standard; DNA; 20 BP.

XX AC AAQ75589;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

AC AAQ75589;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 161
 AAQ75588/c
 ID AAQ75588 standard; DNA; 20 BP.

XX AC AAQ75588;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 161
 AAQ75588/c
 ID AAQ75588 standard; DNA; 20 BP.

XX AC AAQ75588;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 160
 AAQ75589/c
 ID AAQ75589 standard; DNA; 20 BP.

XX AC AAQ75589;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1480 TAAAAAAAAAAAAAAAAA 1496
DB 18 TAAAAAAAAAAAAAAAAA 2
XX
RESULT 162
AAQ75581/c
ID AAQ75581 standard; DNA; 20 BP.
XX
AC AAQ75581;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1480 TAAAAAAAAAAAAAAAAA 1496
DB 18 TAAAAAAAAAAAAAAAAA 2
XX
RESULT 164
AAQ75580/c
ID AAQ75580 standard; DNA; 20 BP.
XX
AC AAQ75580;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
DB 18 TAAAAAAAAAAAAAAAAA 2
XX
RESULT 163
AAQ75583/c
ID AAQ75583 standard; DNA; 20 BP.
XX
AC AAQ75583;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1480 TAAAAAAAAAAAAAAAAA 1496
DB 18 TAAAAAAAAAAAAAAAAA 2
XX
RESULT 164
AAQ75580/c
ID AAQ75580 standard; DNA; 20 BP.
XX
AC AAQ75580;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PN JP06303997-A.
XX
XX
PD 01-NOV-1994.
XX
XX
PF 16-APR-1993; 93JP-00112515.
XX
XX
PR 16-APR-1993; 93JP-00112515.
XX
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
DR WPI; 1995-018287/03.
XX
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AA075547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 165
AAQ75587/c
ID AAQ75587 standard; DNA; 20 BP.
XX
XX
AC AAQ75587;
XX
XX
DT 04-AUG-1995 (first entry)
XX
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX
OS Synthetic.
XX
XX
PN JP06303997-A.
XX
XX
PD 01-NOV-1994.
XX
XX
PF 16-APR-1993; 93JP-00112515.
XX
XX
PR 16-APR-1993; 93JP-00112515.
XX
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
DR WPI; 1995-018287/03.
XX
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 166
AAV07752/c
ID AAV07752 standard; DNA; 20 BP.
XX
XX
AC AAV07752;
XX
XX
DT 07-DEC-1998 (first entry)
XX
XX
DE Phosphorothioate oligonucleotide.
XX
XX
KW phosphorothioate; sulphurisation; heterocycle; automated synthesis;
KW antisense; EDITH; Beaucage reagent; ss.
XX
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT misc_feature 1..20
FT FT /*tag= a
FT FT /note= "phosphorothioate internucleotide linkages"
XX
XX
PN WO9741130-A2.
XX
XX
PD 06-NOV-1997.
XX
XX
PF 29-APR-1997; 97WO-US007118.
XX
XX
PR 30-APR-1996; 96US-00641920.
XX
XX
PA (MINU ) UNIV MINNESOTA.
XX
XX
PA (LOU ) UNIV LOUISIANA STATE & AGRIC.
XX
XX
PI Barany G, Musier-Forsyth K, Xu Q, Chen L, Hammer RP;
XX WPI; 1997-549671/50.
XX
XX
PT Sulphurisation of phosphorus-containing compounds, e.g.
PT oligo:nucleotide(s) - by contacting the compound with a di:sulphide-
XX containing five-membered heterocycle.
XX
XX
PS Example 7; Page 30; 51pp; English.
XX
XX
CC The present invention provides a method for sulphurising phosphorus-
CC containing compounds. It comprises contacting the phosphorus-containing
CC compound which a 1,2,4-dithiazolidine-2,5-dione compound or a 3-
CC substituted-1,2,4-dithiazolin-5-one compound. The method is especially
CC useful for incorporation of phosphorothioate linkages into biologically
CC important molecules such as DNA, RNA and phosphopeptides. Molecules
CC containing such linkages are useful e.g. as antisense compounds for
CC inhibiting gene expression, as reagents for studying DNA-protein or RNA-
CC protein interactions, or as catalytic RNA. The present sequence
CC represents an oligonucleotide with phosphorothioate linkages prepared by
CC the method of the invention
XX
XX
SQ Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;
Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

```

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CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 166
AAV07752/c
ID AAV07752 standard; DNA; 20 BP.
XX
XX
AC AAV07752;
XX
XX
DT 07-DEC-1998 (first entry)
XX
XX
DE Phosphorothioate oligonucleotide.
XX
XX
KW phosphorothioate; sulphurisation; heterocycle; automated synthesis;
KW antisense; EDITH; Beaucage reagent; ss.
XX
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT misc_feature 1..20
FT FT /*tag= a
FT FT /note= "phosphorothioate internucleotide linkages"
XX
XX
PN WO9741130-A2.
XX
XX
PD 06-NOV-1997.
XX
XX
PF 29-APR-1997; 97WO-US007118.
XX
XX
PR 30-APR-1996; 96US-00641920.
XX
XX
PA (MINU ) UNIV MINNESOTA.
XX
XX
PA (LOU ) UNIV LOUISIANA STATE & AGRIC.
XX
XX
PI Barany G, Musier-Forsyth K, Xu Q, Chen L, Hammer RP;
XX WPI; 1997-549671/50.
XX
XX
PT Sulphurisation of phosphorus-containing compounds, e.g.
PT oligo:nucleotide(s) - by contacting the compound with a di:sulphide-
XX containing five-membered heterocycle.
XX
XX
PS Example 7; Page 30; 51pp; English.
XX
XX
CC The present invention provides a method for sulphurising phosphorus-
CC containing compounds. It comprises contacting the phosphorus-containing
CC compound which a 1,2,4-dithiazolidine-2,5-dione compound or a 3-
CC substituted-1,2,4-dithiazolin-5-one compound. The method is especially
CC useful for incorporation of phosphorothioate linkages into biologically
CC important molecules such as DNA, RNA and phosphopeptides. Molecules
CC containing such linkages are useful e.g. as antisense compounds for
CC inhibiting gene expression, as reagents for studying DNA-protein or RNA-
CC protein interactions, or as catalytic RNA. The present sequence
CC represents an oligonucleotide with phosphorothioate linkages prepared by
CC the method of the invention
XX
XX
SQ Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;
Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
QY	1480 TAAAAA	1496									
Db	20 TAAAAA	18									
RESULT 167											
ABZ89546											
ID	ABZ89546	standard; DNA; 20 BP.									
XX	AC	ABZ89546;									
XX	DT	17-OCT-2003 (first entry)									
XX	DE	Human oligonucleotide sequence.									
XX	KW	Human; antisense; lung dysfunction; nasal airway dysfunction;									
XX	KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;									
XX	KW	antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;									
XX	KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;									
XX	KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;									
XX	KW	lung inflammation; respiratory disease; ds.									
XX	OS	Homo sapiens.									
XX	XX	WO200285308-A2.									
XX	PD	31-OCT-2002.									
XX	XX	23-APR-2002; 2002WO-US013135.									
XX	PR	24-APR-2001; 2001US-0286137P.									
XX	PA	(EPIG-) EPIGENESIS PHARM INC.									
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;										
PI	Miller S, Tang L, Shahabuddin S;										
XX	WPI; 2003-229219/22.										
XX	Pharmaceutical composition for treating ailments associated with impaired										
PT	respiration, has oligo(s) antisense to specific gene(s) or its										
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or										
PT	ubiquinone.										
XX	Disclosure; SEQ ID NO 4788; 872pp; English.										
XX	The invention relates to a novel pharmaceutical composition, which has a										
CC	first active agent comprising an oligonucleotide antisense to the										
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,										
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of										
CC	junctions of genes encoding a polypeptide associated with lung and/or										
CC	nasal airway dysfunction and a second active agent comprising an										
CC	antiinflammatory steroid and ubiquinone. A composition of the invention										
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,										
CC	immunosuppressive, and cytostatic activity. The composition may have a										
CC	use in antisense gene therapy. The composition is useful for treating or										
CC	preventing a respiratory, lung or malignant disease or condition, also										
CC	for enhancing the prophylactic or therapeutic respiratory effect of an										
CC	antiinflammatory steroid in a subject, for reducing or depleting levels										
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine										
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or										
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,										
CC	lung inflammation, lung allergies, or a respiratory disease or condition.										
CC	Note: The sequence data for this patent is not represented in the printed										
CC	specification, but was obtained in electronic format directly from WIPO										
CC	at ftp.wipo.int/pub/published_pct_sequences										
XX	Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;										
Query Match 1.1%; Score 17; DB 1; Length 20;											
Best Local Similarity 100.0%; Pred. No. 1.2e+02;											

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
QY	1480 TAAAAA	1496									
Db	2 TAAAAA	18									
RESULT 168											
ABZ8880											
ID	ABZ8880	standard; DNA; 20 BP.									
XX	AC	ABZ8880;									
XX	DT	17-OCT-2003 (first entry)									
XX	DE	Human oligonucleotide sequence.									
XX	KW	Human; antisense; lung dysfunction; nasal airway dysfunction;									
XX	KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;									
XX	KW	antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;									
XX	KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;									
XX	KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;									
XX	KW	lung inflammation; respiratory disease; ds.									
XX	OS	Homo sapiens.									
XX	XX	WO200285308-A2.									
XX	PD	31-OCT-2002.									
XX	XX	23-APR-2002; 2002WO-US013135.									
XX	PR	24-APR-2001; 2001US-0286137P.									
XX	PA	(EPIG-) EPIGENESIS PHARM INC.									
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;										
PI	Miller S, Tang L, Shahabuddin S;										
XX	WPI; 2003-229219/22.										
XX	Pharmaceutical composition for treating ailments associated with impaired										
PT	respiration, has oligo(s) antisense to specific gene(s) or its										
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or										
PT	ubiquinone.										
XX	Disclosure; SEQ ID NO 4122; 872pp; English.										
XX	The invention relates to a novel pharmaceutical composition, which has a										
CC	first active agent comprising an oligonucleotide antisense to the										
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,										
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of										
CC	junctions of genes encoding a polypeptide associated with lung and/or										
CC	nasal airway dysfunction and a second active agent comprising an										
CC	antiinflammatory steroid and ubiquinone. A composition of the invention										
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,										
CC	immunosuppressive, and cytostatic activity. The composition may have a										
CC	use in antisense gene therapy. The composition is useful for treating or										
CC	preventing a respiratory, lung or malignant disease or condition, also										
CC	for enhancing the prophylactic or therapeutic respiratory effect of an										
CC	antiinflammatory steroid in a subject, for reducing or depleting levels										
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine										
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or										
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,										
CC	lung inflammation, lung allergies, or a respiratory disease or condition.										
CC	Note: The sequence data for this patent is not represented in the printed										
CC	specification, but was obtained in electronic format directly from WIPO										
CC	at ftp.wipo.int/pub/published_pct_sequences										
XX	Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;										
Query Match 1.1%; Score 17; DB 1; Length 20;											
Best Local Similarity 100.0%; Pred. No. 1.2e+02;											

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
Qy	1480 TAAAAA	1496									
Db	1 TAAAAA	17									
RESULT 170											
ID	ABZ92865	standard; DNA; 20 BP.									
XX	AC	ABZ92865;									
XX	DT	17-OCT-2003 (first entry)									
XX	DE	Human oligonucleotide sequence.									
XX	KW	Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.									
XX	OS	Homo sapiens.									
XX	PN	WO200285308-A2.									
XX	XX	31-OCT-2002.									
XX	PD	23-APR-2002; 2002WO-US013135.									
XX	PF	24-APR-2001; 2001US-0286137P.									
XX	PR	(EPIG-) EPIGENESIS PHARM INC.									
XX	PA	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Miller S, Tang L, Shahabuddin S; WPI; 2003-229219/22.									
XX	PI	Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.									
XX	PS	Disclosure; SEQ ID NO 8107; 872pp; English.									
XX	CC	The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences									
XX	SQ	Sequence 20 BP; 18 A; 0 C; 1 G; 1 T; 0 U; 0 Other;									
Query Match 1.1%; Score 17; DB 1; Length 20;											
Best Local Similarity 100.0%; Pred. No. 1.2e+02;											

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
Qy	1480 TAAAAA	1496									
Db	1 TAAAAA	17									
RESULT 169											
ID	ABZ89179	standard; DNA; 20 BP.									
XX	AC	ABZ89179;									
XX	DT	17-OCT-2003 (first entry)									
XX	DE	Human oligonucleotide sequence.									
XX	KW	Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.									
XX	OS	Homo sapiens.									
XX	PN	WO200285308-A2.									
XX	XX	31-OCT-2002.									
XX	PD	23-APR-2002; 2002WO-US013135.									
XX	PF	24-APR-2001; 2001US-0286137P.									
XX	PR	(EPIG-) EPIGENESIS PHARM INC.									
XX	PA	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Miller S, Tang L, Shahabuddin S; WPI; 2003-229219/22.									
XX	PI	Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.									
XX	PS	Disclosure; SEQ ID NO 4421; 872pp; English.									
XX	CC	The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences									
XX	SQ	Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;									
Query Match 1.1%; Score 17; DB 1; Length 20;											
Best Local Similarity 100.0%; Pred. No. 1.2e+02;											

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
|||||
4 TAAAAAAAAAAAAAAAAA 20

Db

RESULT 171
ABZ89703
ID ABZ89703 standard; DNA; 20 BP.

XX AC ABZ89703;
XX 17-OCT-2003 (first entry)
XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.

XX PS Disclosure; SEQ ID NO 4945; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
|||||
4 TAAAAAAAAAAAAAAAAA 20

Db

RESULT 172
ABZ88694
ID ABZ88694 standard; DNA; 20 BP.

XX AC ABZ88694;
XX 17-OCT-2003 (first entry)
XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.

XX PS Disclosure; SEQ ID NO 3936; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

```
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
Db 3 TAAAAAAAAAAAAAAAAA 19

RESULT 173
ABZ89014
ID ABZ89014 standard; DNA; 20 BP.
XX
AC ABZ89014;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antiaethmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandkasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Disclosure; SEQ ID NO 4256; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding regions, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antiaethmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAAAAAA 1495
Db 4 CTAATAAAAAAAAAAAAAA 20

RESULT 174
AAD44128
ID AAD44128 standard; DNA; 18 BP.
XX
AC AAD44128;
XX
DT 13-DEC-2002 (first entry)
XX
DE PCR primer #3 designed to bind human MMP PPR region.
XX
KW Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; MMP;
KW propeptide region; PPR; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US6277571-B1.
XX
PD 21-AUG-2001.
XX
PF 30-SEP-1998; 98US-00163485.
XX
PR 03-OCT-1997; 97US-00943162.
XX
PR 03-OCT-1997; 97US-0108152P.
XX
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI Fillmore H, Broadus W, Gillies G;
XX
DR WPI; 2002-412824/44.
XX
PT Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX
PS Example; Col 12; 19pp; English.
XX
CC The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is a PCR
CC primer designed to bind to human matrix metalloproteinase (MMP)
CC propeptide region (PPR). This primer is used to illustrate the method of
CC the invention
XX
SQ Sequence 18 BP; 6 A; 2 C; 5 G; 3 T; 0 U; 2 Other;

Query Match 1.1%; Score 16.6; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 599 AAGGATGTGAAGCAGTTC 616
Db 1 AAGGATGTNAGCAGTTC 18

RESULT 175
AAT69640/c
ID AAT69640 standard; DNA; 19 BP.
XX
AC AAT69640;
XX
DT 20-FEB-1998 (first entry)
XX
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DE Telomerase Oligo-dT-Primer P3.
XX
XX Telomerase; substrate; primer; detection; 5'-region; retrovirus;
KW long terminal repeat 2; LTR-2; diagnosis; tumour; screening;
KW effector compound; PCR; amplification; Oligo-dT-Primer; ss.
XX
OS Synthetic.
XX
XX DE19644302-A1.
XX
XX 05-JUN-1997.
XX
XX 24-OCT-1996; 96DE-01044302.
XX
XX 28-NOV-1995; 95DE-01044317.
XX
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
XX PI Erich T, Leying H, Hinzpeter M, Karl G;
XX WPI; 1997-299542/28.
XX
XX Measuring telomerase activity, useful for tumour diagnosis and compound
PT screening - by extending substrate primer, followed by amplification and
PT immobilising product for detection.
XX
XX Example; Page 11; 21pp; German.
XX
XX The present sequence is a telomerase Oligo-dT-Primer, which can be used
CC in a novel method for detecting telomerase activity. The method comprises
CC adding to a test sample a 1st primer, that serves as telomerase
CC substrate, and nucleoside triphosphate (dNTP) and incubating to allow
CC primer extension by the telomerase, amplifying the extension product,
CC immobilising the amplification product (AP) on a solid phase and
CC qualitative and/or quantitative detection of AP, where the substrate
CC primer is preferably from the 5'-region of the long terminal repeat 2
CC (LTR-2) sequence of a retrovirus. The method can be used to diagnose
CC tumours and screen compounds for effector activity. Immobilisation of AP
CC provides a signal that is reproducibly representative of telomerase
CC activity, eliminates the need for gel electrophoretic separation and
CC provides high sensitivity. Radioactive labels are not required and the
CC method can be automated for routine use. Specific detection is achieved
CC by proper choice of hybridisation conditions, without separation of the
CC telomerase extension product. A specific signal is generated by 1-10 cell
CC equivalents, but for tumour analysis 10-1000 ng of tissue is usually used
XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;

Query Match 1.1%; Score 16.6; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
Db 18 KAAAAAAAAAAAAAAAAA 2

RESULT 176
AAN30173
ID AAN30173 standard; DNA; 18 BP.
XX
XX AAN30173;
AC
XX
XX 05-APR-1992 (first entry)
DT
XX
XX Sequence derived from the L1 region of the bovine papillomavirus (bpv)
DE type 1a genome.
XX
XX Diagnostic reagent; vaccine; medicine; wart; tumour; ss.
XX
XX Bovine papillomavirus.
OS
XX
XX Key Location/Qualifiers

Telomerase Oligo-dT-Primer P3.
FT 1.18
FT /*tag= a
XX
XX EP92456-A.
PN
XX
XX 26-OCT-1983.
PD
XX
XX 01-APR-1983; 83EP-00901081.
PF
XX
XX 05-APR-1982; 82PR-00005887.
PR
XX
XX (INSP ) INST PASTEUR.
PA
XX (DANO/) DANOS O.
PA
XX
XX Danos O, Katinka M, Yaniv M;
PI
XX
XX WPI; 1983-802979/44.
DR
XX P-PSDB; AAP30313.
DR
XX
XX DNA fragment coding for Papillomavirus antigenic proteins - and derived
PT immunogen, vaccine and antibody.
PT
XX
XX Claim 6; Page 16; 25pp; French.
PS
XX
XX The inventors claim DNA fragments capable of expressing, in a host, a
CC prod. contg. at least one antigenic determinant of papillomavirus (PV),
CC (see AAN30170-N30173). Also claimed are immunogens consisting of at least
CC one peptide sequence coded for by the DNA fragments (see AAP30310-
CC 230313), vaccines contg. the immunogens and antibodies raised from them.
CC The vaccines are useful in human and veterinary medicine and the
CC antibodies are useful as diagnostic reagents. The DNA fragments are most
CC esp. derived from the L1 region of human PV type 1a
XX
XX SQ Sequence 18 BP; 16 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAAAAAAAAAAAAA 1495
Db 1 GCAAAAAAAAAAAAAAAAAA 18

RESULT 177
AAT94669/C
ID AAT94669 standard; DNA; 18 BP.
XX
XX AAT94669;
AC
XX
XX 27-MAR-1998 (first entry)
DT
XX
XX Anchored poly(T) oligonucleotide polyT-AnchG.
DE
XX
XX Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW snapdragon; primer; ss.
KW
XX
XX Synthetic.
OS
XX
XX WO9732023-A1.
PN
XX
XX 04-SEP-1997.
PD
XX
XX 28-FEB-1997; 97WO-AU000124.
PF
XX
XX 01-MAR-1996; 96AU-00008386.
PR
XX
XX (FLOR-) FLORIGENE LTD.
PA
XX
XX Brugliera F, Holton TA, Michael MZ;
PI
XX
XX WPI; 1997-448691/41.
DR
XX

```

PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
 PT corresponding DNA, used in the manipulation of pigmentation in plants.
 XX
 PS Example 15; Page 59; 234pp; English.

XX Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
 CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
 CC region of a polyadenylation sequence. They were used to prime cDNA
 CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
 CC were also utilised in the PCR amplification of plant cytochrome P450
 CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
 CC flavonoid 3'-hydroxylase (see AAW35704) was isolated using a differential
 CC display approach. This can be used to manipulate the pigmentation of
 CC transgenic plants
 XX

SQ Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
 DB 18 CAAAAAATAAAAAAAAAA 1

RESULT 178
 AAF75596/C
 ID AAF75596 standard; DNA; 18 BP.

XX AAF75596;

DT 10-MAY-2001 (first entry)

DE Binary encoded sequence tag method anchored primer #1.

XX Binary encoded sequence tag; BEST; nucleic acid analysis;
 KW gene expression; adaptor; PCR primer; ss.

XX Synthetic.

XX WO200112855-A2.

XX 22-FEB-2001.

XX 11-AUG-2000; 2000WO-US022164.

XX 13-AUG-1999; 99US-0148870P.

XX 06-APR-2000; 2000US-00544713.

XX (UYTA) UNIV YALE.

XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;

XX WPI; 2001-202878/20.

XX Producing binary sequence tags, useful for analyzing nucleic acid
 PT sequence tags, gene expression or gene-expression patterns, involves
 PT generating nucleic acid fragments, which are mixed with offset adaptors
 PT and adaptor-indexers.
 XX

PS Disclosure; Page 100; 101pp; English.

XX The present invention describes a method of producing binary sequence
 CC tags from nucleic acid fragments in a sample, involving incubating the
 CC sample with cleaving reagents, mixing offset adaptors with the sample,
 CC incubating with more cleaving reagents and mixing the sample with adaptor
 CC -indexers where the adaptors are coupled to binary sequence tags. The
 CC method is useful in sequence analysis, including analysis and comparison
 CC of gene expression, nucleic acid samples and genomes
 XX

SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAATAAAAAAAAAA 1495
 DB 18 GCAAAAAAATAAAAAAAAAA 1

RESULT 179
 ABK13935/C
 ID ABK13935 standard; DNA; 18 BP.

XX ABK13935;

DT 21-MAY-2002 (first entry)

DE 5'-PCR primer used to produce single pattern characteristic by HaeII.
 XX Identification of transcribed gene; mRNA profile; gene expression;
 KW cellular process; fingerprinting; susceptibility to external factor;
 KW development; disease; PCR; primer; ss.

XX Synthetic.

XX WO200208461-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-IB001539.

XX 21-JUL-2000; 2000GB-00018016.

XX 21-JUL-2000; 2000US-0219925P.

XX (GLOB-) GLOBAL GENOMICS AB.

XX Linnarsson S, Ernfors P, Bauren G;

XX WPI; 2002-217065/27.

XX Providing mRNA profile, by generating two independent patterns
 PT characteristic of sample mRNA population, analyzing patterns, comparing
 PT gene expression by cell types under varied conditions, and identifying
 PT genes.
 XX

PS Disclosure; Fig 1; 67pp; English.

XX The present invention relates to a method for providing a profile of mRNA
 CC molecules present in a sample. The method comprises generating two
 CC independent patterns characteristic of the population of mRNA molecules
 CC expressed in the sample and analysing the patterns using a combinatorial
 CC algorithm, comparing gene expression by different or same cell types
 CC under different conditions, and identifying genes having a role in
 CC various cellular processes. The method is useful for the analysis and
 CC identification of transcribed genes, and fingerprinting. The method can
 CC be used to identify genes which play a role in determining various
 CC cellular processes, including susceptibility to external factors,
 CC development, and disease. The present sequence for a PCR primer is used
 CC in the production of a single pattern characteristic of a sample,
 CC employing a Type II restriction enzyme (i.e. HaeII) in the methods of the
 CC present invention
 XX

SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
 DB 18 CGAAAAAATAAAAAAAAAA 1

RESULT 180
ACF36339/C
ID ACF36339 standard; DNA; 18 BP.
XX AC ACF36339;
XX DT 04-DEC-2003 (first entry)
XX DE Nucleotide sequence of a double stranded product DNA fragment.
XX DE Gene variant identification; restriction enzyme; HaeII; ds.
XX KW Gene variant identification; restriction enzyme; HaeII; ds.
XX OS Synthetic.
XX PN WO2003064689-A2.
XX PD 07-AUG-2003.
XX PF 28-JAN-2003; 2003WO-IB000255.
XX PR 29-JAN-2002; 2002US-0352245P.
XX PA (GLOB-) GLOBAL GENOMICS AB.
XX PI Lonnarberg P, Oldin M, Linnarsson S, Ernfors P;
XX WPI; 2003-627619/59.
XX DR Determining polyadenylation sites within transcribed gene sequences
XX PT present in a sample comprises assigning to gene fragments gene candidates
XX PT within a database by comparing signals in the dataset with the database.
XX PS Example; Fig 2; 81pp; English.
XX CC The invention relates to determining the presence of and/or identifying a
XX CC polyadenylation site within a sequence of a transcribed gene or variants
XX CC present in a sample. The method involves assigning to gene fragments gene
XX CC candidates within a database by comparing signals in the dataset with the
XX CC database, the database comprising data representing mRNAs with known
XX CC polyA sites and/or 'virtual genes' representing a possible
XX CC polyadenylation site within an actual gene. The method is useful for
XX CC determining the presence of and/or identifying a polyadenylation site or
XX CC alternative polyadenylation sites within a sequence of a transcribed gene
XX CC or sequences of transcribed gene variants present or potentially present
XX CC in a sample, in identifying gene features, particularly in identifying
XX CC differences between sequence variants that occur in a population of
XX CC nucleic acid molecules, especially in identifying or discovering polyA
XX CC site usage or determining polyA site usage in a nucleic acid sample, and
XX CC gene variants arising from alternative polyA sites. The present sequence
XX CC represents a double stranded product DNA fragment
XX SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
Query Match 1.1%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTAAGAAAAA 1496
DB 18 CGAAAAA 1

RESULT 181
ACF36364/C
ID ACF36364 standard; DNA; 18 BP.
XX AC ACF36364;
XX DT 04-DEC-2003 (first entry)
XX DE Nucleotide sequence of a double stranded product DNA.
XX DE Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW

XX electrophoresis; type II restriction enzyme; HaeII; ds.
XX Synthetic.
XX PN WO2003064691-A2.
XX PD 07-AUG-2003.
XX PF 28-JAN-2003; 2003WO-IB000843.
XX PR 29-JAN-2002; 2002US-0352215P.
XX PA (GLOB-) GLOBAL GENOMICS AB.
XX PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;
XX PI Montelius A;
XX WPI; 2003-618365/59.
XX DR Producing a population of double-stranded product DNA molecules, useful
XX PT for mRNA profiling, comprises amplification by nested polymerase chain
XX PT reaction.
XX PS Example; Fig 1; 105pp; English.
XX CC The invention relates to producing a population of double-stranded
XX CC product DNA molecules comprising amplification by a nested PCR method.
XX CC The method is useful in profiling mRNA transcribed in a system under
XX CC investigation. The oligonucleotides are used as size standards in
XX CC electrophoresis, and as internal controls allowing for calculation of
XX CC relative amounts of material present. The present sequence represents a
XX CC double stranded product DNA, which aids in outlining an approach to
XX CC production of a single pattern characteristic of a sample, employing a
XX CC type II restriction enzyme (HaeII)
XX SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
Query Match 1.1%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTAAGAAAAA 1496
DB 18 CGAAAAA 1

RESULT 182
AAQ75549/C
ID AAQ75549 standard; DNA; 19 BP.
XX AC AAQ75549;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX DE Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1479 CTAATAAAAAAAAAAAAAA 1496
DB 18 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 183
AAQ75548/c
ID AAQ75548 standard; DNA; 19 BP.

XX
AC AAQ75548;

DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX

SQ Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1479 CTAATAAAAAAAAAAAAAA 1496

DB 18 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 184

AAQ75547/c

ID AAQ75547 standard; DNA; 19 BP.

XX
AC AAQ75547;

DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX

SQ Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1479 CTAATAAAAAAAAAAAAAA 1496
DB 19 CAAAAAAAAAAAAAAAAAAAAA 2

RESULT 185

AAQ75555/c

ID AAQ75555 standard; DNA; 19 BP.

XX
AC AAQ75555;

DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX

PD 01-NOV-1994.
 XX 16-APR-1993; 93JP-00112515.
 XX 16-APR-1993; 93JP-00112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX Disclosure; Page 5; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
 SQ Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1479 CTAATAAAAAAAAAAAAAA 1496
 Db 19 CGAAAAAAAAAAAAAAAAAA 2
 RESULT 186
 AAX18389/C
 ID AAX18389 standard; DNA; 18 BP.
 XX AAX18389;
 AC AAX18389;
 DT 11-MAY-1999 (first entry)
 XX RT-PCR primer of the invention SEQ ID 30.
 DE RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX Synthetic.
 OS JP11032765-A.
 XX JP11032765-A.
 XX 09-FEB-1999.
 XX 18-JUL-1997; 97JP-00208312.
 XX 18-JUL-1997; 97JP-00208312.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX WPI; 1999-183822/16.
 XX Peptides having at least two new nucleotides - useful as primers in RT-
 PT PCR.
 XX Example 1; Page 12; 19pp; Japanese.
 XX This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;
 SQ Query Match 1.1%; Score 16.2; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.4e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1480 TAAAAAATAAAAAAAAAA 1496
 Db 17 BAAAAAATAAAAAAAAAA 1
 RESULT 187
 AAT94431
 ID AAT94431 standard; mRNA; 19 BP.
 XX AAT94431;
 AC AAT94431;
 XX 02-MAR-1998 (first entry)
 DT Template mRNA poly-A tail SEQ ID NO:1 from W09729211.
 XX Primer; detection; characterisation; mRNA; restriction display PCR;
 KW synthesis; cDNA; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX W09729211-A1.
 FN 14-AUG-1997.
 XX 07-FEB-1997; 97WO-US002009.
 XX 09-FEB-1996; 96US-0011379P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Weinstein JN, Boulamwini J;
 XX WPI; 1997-415362/38.
 PT Detection and characterisation of mRNA by restriction display PCR -
 PT comprising synthesis of cDNA, digestion with a restriction endonuclease,
 PT ligation to an adaptor DNA and PCR amplification.
 XX Disclosure; Page 24; 40pp; English.
 XX A method has been improved for detecting and characterising mRNA
 CC molecules which includes synthesising a double stranded (ds) cDNA from
 CC isolated mRNA, digesting the ds cDNA with a restriction endonuclease to
 CC produce cDNA fragments in which at least one end of the cDNA fragments
 CC has a sequence capable of hybridising to an adaptor DNA sequence. The
 CC improvement comprises: (a) hybridising adaptor DNA sequences to at least
 CC one end of the cDNA fragments; (b) ligating the adaptor DNA sequences to
 CC the cDNA fragments; (c) amplifying the cDNA fragments having ligated
 CC adaptor DNA sequences by a PCR using primers that hybridise to the ends
 CC of the cDNA fragments, where the primers have at least one nucleotide at
 CC the 3' end that specifically hybridises to a subset of cDNA molecules;
 CC and (d) detecting the presence of the resulting amplified cDNA fragments.
 CC The present sequence represent a template poly-A tail used in the present
 CC specification. The method designate restriction display PCR can be used
 CC for characterising cells based on their mRNA content, for representing
 CC expressed genes, and for discovery of therapeutics that alter cellular
 CC gene expression. The method is also useful for characterising cells of a
 CC variety of types and under a variety of physiological conditions. The
 CC method is also useful for identifying cells or tissue from particular
 CC individuals or species based on the fingerprint obtained from the mRNA

```

CC content of isolated cells or tissue and comparing it to cells or tissue
CC from a known source
XX
SQ Sequence 19 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 2 Other;

Query Match      1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 2 BAAAAAATAAAAAAAAAA 18

RESULT 188
AAAX18390/C
ID AAAX18390 standard; DNA; 19 BP.
XX
AC AAAX18390;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 31.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
FN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
PS Example 1; Page 12; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;

Query Match      1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 18 BAAAAAATAAAAAAAAAA 2

RESULT 189
AAAX06572/C
ID AAAX06572 standard; DNA; 19 BP.
XX

```

```

AC AAX06572;
XX
DT 06-APR-1999 (first entry)
XX
DE (-)-limonene-6-hydroxylase primer 3.B.
XX
KW (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; L3H; L6H;
KW spear mint; peppermint; enzyme; limonene hydroxylase; trans-carveol;
KW trans-isopipitenol; pathogen defense mechanism; attractant;
KW environmental signal; monoterpene hydroxylase; PCR primer; ss.
XX
OS Synthetic.
OS Mentha spicata.
XX
PN WO9859042-A1.
XX
PD 30-DEC-1998.
XX
PF 15-JUN-1998; 98WO-US012581.
XX
PR 24-JUN-1997; 97US-00881784.
XX
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI Croteau RB, Lupien SL, Karp F;
XX
DR WPI; 1999-105618/09.
XX
PT New isolated limonene hydroxylase nucleic acids - which encode limonene-6
PT -hydroxylase and limonene-3-hydroxylase, which can be used to produce
PT trans-carveol and trans-isopipitenol.
XX
PS Example 4; Page 27; 80pp; English.
XX
CC The invention relates to nucleotide sequences encoding spearmint (-)-
CC limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3- hydroxylase
CC (L3H). Host cells containing a vector comprising the nucleotide sequences
CC can be used for the recombinant production of limonene hydroxylases or of
CC primary enzyme products. The primary enzyme products are trans-carveol in
CC the case of (-)-L6H or trans-isopipitenol in the case of (-)-L3H, which
CC are of subsequent use, to obtain enhanced expression of limonene
CC hydroxylase in plants to attain enhanced trans- carveol or trans-
CC isopipitenol production as a predator or pathogen defense mechanism,
CC attractant or environmental signal. The limonene hydroxylase cDNAs also
CC provide a useful tool for isolating other monoterpene hydroxylase genes
CC and for examining the developmental regulation of monoterpene
CC biosynthesis. Sequences AAX06564-73 represent primers for the PCR
CC amplification of (-)-limonene-6-hydroxylase cDNA
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match      1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 19 DAAAAAATAAAAAAAAAA 3

RESULT 190
AAZ99489/C
ID AAZ99489 standard; DNA; 19 BP.
XX
AC AAZ99489;
XX
DT 03-JUL-2000 (first entry)
XX
DE Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
XX
KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
KW seed germination; seedling growth; gibberellin biosynthetic pathway;

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KW transgenic plant; hypocotyl; epicotyl; PCR primer; ss.

XX

OS Cucurbita maxima.

XX

PN WO200009722-A2.

XX

XX 24-FEB-2000.

XX

XX 10-AUG-1999; 99WO-US018066.

XX

XX 10-AUG-1998; 98US-0096111P.

XX

PR 07-JUN-1999; 99US-0137977P.

XX

XX (MONS) MONSANTO CO.

XX

XX Brown SM, Ellich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;

XX

PI Pillar KJ, Rao S, Ream JE;

PI

XX WPI; 2000-224351/19.

XX

DR Obtaining transgenic plant useful for controlling seed germination and
PT seedling growth comprises transgene comprising a sequence expressing
PT altered levels of an essential hormone.

XX

PS Example 17; Page 262; 267pp; English.

XX

XX The present primer was used to reverse transcribe cDNA encoding a C-20
CC oxidase. The amplification fragment is used in the method of the invention.
CC The specific method describes methods for the inhibition and control of
CC gibberellic acid levels. Gibberellic acid levels may be inhibited or
CC controlled by use of a chimeric expression construct expressing a RNA or
CC protein which suppresses the gibberellin biosynthetic pathway sequence,
CC diverts substrate from the pathway, or degrades pathway substrates or
CC products. The methods uses copayl diphosphate synthase, 3beta-
CC hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a
CC 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is
CC used to control seed germination and seedling growth especially to
CC regulate gene products of gibberellin biosynthetic pathway and
CC restoration of normal seed germination, in transgenic plants. The plants
CC produced are gibberellin deficient, and have shortened hypocotyl and/or
CC epicotyl phenotypes compared to normal plants

XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

XX

Query Match 1.1%; Score 16.2; DB 1; Length 19;

XX

Best Local Similarity 94.1%; Pred. No. 1.6e+02;

XX

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1480 TAAAAAATAAAAAAAAAA 1496

XX

Db :|||||

XX

19 BAAAAAATAAAAAAAAAA 3

XX

RESULT 191

XX

AAD15201/C

XX

ID AAD15201 standard; DNA; 19 BP.

XX

XX AAD15201;

XX

XX 01-NOV-2001 (first entry)

XX

XX 3' sequencing primer #1 to identify and characterise polynucleotides.

XX

XX Fatty lesion development; atherosclerosis; Alzheimer's disease;
KW nervous system disorder; Parkinson's disease; immune system disorder;
KW ischaemia; lymphopaenia; leukocyte adhesion deficiency syndrome;
KW haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
KW coagulation disorder; blood platelet disorder; autoimmune disorder;
KW dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
KW Grave's disease; gene therapy; antiarteriosclerotic; immunostimulant;
KW cardiovascular; antiviral; primer; ss.

XX

XX Unidentified.

XX

OS

XX

XX

PN WO200154651-A2.

XX

XX 02-AUG-2001.

XX

XX 25-JAN-2001; 2001WO-US002439.

XX

XX 25-JAN-2000; 2000US-0177963P.

XX

XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX

XX Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;

XX

XX WPI; 2001-514526/56.

XX

XX New polynucleotides regulated by fatty lesion development and their
XX encoded polypeptides, useful for preventing, treating or ameliorating
XX atherosclerosis, as well as for immune or hyperproliferative disorders.

XX

XX Example 1; Page 79; 188pp; English.

XX

XX The present invention relates to an isolated nucleic acid regulated by
XX fatty lesion development, which comprises any of 55 polynucleotide
XX sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or
XX antibody is useful for preventing, treating, modulating or ameliorating a
XX medical condition, particularly atherosclerosis. The invention is used as
XX a marker or detector of nervous system disorder or disease (e.g.
XX Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
XX invention may also be useful for treating deficiencies or disorders of
XX the immune system (e.g. lymphopaenia, leukocyte adhesion deficiency
XX syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
XX (e.g. Gaucher's disease), infectious disease (e.g. herpes simplex),
XX coagulation disorders, rheumatoid arthritis, dermatitis, Grave's disease
XX (Addison's disease). The polynucleotide sequence is also used in gene therapy. The present
XX sequence is a 3' sequencing primer used in the identification and
XX characterisation of polynucleotides up-regulated by fatty lesion
XX development

XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

XX

Query Match 1.1%; Score 16.2; DB 1; Length 19;

XX

Best Local Similarity 94.1%; Pred. No. 1.6e+02;

XX

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1480 TAAAAAATAAAAAAAAAA 1496

XX

Db :|||||

XX

19 BAAAAAATAAAAAAAAAA 3

XX

RESULT 192

XX

AAH21968/C

XX

ID AAH21968 standard; DNA; 19 BP.

XX

XX AAH21968;

XX

XX 16-AUG-2001 (first entry)

XX

XX Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ.92.
XX Mouse; human; total gene expression analysis; TOGA; DST; EST;
XX digital sequence tag; expressed sequence tag; neuroleptic; antimanic;
XX central nervous system; antidepressant; gene therapy; diagnosis;
XX neuropsychiatric disorder; schizophrenia; bipolar disorder;
XX addiction-related behaviour; chromosome identification; immune response;
XX PCR primer; probe; ss.
XX Mus musculus.
XX OS
XX WO200130972-A2.
XX PD
XX 03-MAY-2001.

sequences. AAS06401-AAS06590 represent these novel sequences and the primer sequences used to isolate them. The PCR-based total gene expression analysis (TOGA) system is used to examine the expression pattern of molecules corresponding to genes that are regulated in unstimulated microglia, activated microglia, unstimulated macrophage and activated macrophage. The polynucleotides of the invention, the polypeptides encoded by them and antibodies that bind to these polypeptides are useful for the diagnosis, prevention, treatment or amelioration of a medical condition, preferably a neuroinflammatory pathology or a neurodegenerative disease such as Alzheimer's disease, senile dementia, Parkinson's disease, obsessive compulsive disorders, epilepsy, schizophrenia, multiple sclerosis, depression and bipolar manic-depressive disorder. The sequences and methods of the invention can also be used for detecting or treating infectious disorders (e.g. AIDS), hyperproliferative disorders (e.g. cancer), immune disorders (e.g. severe combined immunodeficiency, SCID) autoimmune diseases (e.g. insulin dependent diabetes mellitus), inflammatory disorders (e.g. arthritis). The polynucleotides can be used for gene therapy

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1480 TAAAAAATAAAAAAAAAA 1496
Db 19 BAAAAAATAAAAAAAAAA 3

RESULT 195
ID ABK71509/c
XX ABK71509; DNA; 19 BP.
AC ABK71509;
XX
XX 30-JUL-2002 (first entry)
DT
XX
XX CNS related 3' sequencing primer.
XX
KW Central nervous system; CNS; neuroleptic; mouse; human; psychoses;
KW neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
KW Pick's disease; Binswanger's disease; senile dementia; encephalopathy;
KW Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;
KW addiction; multiple sclerosis; depression; manic-depressive disorder;
KW primer; ss.
XX
XX Synthetic.
XX
XX WO200226936-A2.
XX
XX 04-APR-2002.
XX
XX 01-OCT-2001; 2001WO-US030695.
XX
XX 29-SEP-2000; 2000US-0236790P.
XX
XX 18-JAN-2001; 2001US-0263084P.
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
XX Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush BS, Hasel KW;
XX WPI; 2002-383271/41.
XX
XX
XX New polynucleotide useful in gene therapy for preventing, treating
XX modulating or ameliorating a medical condition such as psychoses or a
XX neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a
XX mammal.
XX
XX Example 1; Page 40; 254pp; English.
XX
XX This invention relates to the cDNA sequences of novel isolated

polynucleotides associated with psychoses or other neuropsychiatric disorders. The sequences of the invention may act as blockers of D₂ receptors in the meso-limbic dopamine system. The nucleotide sequences of the invention and the polypeptides encoded by them are useful in the manufacture of a medicament useful for preventing, treating, modulating or ameliorating a medical condition e.g. a neuropsychiatric disorder. An antibody that binds the proteins of the invention is useful for preventing, treating, modulating or ameliorating neurological disorders such as psychoses or a neuro psychiatric disorder in a subject by determining the presence or absence of mutation in the nucleotide sequence of apolipoprotein D or by determining the alteration (increase or decrease) in the expression of apolipoprotein D. The sequences of the invention are useful in treating deficiencies or disorders of the central nervous system or peripheral nervous system by activating or inhibiting the proliferation, differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells or glial cells. The sequences are useful as a marker or detector of a particular nervous system disease or disorder such as Alzheimer's disease, Pick's disease, Binswanger's disease, other senile dementia, Parkinson's disease, obsessive compulsive disorders, epilepsy, encephalopathy, ischaemia, addiction, multiple sclerosis, depression and manic-depressive disorder. The present sequence represents an oligonucleotide primer used in the identification of the cDNA sequences of the invention

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1480 TAAAAAATAAAAAAAAAA 1496
Db 19 BAAAAAATAAAAAAAAAA 3

RESULT 196
ABQ73231/c
ID ABQ73231 standard; DNA; 19 BP.
XX
XX ABQ73231;
AC ABQ73231;
XX
XX 27-SEP-2002 (first entry)
DT
XX
XX Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.
DE
XX
XX Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;
KW TOGA primer; ss.
KW
XX Oryctolagus cuniculus.
OS
XX Synthetic.
XX
XX WO200242420-A2.
XX
XX 30-MAY-2002.
XX
XX 21-NOV-2001; 2001WO-US044072.
XX
XX 21-NOV-2000; 2000US-0252216P.
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
XX Leonardi A, Sartani A, Glass JR, Hasel KW;
XX WPI; 2002:575233/61.
XX
XX New polynucleotides related to regulated genes characteristic of
XX atherosclerosis, useful for diagnosing, preventing, treating, modulating
XX or ameliorating atherosclerosis in a mammalian subject.
XX
XX Disclosure; Page 28; 130pp; English.

XX The present invention describes an isolated polynucleotide (I) and its
 CC complements, and degenerate variants, comprising a sequence selected from
 CC those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag
 CC (DST) corresponding to mRNAs whose expression is regulated by
 CC proliferative lesion development caused by mechanically induced intimal
 CC hyperplasia, or by lecanidipine treatment, or by proliferative lesions
 CC and reversed by lecanidipine treatment. (I) has antiatherosclerotic
 CC activity and can be used in gene therapy. (I) can be used for diagnosing
 CC a medical condition (e.g. atherosclerosis) in a subject which involves
 CC determining the presence or absence of a mutation in (I) and diagnosing
 CC the medical condition based on the presence or absence of the mutation.
 CC (I) is also useful for diagnosing atherosclerosis, or the susceptibility
 CC to atherosclerosis in a subject which involves detecting an alteration
 CC (an increase or decrease) in amount of expression of (I). (I) is also
 CC useful for diagnosing or monitoring the effects of treating a subject
 CC with dihydropyridine calcium antagonist e.g., lercanidipine. (I) can also
 CC be used for preventing, treating, modulating, or ameliorating a medical
 CC condition such as atherosclerosis in a mammalian subject. The present
 CC sequence represents a TOGA primer which is used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAATAAAAAAAAAA 1496
 Db 19 BAAAAAATAAAAAAAAAA 3
 RESULT 197
 AAD34663/c
 ID AAD34663 standard; DNA; 19 BP.
 XX
 AC AAD34663;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE PCR primer #4 used for direct sequencing of TOGA generated PCR products.
 XX
 KW Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;
 KW acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;
 KW TOGA; Total Gene expression Analysis; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200222783-A2.
 XX
 PD 21-MAR-2002.
 XX
 XX 17-SEP-2001; 2001WO-US029123.
 XX
 PR 15-SEP-2000; 2000US-0233176P.
 XX
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX
 PI Chisari FV, Wieland SF, Guidotti LGDVM, Mueller R, Hilbush BS;
 XX
 DR WPI; 2002-339865/37.
 XX
 PT Preventing and treating hepatitis viral infection in a mammal, comprises
 PT administering nucleic acid molecules that up- or down-regulate in
 PT hepatitis B virus infection or polypeptides encoded by the nucleic acid
 PT molecules.
 XX
 PS Disclosure; Page 28; 125pp; English.
 XX
 CC The present invention relates to a method for preventing, treating,
 CC modulating or ameliorating a medical condition. The method involves
 CC administering one or more nucleic acid molecules up- or down-regulated in

CC hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic
 CC acid molecules or antibodies that bind to the polypeptide. The method is
 CC useful for preventing, treating, modulating or ameliorating a medical
 CC condition. It is also useful for determining the presence or absence of a
 CC mutation in the nucleic acid molecules or detecting an alteration in
 CC expression of the polypeptide which is useful for the diagnosis of
 CC hepatitis viral infection. The method is useful for assessing the stage
 CC of hepatitis viral infection (e.g., acute hepatitis versus chronic
 CC hepatitis) or assessing the efficacy or toxicity of therapeutic treatment
 CC for hepatitis viral infection and a gene expression profile is useful for
 CC identifying polypeptides and polynucleotides which are associated with
 CC hepatitis viral infection. Sequences of the invention are used in gene
 CC therapy and as vaccines. Nucleic acid sequences are useful as a
 CC diagnostic markers for HBV infection and for treating infectious
 CC diseases. The present DNA sequence is a PCR primer which is used for
 CC direct sequencing of TOGA (Total Gene expression Analysis) generated PCR
 CC products
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAATAAAAAAAAAA 1496
 Db 19 BAAAAAATAAAAAAAAAA 3
 RESULT 198
 AAD40279/c
 ID AAD40279 standard; DNA; 19 BP.
 XX
 AC AAD40279;
 XX
 DT 22-OCT-2002 (first entry)
 XX
 DE HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
 XX
 KW Gibberellin; transgenic plant; seed germination; seedling growth; GA;
 KW transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.
 XX
 OS Cucurbita pepo.
 XX
 PN US2002053095-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 10-AUG-1999; 99US-00371307.
 XX
 PR 10-AUG-1999; 99US-00371307.
 XX
 PA (BROW/) BROWN S M.
 XX
 PI Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Piller KJ, Rac S, Ream JE;
 XX
 DR WPI; 2002-489107/52.
 XX
 PT Control of gibberellin levels in plants useful to avoid unfavorable
 PT conditions in crops to increase yields, using transgenic plants having
 PT reduced seed germination and early seedling growth then treatment to
 PT restore these properties.
 XX
 PS Example 19; Page 104; 155pp; English.
 XX
 CC The invention relates to control of gibberellin (GA) levels in plants.
 CC The invention involves producing transgenic plants having a phenotype of
 CC reduced seed germination and reduced early seedling growth, then
 CC restoring seed germination and early seedling growth by treating plants
 CC with an appropriate compound when conditions are favourable. The method
 CC is useful to control seed germination and/or early seedling growth in
 CC agricultural production so that unfavorable environmental conditions

CC normally reducing agronomic output can be avoided and yields increased.
 CC Plants also demonstrate increased uniformity of germination, emergence
 CC and seedling vigor, so increasing yields at harvest. The method is
 CC especially useful in crop plants such as e.g. canola, soybean, cotton,
 CC etc., and is also useful in storage and transport of seeds to reduce
 CC premature germination which may affect agronomic or food quality of the
 CC seeds. The present sequence is a PCR primer used to isolate pumpkin 2beta
 CC -3beta hydroxylase cDNA. This primer is used in the exemplification of
 CC the invention

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
 Db :|||||
 19 BAAAAAAAAAAAAAAAAA 3

RESULT 199
 ABZ68389/c
 ID ABZ68389 standard; DNA; 19 BP.

XX AC ABZ68389;

XX DT 22-APR-2003 (first entry)

XX DE Reverse transcription primer used to produce yeast cDNA.

XX KW Histone acetyltransferase; histone deacetylase; gene expression profile;
 KW chromatin-associated protein; gene expression; primer; ss.

XX OS Synthetic.

XX PN WO2003000715-A1.

XX PD 03-JAN-2003.

XX PF 21-JUN-2002; 2002WO-US019750.

XX PR 22-JUN-2001; 2001US-0300135P.

XX PA (CERE-) CERES INC.

XX PI Dang V, Okamuro J;

XX DR WPI; 2003-175280/17.

XX PT New chimeric polypeptide comprising a histone acetyltransferase

PT polypeptide segment and a segment comprising a histone deacetylase
 PT chromatin-associated protein complex subunit, useful for modulating gene
 PT expression in cells.

XX PS Example 10; Page 54; 85pp; English.

XX CC The specification describes chimeric histone acetyltransferase
 CC polypeptides. The chimeric polypeptides comprise a polypeptide segment
 CC that exhibits histone acetyltransferase activity, and a polypeptide
 CC segment having 40% or greater sequence identity to a subunit of a histone
 CC deacetylase chromatin-associated protein complex. The chimeric
 CC polypeptides are useful for determining gene expression profiles in
 CC specific cells, for modulating gene expression in specific cells, and for
 CC making genetically modified eukaryotes. The present sequence represents a
 CC reverse transcription primer used in the method of the invention

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
 Db :|||||
 19 BAAAAAAAAAAAAAAAAA 3

RESULT 200
 ACC79402/c
 ID ACC79402 standard; DNA; 19 BP.

XX AC ACC79402;

XX DT 04-AUG-2003 (first entry)

XX DE M13 sequencing primer 3' primer SEQ ID NO:84.

XX KW Pathological condition; ataxia telangiectasia; AT; tumour; cancer;
 KW cytostatic; vaccine; gene therapy; PCR primer; ss.

XX OS Enterobacteria phage M13.

XX OS Synthetic.

XX PN WO2003033668-A2.

XX PD 24-APR-2003.

XX PF 17-OCT-2002; 2002WO-US033311.

XX PR 17-OCT-2001; 2001US-0330206P.

XX PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX PI Barlow C, Winrow CJ, Callahan MLA, Pankratz DG, Vibat CRT;
 PI Warren AJ;

XX DR WPI; 2003-393520/37.

XX PT Preventing or treating a pathological condition e.g., ataxia
 PT telangiectasia (AT), AT tumors or other cancers comprises administering
 PT polynucleotides.

XX PS Example 1; Page 76; 184pp; English.

XX CC The present invention describes a method for preventing or treating a
 CC pathological condition (comprising ataxia telangiectasia (AT), AT tumors
 CC or other cancers), which comprises administering to a mammalian subject
 CC at least one of: (a) a first polynucleotide comprising a sequence having
 CC 38-889 bp (consisting of the sequences in ACC79319 to ACC79392 (I)) or a
 CC second polynucleotide at least 95% identical to the first polynucleotide;
 CC (b) a third polynucleotide comprising at least 10-bp sequence that is
 CC hybridisable to the first polynucleotide under stringent conditions; or
 CC (c) a gene corresponding to any of (1)-(2) or another gene at least 95%
 CC identical to the gene. (1) have cytostatic activities, and can be used in
 CC vaccines and in gene therapy. The method is useful for preventing or
 CC treating e.g., ataxia telangiectasia (AT), AT tumors or other cancers.
 CC ACC79393 to ACC79423 represent primers used in the exemplification of the
 CC present invention

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
 Db :|||||
 19 BAAAAAAAAAAAAAAAAA 3

RESULT 201
 AAD49149/c
 ID AAD49149 standard; DNA; 19 BP.

XX AC AAD49149;

```

XX DT 07-MAR-2003 (first entry)
XX DE
XX 3' sequencing primer #1 used in the invention.
XX KW
XX OS Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
XX KW Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;
XX KW autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;
XX KW haemolytic anaemia; graft-versus-host disease; inflammation; infection;
XX KW epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;
XX KW food additive; food preservative; primer; ss.
XX OS
XX PN WO200281726-A2.
XX PD
XX PF 17-OCT-2002.
XX PN
XX PD
XX PF 15-NOV-2001; 2001WO-US043741.
XX PR 15-NOV-2000; 2000US-0248992P.
XX PR 28-NOV-2000; 2000US-0253623P.
XX PR
XX PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX PI Leonardi A, Sartani A, Glass J, Sutcliffe JG, Hasel KW;
XX DR WPI; 2003-058561/05.
XX XX
XX XX New polypeptide associated with atherosclerosis, useful for treating
XX PT atherosclerosis, nervous system disorders, immune disorders,
XX PT hyperproliferative disorders and infectious diseases.
XX XX
XX PS Disclosure; Page 139; 146pp; English.
XX CC
XX CC The invention relates to polynucleotides and polypeptides associated with
XX CC atherosclerosis. Polynucleotides of the invention are useful for delivery
XX CC of genes, DNA vaccines, diagnostic reagents, peptides, proteins or
XX CC macromolecules. Sequences of the invention are useful for treating
XX CC nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease,
XX CC multiple sclerosis, epilepsy), immune disorders (e.g., autoimmune
XX CC disorders such as rheumatoid arthritis, Addison's disease, haemolytic
XX CC anaemia, graft-versus-host disease, inflammation), hyperproliferative
XX CC disorders (e.g., neoplasms) and infectious diseases (e.g., viral,
XX CC bacterial, fungal or parasite infection). They are used for regeneration
XX CC of tissues, to repair, replace or protect damage tissues, for increasing
XX CC chemotaxis activity of cells, for increasing or decreasing the
XX CC differentiation or proliferation of embryonic stem cells from a lineage,
XX CC for modulating mammalian characteristics, (such as body weight or
XX CC height), for modulating mammalian metabolism affecting catabolism,
XX CC anabolism, processing utilisation and storage of energy, to change a
XX CC mammal's mental or physical state, or as a food additive or preservative.
XX CC The invention is useful in gene therapy. The present sequence is a
XX CC sequencing primer used in the invention
XX XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
XX
XX Query Match 1.1%; Score 16.2; DB 1; Length 19;
XX Best Local Similarity 94.1%; Pred. No. 1.6e+02;
XX Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1480 TAAAAAAAAAAAAAAAAA 1496
DB 19 BAAAAAAAAAAAAAAAAA 3

RESULT 202
AAD50267/C
XX ID AAD50267 standard; DNA; 19 BP.
XX AC
XX XX AAD50267;
XX DT 24-MAR-2003 (first entry)
XX
XX QY 1480 TAAAAAAAAAAAAAAAAA 1496
XX DB 19 BAAAAAAAAAAAAAAAAA 3

RESULT 202
AAD50267/C
XX ID AAD50267 standard; DNA; 19 BP.
XX AC
XX XX AAD50267;
XX DT 24-MAR-2003 (first entry)
XX
XX 3' sequencing primer #1 used to illustrate the method of the invention.
XX DE
XX KW Gene expression; drug interaction mechanism; drug screening; primer;
XX KW genomic mapping; ss.
XX OS
XX PN WO200261045-A2.
XX PD
XX PF 08-AUG-2002.
XX PF
XX PF 01-FEB-2002; 2002WO-US002666.
XX PR 01-FEB-2001; 2001US-00775217.
XX PR
XX PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX PA (QUAN/) QUAN J.
XX PI Quan J, Hilbush BS, Hasel KWPD, Sutcliffe GJ, Chang HW;
XX PI Callahan MA;
XX DR WPI; 2003-092784/08.
XX XX
XX XX Simplified TOGA method for simultaneous sequence-specific identification
XX PT of multiple mRNA molecules in mRNA population, useful for determining
XX PT tissue-specific patterns of gene expression or mechanisms of drug
XX PT interaction.
XX XX
XX PS Disclosure; Page 39; 93pp; English.
XX CC
XX CC The present invention relates to a novel simplified TOGA (RTM) method for
XX CC simultaneous sequence-specific identification of multiple mRNA molecules
XX CC in a RNA population. The method involves characterising each of the
XX CC sequence-specific polymerase chain reaction (PCR) products by partial
XX CC patterns and length. The method is useful for determining tissue-specific
XX CC patterns of gene expression or mechanisms of drug interaction. It is also
XX CC useful for drug screening, studying physiological processes, genomic
XX CC mapping or manufacture of diagnostic, prognostic or therapeutic reagents.
XX CC The present sequence is a primer used to illustrate the method of the
XX CC invention
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
XX
XX Query Match 1.1%; Score 16.2; DB 1; Length 19;
XX Best Local Similarity 94.1%; Pred. No. 1.6e+02;
XX Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1480 TAAAAAAAAAAAAAAAAA 1496
DB 19 BAAAAAAAAAAAAAAAAA 3

RESULT 203
ADC21495/C
XX ID ADC21495 standard; DNA; 19 BP.
XX XX
XX AC ADC21495;
XX DT 18-DEC-2003 (first entry)
XX XX
XX DE Human PRDI-BF1 RT-PCR primer.
XX XX
XX KW tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;
XX KW multiple myeloma cell; human; PRDI-BF1;
XX KW positive regulatory domain I-binding factor-1; MHC;
XX KW major histocompatibility complex Class I; cytostatic; vaccine; ss;
XX KW primer; PCR.
XX XX
XX OS Homo sapiens.
XX PN WO2003029282-A2.
XX XX

```

PD 10-APR-2003.
 PF 24-SEP-2002; 2002WO-EP010701.
 XX
 PR 29-SEP-2001; 2001DE-01048236.
 XX (IMMU-) IMMUGENICS AG.
 PA
 XX Theobald M, Lotz C;
 PI WPI; 2003-354724/33.
 XX
 XX New tumor-associated oligopeptide, useful particularly for treating
 PT multiple myeloma, is recognized by CD8 cytotoxic T cells, also
 PT derivatives and related nucleic acid.
 PT
 PS Disclosure; Page 22; 64pp; German.
 XX
 XX This invention describes a novel tumor-associated oligopeptide that is
 CC recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes
 CC CTL-induced lysis and/or apoptosis of tumor cells, especially multiple
 CC myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive
 CC regulatory domain I-binding factor-1) which is able to induce an MHC
 CC (major histocompatibility complex) Class I allele variant A2-restricted
 CC immune response of CD8+ CTL against tumor cells. The products of the
 CC invention have cytostatic activity and can be used in a vaccine. The
 CC peptide of the invention, also related retro-inverse and pseudopeptides,
 CC fusion proteins (FP), polynucleotides, vectors, host cells and antibodies
 CC and T cell receptors specific for PRDI-BF1 peptides are useful for
 CC treating diseases associated with PRDI-BF1, particularly tumors. The
 CC products of the invention are also useful as diagnostic, therapeutic and
 CC prophylactic agents for detecting, modifying, generating, expanding
 CC and/or regulating activation and functional status of T cells, and for
 CC preparation of poly- or mono-clonal or recombinant A2-restricted T cell
 CC receptors and their functional equivalents. This sequence represents an
 CC RT-PCR primer used to amplify the human PRDI-BF1 gene described in the
 CC invention.
 XX
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 SQ
 Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAATAAAAAAAAAA 1496
 :|||||
 Db 19 BAAAAAATAAAAAAAAAA 3
 RESULT 204
 AAX18368/c
 ID AAX18368 standard; DNA; 16 BP.
 XX
 XX AAX18368;
 AC
 XX 11-MAY-1999 (first entry)
 DT
 XX RT-PCR primer of the invention SEQ ID 9.
 DE
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 KW
 XX Synthetic.
 OS
 XX JPI1032765-A.
 PN
 XX 09-FEB-1999.
 PD
 XX 18-JUL-1997; 97JP-00208312.
 PF
 XX 18-JUL-1997; 97JP-00208312.
 PR
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX

DR WPI; 1999-183822/16.
 XX Peptides having at least two new nucleotides - useful as primers in RT-
 PT PCR.
 XX
 XX Disclosure; Page 10; 19pp; Japanese.
 PS
 XX This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX
 XX Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1479 CTAAAAAATAAAAAAAAA 1494
 :|||||
 Db 16 CTAAAAAATAAAAAAAAA 1
 RESULT 205
 AAX07568
 ID AAX07568 standard; cDNA; 16 BP.
 XX
 XX AAX07568;
 AC
 XX 21-JUN-1999 (first entry)
 DT
 XX Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.
 DE
 XX Secreted protein; fetal kidney; ds.
 KW
 XX Homo sapiens.
 OS
 XX WO9900405-A1.
 PN
 XX 07-JAN-1999.
 PD
 XX 29-JUN-1998; 98WO-US013530.
 PF
 XX 30-JUN-1997; 97US-00885610.
 PR
 XX (GEMY) GENETICS INST INC.
 PA
 XX Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Evans C, Agostino MJ;
 PI
 XX WPI; 1999-095671/08.
 DR
 XX New polynucleotides encoding secreted human proteins - are derived from
 PT foetal kidney or adult retina cDNA libraries, used as; e.g. potential
 PT vaccines.
 PT
 XX Disclosure; Page 54; 76pp; English.
 PS
 XX The sequence is that of the 3' end of a sequence encoding a secreted
 CC protein from a human fetal kidney clone AK296. Such a sequence is
 CC predicted to have biological activities which would make them suitable
 CC for treating, preventing or ameliorating medical conditions in humans and
 CC animals, although no supporting data is given. Suggested activities
 CC include nutritional activity, cytokine and cell
 CC proliferation/differentiation activity, immune stimulating (e.g. as

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CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
CC invasion suppressor activity, and tumour inhibition activity. It is also
CC stated to be useful for gene therapy
XX
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match          1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 1 AAAAAAAAAAAAAA 16

RESULT 206
AAC66068
ID AAC66068 standard; DNA; 16 BP.
XX
AC AAC66068;
XX
DT 22-FEB-2001 (first entry)
XX
DE DNA chip primer #4.
XX
KW DNA chip; primer; nucleoside derivative; photolabile protecting group;
KW photolithographic nucleic acid chip; ss.
XX
OS Synthetic.
XX
PN WO200061594-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-DE001148.
XX
PR 08-APR-1999; 99DE-01015867.
XX
PT 28-JAN-2000; 2000DE-01003631.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Beier M, Hoheisel J;
XX
WPI; 2000-679457/66.
XX
New nucleoside derivatives with photolabile protecting groups, useful in
PT oligonucleotide synthesis, particularly on solid phases, e.g. for
PT hybridization testing.
XX
PS Disclosure; Fig 9; 48pp; German.
XX
This invention describes nucleoside derivatives (I) with photolabile
CC protecting groups. (I) are used to synthesize oligonucleotides using the
CC photolithographic nucleic acid chip method, particularly where these are
CC intended for performing enzymatic reactions initiated from a free 3'-
CC hydroxy (especially solid-phase polymerase reactions or ligase reactions,
CC but also reverse transcription, cDNA synthesis etc.), also for
CC hybridization testing, sequencing and in DNA computing. (I) are produced
CC with high selectivity by reaction with a mild acylating agent that has
CC high specificity for the 3'-position, without significant side-reactions
CC (cf. more reactive acylating agents such as chloroformates)
XX
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match          1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 1 AAAAAAAAAAAAAA 16

```

```

Db 1 AAAAAAAAAAAAAA 16

RESULT 207
ABA04585/c
ID ABA04585 standard; DNA; 16 BP.
XX
AC ABA04585;
XX
DT 15-FEB-2002 (first entry)
XX
DE Oligonucleotide #5.
XX
KW Analytical support; genomic sequencing; mutation detection;
KW pharmaceutical development; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = Fl(CH2)6-PO-thymine, where Fl is flavine
FT and PO is a phosphate group"
XX
PN FR2805348-A1.
XX
PD 24-AUG-2001.
XX
PF 23-FEB-2000; 2000FR-00002236.
XX
PR 23-FEB-2000; 2000FR-00002236.
XX
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI Cuzin M, Feltie P, Fontecave M, Decout JL, Dueymes C;
XX
WPI; 2001-628265/73.
XX
Support for hybridization analysis of nucleic acids for sequencing
PT techniques, comprises an array of oligonucleotides having a label where
PT the fluorescence changes follow hybridization.
XX
PS Example 1; Page 12; 33pp; French.
XX
The present invention relates to an analytical support, to which a number
CC of oligonucleotides are fixed. The oligonucleotides are labelled with a
CC fluorescent compound, the fluorescence of which varies when the
CC oligonucleotide hybridises to its complement. The analytical support is
CC useful in hybridisation testing for identification of specific nucleic
CC acids, such as genomic sequencing, detecting mutations or pharmaceutical
CC development. The present oligonucleotide was used to illustrate the
CC invention
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match          1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 16 AAAAAAAAAAAAAA 1

RESULT 208
AAF30895/c
ID AAF30895 standard; DNA; 16 BP.
XX
AC AAF30895;
XX
DT 09-JUL-2001 (first entry)
XX

```

DE Oligonucleotide-minor groove binder complex.

KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;

KW hybridisation; detection; fluorescence; probe; ss.

XX Synthetic.

OS

FH Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /note= "thymine modified by a minor groove binder (2-

FT dimethylaminonaphthalene-6- sulfonamide"

XX

PN WO200131063-A1.

XX

PD 03-MAY-2001.

XX

PF 26-OCT-2000; 2000WO-US029786.

XX

PR 26-OCT-1999; 99US-00428236.

XX

PA (EPOC-) EPOCH BIOSCIENCES INC.

XX

PI Dempcy RO, Afonina IA, Vermeulen NMJ;

XX

DR WPI; 2001-328656/34.

XX

CC Conjugate of oligonucleotide, minor groove binder and latent fluorophore,

PT useful for detecting specific nucleic acids, e.g. for single-nucleotide

PT mismatch discrimination.

XX

PS Disclosure; Page 101; 105pp; English.

XX

CC The present sequence is that of an oligonucleotide (ODN)-minor groove

CC binder (MGB) complex. MGBs bind in a non-intercalating manner to the

CC minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF

CC conjugates of the invention also comprise a latent fluorophore (LF),

CC which binds similarly to the MGB but in an intercalating manner, or lies

CC in the minor groove, or is oriented in some other way to the DNA molecule

CC by MGB, such that it becomes fluorescent (or its fluorescent properties

CC change detectably). The conjugates are used as hybridisation probes and

CC amplification primers for fluorescent detection of specifically

CC hybridising sequences, for analysis or diagnosis, especially (real-time)

CC PCR, for single-nucleotide mismatch discrimination, target or signal

CC amplification, array-based assays and sequencing, including detection of

CC double-stranded DNA by triplex formation

XX

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496

Db 16 AAAAAAAAAAAAAA 1

RESULT 209

AAF30880/c

ID AAF30880 standard; DNA; 16 BP.

XX

AC AAF30880;

XX

DT 09-JUL-2001 (first entry)

XX

DE Oligonucleotide portion of ODN-MGB-LF conjugate.

XX

KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;

KW hybridisation; detection; fluorescence; probe; ss.

XX

OS Synthetic.

XX

PN WO200131063-A1.

XX

PD 03-MAY-2001.

XX

PF 26-OCT-2000; 2000WO-US029786.

XX

PR 26-OCT-1999; 99US-00428236.

XX

PA (EPOC-) EPOCH BIOSCIENCES INC.

XX

PI Dempcy RO, Afonina IA, Vermeulen NMJ;

XX

DR WPI; 2001-328656/34.

XX

CC Conjugate of oligonucleotide, minor groove binder and latent fluorophore,

PT useful for detecting specific nucleic acids, e.g. for single-nucleotide

PT mismatch discrimination.

XX

PS Disclosure; Page 101; 105pp; English.

XX

CC The present sequence is that of an oligonucleotide (ODN)-minor groove

CC binder (MGB) complex. MGBs bind in a non-intercalating manner to the

CC minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF

CC conjugates of the invention also comprise a latent fluorophore (LF),

CC which binds similarly to the MGB but in an intercalating manner, or lies

CC in the minor groove, or is oriented in some other way to the DNA molecule

CC by MGB, such that it becomes fluorescent (or its fluorescent properties

CC change detectably). The conjugates are used as hybridisation probes and

CC amplification primers for fluorescent detection of specifically

CC hybridising sequences, for analysis or diagnosis, especially (real-time)

CC PCR, for single-nucleotide mismatch discrimination, target or signal

CC amplification, array-based assays and sequencing, including detection of

CC double-stranded DNA by triplex formation

XX

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496

Db 16 AAAAAAAAAAAAAA 1

RESULT 210

AAH42481/c

ID AAH42481 standard; DNA; 16 BP.

XX

AC AAH42481;

XX

DT 01-OCT-2001 (first entry)

XX

DE Oligonucleotide used to produce branched chain compounds.

XX

KW Branched chain compound; nucleic acid synthesis; primer extension;

KW reverse transcription; nucleic acid hybridization;

KW nucleic acid amplification; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /note= "COOH attached"

FT misc_feature 2.3

XX

```

FT      /*tag= c
FT      /note= "branch present"
FT      modified_base 2
FT      /*tag= b
FT      /note= "COOH attached"
XX      EP1111068-A1.
XX      27-JUN-2001.
XX      21-DEC-1999; 99EP-00125484.
XX      21-DEC-1999; 99EP-00125484.
XX      (LION-) LION BIOSCIENCE AG.
XX      (VBCG-) VBC GENOMICS GMBH.
XX      Schmidt W, Hiller R, Huber M, Mueller M;
XX      WPI; 2001-466959/51.
XX      Branched compounds useful in e.g. nucleic acid synthesis reaction
XX      comprises nucleic acid moieties optionally extended by a polymerase.
XX      Example 1; Page 10; 31pp; English.
XX      The specification describes branched compounds containing nucleic acid
XX      moieties optionally extended by a polymerase. The branched chain
XX      compounds of the invention are used in nucleic acid synthesis reaction,
XX      primer extension reaction, reverse transcription reaction of RNA into
XX      DNA, nucleic acid hybridization experiment (for identifying sequence of a
XX      nucleic acid), and nucleic acid amplification experiment (for analysing
XX      the expression pattern of genes). The compounds are also used in solid-
XX      phase enzymatic reactions. The present sequence was used in the course of
XX      the invention to produce branched chain compounds
XX      Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1496
DB      16 AAAAAAAAAAAAAA 1

RESULT 212
AAB56451/c
ID      AAB56451 standard; DNA; 16 BP.
XX      AAB56451;
XX      07-AUG-2003 (first entry)
XX      2'-F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
XX      Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX      antisense; ss.
XX      Unidentified.
XX      Key      Location/Qualifiers
FH      modified_base 1..16
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT      misc_feature 8..9
FT      /*tag= b
FT      /note= "Bases 8 and 9 are linked by two secouridine
FT      linkers which is represented as S in page 49 and X in
FT      page 57 and Fig 7 and 8 of the specification"
XX      WO2003037909-A1.
XX      08-MAY-2003.
XX      29-OCT-2002; 2002WO-CA001628.
XX      29-OCT-2001; 2001US-0330719P.
XX      (UYMC-) UNIV MCGILL.

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FT      /*tag= c
FT      /note= "branch present"
FT      modified_base 2
FT      /*tag= b
FT      /note= "COOH attached"
XX      EP1111068-A1.
XX      27-JUN-2001.
XX      21-DEC-1999; 99EP-00125484.
XX      21-DEC-1999; 99EP-00125484.
XX      (LION-) LION BIOSCIENCE AG.
XX      (VBCG-) VBC GENOMICS GMBH.
XX      Schmidt W, Hiller R, Huber M, Mueller M;
XX      WPI; 2001-466959/51.
XX      Branched compounds useful in e.g. nucleic acid synthesis reaction
XX      comprises nucleic acid moieties optionally extended by a polymerase.
XX      Example 1; Page 10; 31pp; English.
XX      The specification describes branched compounds containing nucleic acid
XX      moieties optionally extended by a polymerase. The branched chain
XX      compounds of the invention are used in nucleic acid synthesis reaction,
XX      primer extension reaction, reverse transcription reaction of RNA into
XX      DNA, nucleic acid hybridization experiment (for identifying sequence of a
XX      nucleic acid), and nucleic acid amplification experiment (for analysing
XX      the expression pattern of genes). The compounds are also used in solid-
XX      phase enzymatic reactions. The present sequence was used in the course of
XX      the invention to produce branched chain compounds
XX      Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1496
DB      16 AAAAAAAAAAAAAA 1

RESULT 211
ABA97402/c
ID      ABA97402 standard; DNA; 16 BP.
XX      ABA97402;
XX      18-JUN-2002 (first entry)
XX      Nucleotide sequence of oligomer # 1 used to test thermal stability.
XX      Protein nucleic acid molecule; PNA; ds.
XX      Synthetic.
XX      WO200168673-A1.
XX      20-SEP-2001.
XX      13-MAR-2001; 2001WO-US008111.
XX      14-MAR-2000; 2000US-0189190P.
XX      30-NOV-2000; 2000US-0250334P.
XX      (ACTI-) ACTIVE MOTIF.
XX      Efimov V, Fernandez J, Archdeacon D, Archdeacon J;

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PI      Chakhmakheau O, Buryakova A, Choob M, Hondorp K;
XX      WPI; 2002-041177/05.
XX      Oligonucleotides analogs useful in detection, separation and purification
XX      of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX      Example 17; Page 118; 197pp; English.
XX      This invention relates to oligonucleotide analogues comprising a protein
XX      nucleic acid molecule (PNA) monomer. They are used in the detection and
XX      separation of nucleic acid molecules and as probes, primers, linkers,
XX      adapters and antisense agents on solid supports. Modifications enhance
XX      their use as capture and detection probes e.g. by the incorporation of
XX      biotin, digoxigenin, radioisotopes, fluorescent labels such as
XX      fluorescein and reporter molecules such as alkaline phosphatase. They are
XX      also used for enhancing or inhibiting the activity of an enzyme or
XX      cellular activity. The compounds are stable to nucleases and proteases,
XX      have high affinity, binding specificity and solubility. The polyamide
XX      backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
XX      nucleic acid molecules with greater affinity than DNA or RNA
XX      concentration. The compounds are relatively simple to synthesize and are
XX      used in a wide variety of applications. This sequence represents a DNA
XX      oligomer which is used to represent the thermal stability of the
XX      oligomers of the invention
XX      Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1496
DB      16 AAAAAAAAAAAAAA 1

RESULT 212
AAB56451/c
ID      AAB56451 standard; DNA; 16 BP.
XX      AAB56451;
XX      07-AUG-2003 (first entry)
XX      2'-F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
XX      Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX      antisense; ss.
XX      Unidentified.
XX      Key      Location/Qualifiers
FH      modified_base 1..16
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT      misc_feature 8..9
FT      /*tag= b
FT      /note= "Bases 8 and 9 are linked by two secouridine
FT      linkers which is represented as S in page 49 and X in
FT      page 57 and Fig 7 and 8 of the specification"
XX      WO2003037909-A1.
XX      08-MAY-2003.
XX      29-OCT-2002; 2002WO-CA001628.
XX      29-OCT-2001; 2001US-0330719P.
XX      (UYMC-) UNIV MCGILL.

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PI Danha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 7; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1496
DB 16 AAAAAAAAAAAAAA 1
XX
RESULT 213
AAL54078/c
ID AAL54078 standard; DNA; 16 BP.
XX
XX AAL54078;
XX
XX 06-MAR-2003 (first entry)
XX
XX Oligo-homodexyribonucleotide sequence, oligo dT.
XX
XX Detection; single-stranded sensor; detectable fluorescence emission;
XX forensic testing; paternity testing; tissue typing; hereditary disorder;
XX human population genetics; human evolutionary history; cystic fibrosis;
XX human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
XX
XX Unidentified.
XX
XX WO200284271-A2.
XX
XX 24-OCT-2002.
XX
XX 16-APR-2002; 2002WO-US012176.
XX
XX 16-APR-2001; 2001US-00836579.
XX
XX (REGC ) UNIV CALIFORNIA.
XX (CHAJ/) CHA J N.
XX
XX Cha JN, Morse DE, Stucky GD;
XX
XX WPI; 2003-103378/09.
XX
XX Detecting polynucleotides, for pharmacogenetic testing, comprises
XX contacting a target polynucleotide with a complementary single-stranded
XX sensor polynucleotide and an agent that allows the sensor to fluoresce
XX upon excitation.
XX
XX Example 1; Page 25; 41pp; English.
XX
```

```
XX
XX The invention relates to a novel assay for detecting a polynucleotide in
XX a sample, which comprises: contacting a sample suspected of containing a
XX target polynucleotide with a predetermined single-stranded sensor
XX polynucleotide complementary to the target polynucleotide, in a solution
XX comprising an agent that is a nonaqueous solvent that allows the sensor
XX polynucleotide to produce a detectable fluorescence emission; exciting
XX the sensor polynucleotide; and determining fluorescence emission. The
XX assay is useful for detecting a single or double-stranded target
XX polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a
XX wide variety of different applications including pharmacogenetic testing,
XX forensic testing to identify the species or individual which was the
XX source of a forensic specimen, in anthropological setting, paternity
XX testing, testing for compatibility between prospective tissue or blood
XX donors and patients and in screening for hereditary disorders. The method
XX is also useful to study alterations of gene expression in response to a
XX stimulus, disease, drug or medication, and other applications include
XX human population genetics, analyses of human evolutionary history and
XX characterisation of human haplotype diversity. The method is useful for
XX detecting polynucleotide sequences from contaminants or pathogens
XX including bacteria, yeast, and viruses to detect single nucleotide
XX polymorphisms, which may be associated with particular alleles or subsets
XX of alleles. The method is useful for detection of mutations and to detect
XX nucleotide sequences associated with increased risk of diseases or
XX disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.
XX This polynucleotide sequence represents an oligonucleotide sequence used
XX in a fluorescence technique of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1496
DB 16 AAAAAAAAAAAAAA 1
XX
RESULT 214
ADB68519/c
ID ADB68519 standard; DNA; 16 BP.
XX
XX ADB68519;
XX
XX 04-DEC-2003 (first entry)
XX
XX DNA hybridisation oligomer SEQ ID 9.
XX
XX hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
XX gene expression; respiration; secretion; signalling;
XX ion-channel activity; cell motility; developmental phenotype;
XX tumour regression; hybridisation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_difference 1 /tag= a
XX /note= "Optional N-terminal acetyl"
XX
XX WO2003068798-A2.
XX
XX 21-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003904.
XX
XX 09-FEB-2002; 2002US-00072975.
XX
XX (ACTI-) ACTIVE MOTIF.
XX
XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
XX
```

```

DR WPI; 2003-689653/65.
XX
PT Method of inhibiting expression of genes or RNA transcripts, useful for
PT therapy and determining effects of genes, by administering oligomers
PT containing hydroxyproline nucleic acid.
XX
PS Example 17; Page 233; 240pp; English.
XX
CC The invention relates to a novel method of inhibiting the expression of
CC one or more genes or RNA transcripts by administering at least one
CC oligonucleotide analogue that includes at least one hydroxyproline
CC nucleic acid (HyPNA) monomer to a cell or organism or their extracts. The
CC oligonucleotides of the invention may be used to monitor properties
CC including gene expression, respiration, secretion, signalling, ion-
CC channel activity, cell motility, developmental phenotype and tumour
CC regression. Furthermore, they may be utilised to determine the effects of
CC particular genes, as antisense or homologous recombination constructs
CC e.g. for creating animal models of disease and finally, for increasing
CC the activity of some enzymes, such as polymerases. The current sequence
CC is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This
CC sequence may also comprise a peptide nucleic acid (PNA).
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 16 AAAAAAAAAAAAAA 1
RESULT 215
AAAX69800/c
ID AAAX69800 standard; RNA; 17 BP.
AC AAAX69800;
XX
DT 28-JUL-1999 (first entry)
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability- useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 79; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 17 AAAAAAAAAAAAAA 2
RESULT 216
AAAX69801/c
ID AAAX69801 standard; RNA; 17 BP.
AC AAAX69801;
XX
DT 28-JUL-1999 (first entry)
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 79; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX

```

SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 DB 16 AAAAAAAAAAAAAA 1

RESULT 217
 AAV49503/C
 ID AAV49503 standard; cDNA to mRNA; 17 BP.
 XX AC AAV49503;
 XX DT 18-NOV-1998 (first entry)
 XX DE Human eosinophil cell activator HVC002 primer #1.
 XX KW Eosinophil cell activator; treatment; diagnosis; malignant tumour;
 KW parasitic infection; allergic inflammation; eosinophilic pneumonia;
 KW rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.
 XX OS Synthetic.
 OS Homo sapiens.
 XX WO9824817-A1.
 XX PD 11-JUN-1998.
 XX PF 05-DEC-1997; 97WO-JP004470.
 XX PR 05-DEC-1996; 96JP-00325762.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Yoshieue H, Saito A, Nakagawa S, Kuga T, Shinkai A, Koike M;
 PI Nishi T;
 XX WPI; 1998-333261/29.
 XX DT DNA and encoded protein which activates eosinophil cells - for treatment
 PT of cancer, parasite infection, autoimmune disease and allergic
 PT inflammation.
 XX Example 1; Page 64; 92pp; Japanese.
 XX AAV49503-V49507 are primers used in the isolation of a human eosinophil
 CC cell activator. This protein and antibodies generated from the protein
 CC can be used for treatment and diagnosis of malignant tumours, parasitic
 CC infections, allergic inflammation, eosinophilic pneumonia, rapid onset
 CC eosinophilia, and autoimmune diseases. DNA can be used for diagnosis, and
 CC the antisense DNA in gene therapy of these disorders. The protein can be
 CC used for screening of potential agonists or antagonists of its activity
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
 DB 17 TAAAAAAAAAAAAA 2

RESULT 218
 AAX18371/C
 ID AAX18371 standard; DNA; 17 BP.
 XX AC AAX18371;

11-MAY-1999 (first entry)
 RT-PCR primer of the invention SEQ ID 12.
 RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 Synthetic.
 JP11032765-A.
 09-FEB-1999.
 18-JUL-1997; 97JP-00208312.
 18-JUL-1997; 97JP-00208312.
 (TAKI) TAKARA SHUZO CO LTD.
 WPI; 1999-183822/16.
 Peptides having at least two new nucleotides - useful as primers in RT-PCR.
 Disclosure; Page 11; 19pp; Japanese.
 This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences

Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
 DB 16 TAAAAAAAAAAAAA 1

RESULT 219
 AAX18370/C
 ID AAX18370 standard; DNA; 17 BP.
 AC AAX18370;
 11-MAY-1999 (first entry)
 RT-PCR primer of the invention SEQ ID 11.
 RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 Synthetic.
 JP11032765-A.
 09-FEB-1999.
 18-JUL-1997; 97JP-00208312.
 18-JUL-1997; 97JP-00208312.
 (TAKI) TAKARA SHUZO CO LTD.

XX WPI; 1999-183822/16.
XX Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
XX Disclosure; Page 11; 19pp; Japanese.
XX
XX This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
XX Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAA 1495
DB 16 TAAAAAATAAAAAA 1
RESULT 220
AAA30179/C
ID AAA30179 standard; DNA; 17 BP.
XX
XX AAA30179;
AC
XX
XX 16-AUG-2000 (first entry)
DT
XX
DE PCR primer GT15A used in pollenosis associated gene identification.
XX
XX Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
KW
XX
XX Synthetic.
OS
XX
XX WO200020575-A1.
FN
XX
XX 13-APR-2000.
PD
XX
XX 06-OCT-1999; 99WO-JP005506.
PF
XX
XX 06-OCT-1998; 98JP-00284610.
PR
XX
XX (GENO-) GENOX RES INC.
PA
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
PI
XX
XX WPI; 2000-317712/27.
DR
XX
XX Gene highly expressed in patients with high cedar pollen-specific IGE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
PT
XX
XX Example 6; Page 38; 44pp; Japanese.
PS
XX
XX This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IGE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate

CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAA 1495
DB 17 TAAAAAATAAAAAA 2
RESULT 221
AAx82720/C
ID AAX82720 standard; DNA; 17 BP.
XX
XX AAX82720;
AC
XX
XX 10-NOV-2000 (first entry)
DT
XX
DE Human IGA nephropathy-associated CDNA primer #61.
DE
XX
KW IGA nephropathy-associated protein; diagnosis; treatment; antisense;
KW human; primer; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO963085-A1.
FN
XX
XX 09-DEC-1999.
PD
XX
XX 28-MAY-1999; 99WO-JP002855.
PF
XX
XX 02-JUN-1998; 98JP-00152603.
PR
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX
XX Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
PI Sawada S, Takei M, Shibata K, Furuya A;
PI
XX
XX WPI; 2000-097328/08.
DR
XX
XX DNA sequences preferentially expressed in IGA nephropathy patients,
PT proteins encoded by them, and antibodies to those proteins.
PT
XX
XX Claim 3; Page 169; 180pp; Japanese.
PS
XX
XX This invention describes novel DNA sequences preferentially expressed in
CC IGA nephropathy patients, and DNA sequences stringently hybridizing to
CC them. Independent claims cover diagnostic reagents for IGA nephropathy
CC incorporating the antisense sequences; the treatment of IGA nephropathy
CC using the antisense sequences for mRNA inhibition; proteins associated
CC with IGA nephropathy, containing sequences encoded by the DNA sequences;
CC antibodies recognizing these proteins; the production of the proteins by
CC culture of host cells transfected with DNA encoding them; diagnostic
CC reagents for IGA nephropathy containing the antibodies; and compositions
CC for the treatment of IGA nephropathy which contain the antibodies. The
CC products of the invention can be used for the diagnosis and treatment of
CC IGA nephropathy. This sequence represents a primer used in the isolation
CC and identification of the human IGA nephropathy-associated proteins
CC described in the method of the invention
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAA 1495
DB 17 TAAAAAATAAAAAA 2

```

Db      17 TAAAAAAAAAAAAAAAAA 2

RESULT 222
AAZ36739/c
ID      AAZ36739 standard; DNA; 17 BP.
XX
XX
AC      AAZ36739;
XX
XX      13-MAR-2000 (first entry)
DE
DE      Anchored oligo(dT) primer AT15A used for modified differential display.
KW
KW      Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW      differentially expressed nucleic acid; disease state; cancer;
KW      autoimmune disease; infectious disease; aging; developmental disorder;
KW      proliferative disorder; neurological disorder; toxicity; primer;
KW      treatment resistance; differential expression; drug discovery;
KW      growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
OS      Synthetic.
XX
XX
XX      WO9955913-A2.
PN
PD      04-NOV-1999.
XX
XX      27-APR-1999; 99WO-US009119.
PF
XX
XX      27-APR-1998; 98US-0083331P.
PR
PR      27-AUG-1998; 98US-0098070P.
PR      04-FEB-1999; 99US-0118624P.
XX
XX      (KIMM-) KIMMEL CANCER CENT SIDNEY.
PA
XX
XX      McClelland M, Welsh J, Trenkle T;
PI
XX
XX      WPI; 2000-086388/07.
DR
XX
XX      Measuring expression of low abundance reduced complexity target nucleic
XX      acid molecules.
PT
XX
XX      Example 3; Page 91; 187pp; English.
PS
XX
XX      AAZ36739-41 represent oligo(dT) primers used for modified differential
XX      display, in the method of the invention. The specification describes a
XX      method for measuring the level of two or more nucleic acid molecules in a
XX      target. The method comprises contacting a probe with an arbitrarily or
XX      statistically sampled target and detecting the amount of specific binding
XX      of the target to the probe. The methods can be used to identify
XX      differentially expressed nucleic acid molecules associated with disease
XX      states, such as cancer, autoimmune disease, infectious disease, aging,
XX      developmental disorder, proliferative disorder or neurological disorder.
XX      Alternatively the methods can be used to assess the efficacy or toxicity
XX      of or a resistance to a treatment. Also the methods can be used to
XX      determine differential expression of nucleic acid molecules in response
XX      to a stimulus, e.g. a chemical, drug or growth factor (especially
XX      epidermal growth factor), radiation, stress or a pathogen. The methods
XX      can also be used to determine co-regulated genes that can be potential
XX      targets for drug discovery
SQ      Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAAAAAAAAAAAAA 1495
Db      17 TAAAAAAAAAAAAAAAAA 2

RESULT 223
AAZ25450/c

```

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ID      AAA25450 standard; DNA; 17 BP.
XX
XX      AAA25450;
XX
XX      19-JUL-2000 (first entry)
DE
DE      Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.
KW
KW      Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
KW      hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW      gene expression modification; cancer; phosphorothioate; endonuclease;
KW      anticancer; breast cancer; endometrium cancer; ss.
XX
XX      Homo sapiens.
OS
XX
XX      WO9954459-A2.
PN
XX
XX      28-OCT-1999.
PD
XX
XX      19-APR-1999; 99WO-US008547.
PF
XX
XX      20-APR-1998; 98US-0082404P.
PR
PR      23-JUN-1998; 98US-00103636.
XX
XX      (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX      Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
XX      Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX      Matulic-Adamic J;
DR      WPI; 2000-013248/01.
XX
XX      New nucleic acids that interact, and optionally cleave, target sequences,
XX      used to treat cancer.
PT
XX
XX      Claim 77; Page 79; 148pp; English.
PS
XX
XX      The present invention describes nucleic acids (A) that interact stably
XX      with a target sequence and contain at least one phosphoro(di)thioate
XX      link, having endonuclease activity. (A), and more generally any catalytic
XX      nucleic acid (A') that modulates expression of the oestrogen receptor
XX      gene, are used to treat cancer (particularly of breast or endometrium),
XX      in vivo or by transforming cells ex vivo and implanting treated cells, or
XX      for other conditions associated with levels of oestrogen receptor.
XX      Because of the high selectivity for targeted RNA, (A) can also be used to
XX      correlate inhibition of gene expression with alterations in phenotype,
XX      particularly for identification of therapeutic targets, and as research
XX      reagents (for RNA, in the same way that restriction endonucleases are
XX      used with DNA). The combination of modifications in (A) improves
XX      resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX      AAA24748 represent oestrogen receptor hammerhead ribozyme sequences, and
XX      AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
XX      sequences, and AAA26107 to AAA26218 represent their corresponding target
XX      sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX      antisense oligonucleotides used in the exemplification of the present
XX      invention
XX
XX      Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
SQ      Query Match      1.1%; Score 16; DB 1; Length 17;
          Best Local Similarity 100.0%; Pred. No. 1.4e+02;
          Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
Db      17 AAAAAAAAAAAAAAAAAA 2

RESULT 224
AAZ25449/c
ID      AAA25449 standard; DNA; 17 BP.
XX

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```

AC AAA25449;
XX
XX
DT 19-JUL-2000 (first entry)
DE
XX
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.
XX
XX
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO954459-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US008547.
PF
XX
XX 20-APR-1998; 98US-0082404P.
PR
XX
XX 23-JUN-1998; 98US-00103636.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX
XX Claim 77; Page 79; 148pp; English.
PS
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA25993 to AAA26105 represent their corresponding target sequences.
CC AAA24748 to AAA25992 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 17 AAAAAAAAAAAAAA 2
RESULT 225
AAA25451/C
ID AAA25451 standard; DNA; 17 BP.
XX
XX AAA25451;
XX
XX 30-JAN-2001 (first entry)
XX

```

DE Human retrovirus HERV LTR PCR primer #31.
 XX Cell-specific expression; tissue-specific expression; gene therapy; LTR;
 KW U3-R segment; long terminal repeat; retroviral expression vector;
 KW PCR primer; ss.
 XX Human endogenous retrovirus.
 OS
 XX WO200053789-A2.
 XX 14-SEP-2000.
 XX 09-MAR-2000; 2000WO-EP002064.
 XX 10-MAR-1999; 99DE-01010650.
 XX (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
 XX Leib-Moesch C, Schoen U, Baust C;
 XX WPI; 2000-587442/55.
 XX Retroviral expression vector, useful in gene therapy, contains a promoter
 PT from a human endogenous retrovirus to provide cell-specific expression.
 XX Disclosure; Page 27; 67pp; German.
 XX This invention describes a novel retroviral expression vector (A)
 CC containing DNA sequences (I) for packaging vector RNA and for cell-
 CC specific expression of proteins or peptides encoding by heterologous DNA
 CC (II). The sequences controlling cell-specific expression contain a cell-
 CC specifically regulatable promoter region (P) from a human endogenous
 CC retrovirus (HERV) DNA sequence. The invention also describes (a) mRNA and
 CC RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c)
 CC eukaryotic cells containing (A) in integrated form; (d) virions
 CC containing a retroviral expression vector RNA derived from (A); (e) a
 CC method for producing the virions of (d); (f) a method for incorporating
 CC protein-encoding nucleic acid sequences into a eukaryotic cell by
 CC infection with the virions of (d); and (g) a retroviral vector system
 CC containing (A) and a packaging cell line, that contains at least one
 CC (recombinant) retrovirus construct that encodes for the packaging
 CC proteins of (A). (A) are used for cell- or tissue-specific expression of
 CC foreign genes for gene therapy and to produce virions for introducing
 CC (II) into the chromosomal DNA of eukaryotic cells, preferably mammalian
 CC and specifically human. (A) retain the advantages of usual retroviral
 CC promoters with all the signal structures required for transcription in a
 CC small region within the U3-R segment, but without their disadvantages
 CC (excessive strength and limited cell specificity). Since (A) are derived
 CC from endogenous (harmless) viral sequences, they do not introduce any new
 CC viral sequences into the genome and recombination will not create new
 CC types of retrovirus. The promoters provide cell or tissue specific
 CC expression, according to which HERV they are derived from
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 Db 17 AAAAAAAAAAAAAA 2
 RESULT 227
 AAA50197/c
 ID AAA50197 standard; DNA; 17 BP.
 XX
 AC AAA50197;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE 2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.

XX Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.
 KW Synthetic.
 OS
 XX Key Location/Qualifiers
 PH modified_base 1..19
 FT /*tag= a
 FT /note= "2'-methoxyethoxy modified thymidine"
 FT modified_base 1..17
 FT /*tag= b
 FT /note= "phosphorothioate internucleoside linkages"
 XX
 PN WO200047593-A1.
 XX 17-AUG-2000.
 XX 11-FEB-2000; 2000WO-US003543.
 XX 12-FEB-1999; 99US-00250075.
 XX (ISIS-) ISIS PHARM INC.
 PA Manoharan M, Maier MA;
 PI
 XX WPI; 2000-558188/51.
 XX Preparation of mixed backbone oligomeric compounds useful as e.g. primers
 PT for diagnostic tests, involves oxidation of H-phosphonate internucleoside
 PT linkages to phosphodiester internucleoside linkages.
 XX
 PS Example 12; Page 34; 49pp; English.
 XX The present sequence is that of a phosphorothioate oligonucleotide
 CC containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its
 CC 5' ribosyl sugar moiety. It is an example of an oligomeric compound
 CC produced according to the methods of the invention. The invention
 CC provides compounds and methods for the preparation of mixed backbone
 CC oligomeric, or chimeric, compounds having phosphodiester internucleoside
 CC linkages in addition to phosphorothioate and/or phosphoramidate
 CC internucleoside linkages. The methods also include incorporation of
 CC boranophosphate internucleoside linkages. The methods utilize H-
 CC phosphonate intermediates that are coupled together forming contiguous
 CC regions of 1 or more H-phosphonate internucleoside linkages. Each
 CC contiguous region is subsequently oxidized to phosphodiester,
 CC phosphorothioate, phosphoramidate or boranophosphate internucleoside
 CC linkages prior to further elongation. Mixed backbone oligomeric compounds
 CC are prepared in this manner by oxidizing adjacent regions with different
 CC reagents. Oligomeric compounds of the invention are prepared using novel
 CC oxidation steps that oxidize a region of 1 or more H-phosphonate
 CC internucleoside linkages without degrading existing linkages that have
 CC been previously oxidized. The oligonucleotides obtained are useful as
 CC primers in PCR, probes, linkers, gene fragments and for other diagnostic
 CC tests on e.g. biological tissue, fluid, cells etc., as research reagents,
 CC and as antiviral agents
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 Db 17 AAAAAAAAAAAAAA 2
 RESULT 228
 AAC64202/c
 ID AAC64202 standard; DNA; 17 BP.
 XX
 AC AAC64202;
 XX

CC The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention

XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
DB 17 TAAAAAAAAAAAAA 2

RESULT 235
AAC91719/c
ID AAC91719 standard; DNA; 17 BP.
XX
AC AAC91719;
XX
DT 27-MAR-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.
XX
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 19-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-032159/04.
XX
PT Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 40; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-

CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA

XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
DB 17 TAAAAAAAAAAAAA 2

RESULT 236
AAC82874/c
ID AAC82874 standard; DNA; 17 BP.
XX
AC AAC82874;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 441 primer #1.
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073435-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003190.
XX
PR 27-MAY-1999; 99JP-00148783.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2001-061526/07.
XX
PT Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 35; 42pp; Japanese.
XX
CC This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen

XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
DB 17 TAAAAAAAAAAAAA 2

RESULT 237

```
AAH47126/c
ID AAH47126 standard; DNA; 17 BP.
XX
AC AAH47126;
XX
DT 30-NOV-2001 (first entry)
XX
DE Nucleotide sequence of primer Grl5A.
XX
KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
XX PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200165259-A1.
XX
PD 07-SEP-2001.
XX
PF 23-FEB-2001; 2001WO-JP001372.
XX
PR 02-MAR-2000; 2000JP-00061832.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX WPI; 2001-557789/62.
DR
PT Diagnosis of allergies including atopic dermatitis.
XX
PS Example 6; Page 65; 83pp; Japanese.
XX
CC The invention provides a method of diagnosis of allergies that involves:
CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC in T-cells; and comparing them with the level of expression in healthy T-
CC cells. The method is useful for diagnosing allergies, particularly atopic
CC dermatitis. The present sequence represents a PCR primer used for
CC analysis of the expression of the above genes
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAAAAAA 2

RESULT 238
ABK13941/c
ID ABK13941 standard; DNA; 17 BP.
XX
AC ABK13941;
XX
DT 21-MAY-2002 (first entry)
XX
DE 5'-PCR primer used to produce single pattern characteristic by FokI.
XX
KW Identification of transcribed gene; mRNA profile; gene expression;
XX cellular process; fingerprinting; susceptibility to external factor;
XX development; disease; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200208461-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-IB001539.
XX
```

```
PR 21-JUL-2000; 2000GB-00018016.
PR 21-JUL-2000; 2000US-0219925P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfors P, Bauren G;
XX WPI; 2002-217065/27.
XX
DR
XX
PT Providing mRNA profile, by generating two independent patterns
PT characteristic of sample mRNA population, analyzing patterns, comparing
PT gene expression by cell types under varied conditions, and identifying
PT genes.
XX
PS Disclosure; Fig 2; 67pp; English.
XX
CC The present invention relates to a method for providing a profile of mRNA
CC molecules present in a sample. The method comprises generating two
CC independent patterns characteristic of the population of mRNA molecules
CC expressed in the sample and analysing the patterns using a combinatorial
CC algorithm, comparing gene expression by different or same cell types
CC under different conditions, and identifying genes having a role in
CC various cellular processes. The method is useful for the analysis and
CC identification of transcribed genes, and fingerprinting. The method can
CC be used to identify genes which play a role in determining various
CC cellular processes, including susceptibility to external factors,
CC development, and disease. The present sequence for a PCR primer is used
CC in the production of a single pattern characteristic of a sample,
CC employing a Type IIS restriction enzyme (i.e. FokI) in the methods of the
CC present invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 239
ABK49634/c
ID ABK49634 standard; DNA; 17 BP.
XX
AC ABK49634;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; Grl5A.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008246.
XX
PR 25-SEP-2000; 2000JP-00291318.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA ) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
PI Takahashi E;
XX WPI; 2002-315738/35.
XX
```

XX Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX Example 1; Page 56; 72pp; Japanese.
XX
XX The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1480 TAAAAAATAAAAAAAAAA 1495
Db 17 TAAAAAATAAAAAAAAAA 2
RESULT 240
ABL59038/c
ID ABL59038 standard; DNA; 17 BP.
XX AC ABL59038;
XX DT 20-AUG-2002 (first entry)
XX DE Nucleotide sequence of PCR primer GT15A.
XX KW Human; allergosis; eosinophil; PCR; primer; ss.
XX OS Homo sapiens.
XX PN JP2002095500-A.
XX PD 02-APR-2002.
XX PP 25-SEP-2000; 2000JP-00291316.
XX PR 25-SEP-2000; 2000JP-00291316.
XX PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
XX PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX DR WPI; 2002-439993/47.
XX Examining allergosis, involves measuring the expression levels of a
PT specific gene, and comparing it to the levels in the eosinophils of a
PT healthy control.
XX
XX Example 1; Page 17; 20pp; Japanese.

CC The specification describes a method for examining allergosis. The method
CC comprises measuring the expression level of the gene given in ABL59037,
CC and comparing it with the expression level of the gene in the eosinophils
CC of a healthy person. The method is used for the examination of
CC allergosis. The present sequence represents a PCR primer, which is used
CC in the course of the invention
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1480 TAAAAAATAAAAAAAAAA 1495
Db 17 TAAAAAATAAAAAAAAAA 2
RESULT 241
ABN99829/c
ID ABN99829 standard; DNA; 17 BP.
XX AC ABN99829;
XX DT 15-AUG-2002 (first entry)
XX DE Human allergic disease related PCR primer SEQ ID NO: 18.
XX KW Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
XX KW primer; ss.
XX OS Homo sapiens.
XX PN WO200233069-A1.
XX PD 25-APR-2002.
XX PF 28-SEP-2001; 2001WO-JP008574.
XX PR 13-OCT-2000; 2000JP-00314093.
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX DR WPI; 2002-372311/40.
XX Method for examining allergic diseases by differential display of
PT seventeen genes showing different expression particularly significant
PT increase in eosinophils in patients with mild atopic dermatitis, also
PT applicable in screening compounds.
XX
XX Example 1; Page 109; 165pp; Japanese.
XX
XX The present invention relates to a method for examining allergic diseases
CC which involves determining the expression level of a gene, having one of
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC eosinophils in a patient and comparing the expression level with that in
CC the eosinophils of a healthy individual. The method can be used to
CC examine allergic diseases, particularly atopic dermatitis, and its early
CC diagnosis, which is also applicable in screening candidate compounds for
CC remedies. The present sequence is a PCR primer described in the
CC exemplification of the invention
XX
XX Sequence: 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1480 TAAAAAATAAAAAAAAAA 1495
Db 17 TAAAAAATAAAAAAAAAA 2

```

Db      17 TAAAAAAAAAAAAAAAAA 2

RESULT 242
AAL49948/c
ID      AAL49948 standard; DNA; 17 BP.
XX
XX      AAL49948;
AC
XX      10-DEC-2002 (first entry)
DT
XX      Human B1153 expression in allergic disease related PCR primer GT15A.
DE
XX      Human; allergy; B1153; differential expression; antiallergic; asthma;
KW      antisaethmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW      ss.
XX
XX      Unidentified.
OS
XX
XX      WO200250269-A1.
PN
XX      27-JUN-2002.
PD
XX      21-DEC-2001; 2001WO-JP011286.
PF
XX      21-DEC-2000; 2000JP-00389476.
PR
XX      (GENO-) GENOX RES INC.
PA      (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX      Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
PI      WPI; 2002-713252/77.
DR
XX
XX      Examination of allergic diseases comprises detecting gene B1153 over-
PT      expressed in T cells of allergy patients for diagnosis treatment and
PT      investigation of atopic skin inflammation and asthma.
PT
XX
XX      Example 6; Page 81; 102pp; Japanese.
PS
XX
CC      The present invention relates to a method of examining allergic diseases
CC      which comprises comparing the expression level of gene B1153 in allergy
CC      patients with the expression level in healthy subjects. The method is
CC      useful for the treatment, prevention, diagnosis and study of allergic
CC      diseases including atopic skin inflammation and asthma. The present
CC      sequence is a PCR primer described in the exemplification of the
CC      invention
CC
XX      Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ      Query Match      1.1%; Score 16; DB 1; Length 17;
          Best Local Similarity 100.0%; Pred. No. 1.4e+02;
          Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAAAAAAAAAAAAA 1495
          |||
          17 TAAAAAAAAAAAAAAAAA 2
Db
RESULT 243
AAL47234/c
ID      AAL47234 standard; DNA; 17 BP.
XX
XX      AAL47234;
AC
XX      22-AUG-2002 (first entry)
DT
XX      Allergic disease examination method related anchor primer SEQ ID NO: 2.
DE
XX      Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW      atopic dermatitis; human; PCR; primer; ss.
XX
XX      Unidentified.
OS

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```

XX      WO200233122-A1.
PN
XX      25-APR-2002.
PD
XX      11-OCT-2001; 2001WO-JP008937.
PF
XX      13-OCT-2000; 2000JP-00314093.
PR
XX      (GENO-) GENOX RES INC.
PA      (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX      (EISA) EISAI CO LTD.
XX
XX      Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
PI      Takahashi E;
XX      WPI; 2002-372313/40.
DR
XX
XX      Method for examining allergic diseases by differential display of
PT      intersectin 2 gene showing different expression particularly significant
PT      increase in eosinophils in patients.
PT
XX      Example 1; Page 52; 90pp; Japanese.
PS
XX
CC      The present invention relates to a method for examining allergic diseases
CC      with intersectin 2 gene or a gene with equivalent function of intersectin
CC      2 as an indicator gene, which comprises determining the expression level
CC      of the gene in the eosinophils in a patient, and comparing the expression
CC      level with that in the eosinophils of a healthy individual. The method is
CC      for examining allergic diseases, particularly atopic dermatitis, which is
CC      also applicable in screening candidate compounds for remedies. The
CC      present sequence is an anchor primer described in the exemplification of
CC      the invention
CC
XX      Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ      Query Match      1.1%; Score 16; DB 1; Length 17;
          Best Local Similarity 100.0%; Pred. No. 1.4e+02;
          Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAAAAAAAAAAAAA 1495
          |||
          17 TAAAAAAAAAAAAAAAAA 2
Db
RESULT 244
ABK49756/c
ID      ABK49756 standard; DNA; 17 BP.
XX
XX      ABK49756;
AC
XX      15-JUL-2002 (first entry)
DT
XX      Human atopic dermatitis cDNA related PCR primer GT15a.
DE
XX      Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW      allergic disease; antiallergic; dermatological; GT15a.
XX
XX      Synthetic.
OS
XX      WO200226962-A1.
PN
XX      04-APR-2002.
PD
XX      21-SEP-2001; 2001WO-JP008247.
PF
XX      26-SEP-2000; 2000JP-00293021.
PR
XX      (GENO-) GENOX RES INC.
PA      (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX      Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
PI
XX

```

DR WPI; 2002-330097/36.
 XX Examining allergic diseases by differential display of genes showing
 PT different expression particularly increase in remission stage in
 PT eosinophils in patients.
 XX Example 1; Page 54; 74pp; Japanese.
 XX This invention relates to gene sequences that are differentially
 CC expressed in eosinophils from patients with atopic dermatitis in the
 CC increment stage as compared with those in the remission stage. These
 CC sequences are used in a novel method for examining allergic diseases
 CC comprising determining the expression levels of these genes and comparing
 CC the expression level with that in the eosinophils of a healthy
 CC individual. The method of the invention may have antiallergic or
 CC dermatological activities. The method can be used to diagnose allergic
 CC diseases particularly atopic dermatitis, and may also be used to screen
 CC candidate compounds for remedies. The method of the invention can be
 CC performed in high throughput, at low cost. The present sequence
 CC represents the G15a PCR primer used to amplify the differentially
 CC amplified atopic dermatitis related cDNA sequences of the invention
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1480 TAAAAAATAAAAAA 1495
 Db |||||
 17 TAAAAAATAAAAAA 2
 RESULT 245
 ADB04271/c
 ID ADB04271 standard; DNA; 17 BP.
 XX ADB04271;
 XX 20-NOV-2003 (first entry)
 DT Human MD27 scanning oligonucleotide SEQ ID 5257.
 DE Cytostatic; immunostimulant; gene therapy; vaccine; human;
 XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 OS
 XX EP1281758-A2.
 XX 05-FEB-2003.
 XX 30-JUL-2002; 2002EP-00016874.
 XX 02-AUG-2001; 2001US-00922181.
 XX (AEOM-) AEOMICA INC.
 XX Shannon M, Gu Y, Nguyen C;
 XX WPI; 2003-423107/40.
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX Example 8; SEQ ID NO 5257; 103pp; English.
 XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1481 AAAAAAATAAAAAA 1496
 Db |||||
 17 AAAAAAATAAAAAA 2
 RESULT 246
 ADB04272/c
 ID ADB04272 standard; DNA; 17 BP.
 XX ADB04272;
 XX 20-NOV-2003 (first entry)
 DT Human MD27 scanning oligonucleotide SEQ ID 5258.
 DE Cytostatic; immunostimulant; gene therapy; vaccine; human;
 XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 OS
 XX EP1281758-A2.
 XX 05-FEB-2003.
 XX 30-JUL-2002; 2002EP-00016874.
 XX 02-AUG-2001; 2001US-00922181.
 XX (AEOM-) AEOMICA INC.
 XX Shannon M, Gu Y, Nguyen C;
 XX WPI; 2003-423107/40.
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX Example 8; SEQ ID NO 5258; 103pp; English.
 XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 247
ABZ70578/c
ID ABZ70578 standard; DNA; 17 BP.
XX
AC ABZ70578;
XX
DT 23-MAY-2003 (first entry)
DE Primer.
XX
KW Aspergillus phenolics; oxalate decarboxylase; APOXD; transgenic plant;
KW crop protection; primer; ss.
XX
OS Synthetic.
XX
PN CA2350328-A1.
XX
PD 26-DEC-2002.
XX
PF 26-JUN-2001; 2001CA-02350328.
XX
PR 26-JUN-2001; 2001CA-02350328.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Scelonge C, Bidney D;
XX
DR WPI; 2003-248733/25.
XX
PT New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus
PT phenolics, for degrading oxalic acid, identifying transformed plant
PT cells, and preventing pathogenic disease in plants.
XX
PS Disclosure; Page 50; 60pp; English.
XX
SQ The present sequence is that of a primer used in the invention. The
CC invention relates to a novel nucleic acid (see ABZ70560) encoding
CC Aspergillus phenolics oxalate decarboxylase (APOXD) (see ABP72475). The
CC gene and its encoded protein are useful in degrading oxalate, in
CC diagnostic assays, for protecting plants against disease, and as a
CC selectable marker
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 248
AAD56441/c
ID AAD56441 standard; DNA; 17 BP.

XX
AC AAD56441;
XX
DT 07-AUG-2003 (first entry)
DE
DE Antisense oligo #2, to elicit RNase H degradation of target RNA.
XX
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 9..10
FT /tag= a
FT /note= "Bases 9 and 10 are linked by a butanediol linker
FT which is represented as B in page 49 and X in page 59,
FT Fig 9 and 10 of the specification"
XX
PN WC2003037909-A1.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-CA001628.
XX
PR 29-OCT-2001; 2001US-0330719P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS Example 2; Page 90; 104pp; English.
XX
CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 249
AAD56448/c
ID AAD56448 standard; DNA; 17 BP.
XX
AC AAD56448;
XX
DT 07-AUG-2003 (first entry)
DE 2'F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.


```

XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX Unidentified.
XX Key Location/Qualifiers
XX modified_base 1..17
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT misc_feature 9..10
FT /tag= b
FT /note= "Bases 9 and 10 are linked by a butanediol linker
FT which is represented as B in page 49 and Fig 5 and as X
FT in page 52, 55 and Fig 6 of the specification"
XX WO2003037909-A1.
XX 08-MAY-2003.
XX 29-OCT-2002; 2002WO-CA001628.
XX 29-OCT-2001; 2001US-0330719P.
XX (UYMC-) UNIV MCGILL.
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX Example 2; Fig 5; 104pp; English.
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1..17; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2
RESULT 250
AAD56449/C
ID AAD56449 standard; DNA; 17 BP.
XX AAD56449;
XX AAD56449;
XX 07-AUG-2003 (first entry)
XX 2'-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;

```

```

KW antisense; ss.
XX Unidentified.
XX Key Location/Qualifiers
XX modified_base 1..17
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT misc_feature 12..13
FT /tag= b
FT /note= "Bases 12 and 13 are linked by a butanediol linker
FT which is represented as B in page 49 and Fig 5 and as X
FT in page 55 and Fig 6 of the specification"
XX WO2003037909-A1.
XX 08-MAY-2003.
XX 29-OCT-2002; 2002WO-CA001628.
XX 29-OCT-2001; 2001US-0330719P.
XX (UYMC-) UNIV MCGILL.
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX Example 2; Fig 5; 104pp; English.
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1..17; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2
RESULT 251
AAD56447/C
ID AAD56447 standard; DNA; 17 BP.
XX AAD56447;
XX AAD56447;
XX 07-AUG-2003 (first entry)
XX 2'-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX antisense; ss.

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OS Unidentified.
XX
XX Key Location/Qualifiers
FT modified_base 1..17
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT misc_feature 4..5
FT /tag= b
FT /note= "Bases 4 and 5 are linked by a butanediol linker
FT which is represented as B in page 49 and Fig 5 and as X
FT in page 55 and Fig 6 of the specification"
XX
XX WO2003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 5; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX
XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
Db |||||
17 AAAAAAAAAAAAAA 2
RESULT 252
AAD56450/c
ID AAD56450 standard; DNA; 17 BP.
XX
XX AAD56450;
AC
XX
XX 07-AUG-2003 (first entry)
DT
XX
XX 2'F-RNA antisense oligo #5, to elicit RNase H degradation of target RNA.
DE
XX
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
KW
XX
XX Unidentified.
OS
XX

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```

FH Key Location/Qualifiers
FT modified_base 1..17
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT misc_feature 9..10
FT /tag= b
FT /note= "Bases 9 and 10 are linked by a secouridine linker
FT which is represented as S in page 49 and X in page 57 and
FT Fig 1, 2, 7 and 8 of the specification"
XX
XX WO2003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 7; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX
XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
Db |||||
17 AAAAAAAAAAAAAA 2
RESULT 253
ACF36345/c
ID ACF36345 standard; DNA; 17 BP.
XX
XX ACF36345;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX
XX Nucleotide sequence of a double stranded product DNA fragment.
DE
XX
XX Gene variant identification; restriction enzyme; FokI; ds.
KW
XX
XX Synthetic.
OS
XX
XX WO2003064689-A2.
XX
XX 07-AUG-2003.
XX

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XX 28-JAN-2003; 2003WO-IB000255.
 XX 29-JAN-2002; 2002US-0352245P.
 XX (GLOB-) GLOBAL GENOMICS AB.
 XX Lonnberg P, Oldin M, Linnarsson S, Ernfors P;
 XX WPI; 2003-627619/59.
 XX Determining polyadenylation sites within transcribed gene sequences
 XX present in a sample comprises assigning to gene fragments gene candidates
 XX within a database by comparing signals in the dataset with the database.
 XX Example; Fig 3; 81pp; English.
 XX The invention relates to determining the presence of and/or identifying a
 XX polyadenylation site within a sequence of a transcribed gene or variants
 XX present in a sample. The method involves assigning to gene fragments gene
 XX candidates within a database by comparing signals in the dataset with the
 XX database, the database comprising data representing mRNAs with known
 XX polyA sites and/or 'virtual genes' representing a possible
 XX polyadenylation site within an actual gene. The method is useful for
 XX determining the presence of and/or identifying a polyadenylation site or
 XX alternative polyadenylation sites within a sequence of a transcribed gene
 XX or sequences of transcribed gene variants present or potentially present
 XX in a sample, in identifying gene features, particularly in identifying
 XX differences between sequence variants that occur in a population of
 XX nucleic acid molecules, especially in identifying or discovering polyA
 XX site usage or determining polyA site usage in a nucleic acid sample, and
 XX gene variants arising from alternative polyA sites. The present sequence
 XX represents a double stranded product DNA fragment
 XX Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 SQ Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1481 AAAAAAAAAAAAAA 1496
 Db |||||
 16 AAAAAAAAAAAAAA 1
 RESULT 254
 ACF36370/C
 ID ACF36370 standard; DNA; 17 BP.
 XX ACF36370;
 XX 04-DEC-2003 (first entry)
 XX Nucleotide sequence of a double stranded product DNA.
 XX Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
 XX electrophoresis; type II restriction enzyme; FokI; ds.
 XX Synthetic.
 XX WO2003064691-A2.
 XX 07-AUG-2003.
 XX 28-JAN-2003; 2003WO-IB000843.
 XX 29-JAN-2002; 2002US-0352215P.
 XX (GLOB-) GLOBAL GENOMICS AB.
 XX Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;
 XX Montelius A;

DR WPI; 2003-618365/58.
 XX Producing a population of double-stranded product DNA molecules, useful
 XX for mRNA profiling, comprises amplification by nested polymerase chain
 XX reaction.
 XX Example; Fig 2; 105pp; English.
 XX The invention relates to producing a population of double-stranded
 XX product DNA molecules comprising amplification by a nested PCR method.
 XX The method is useful in profiling mRNA transcribed in a system under
 XX investigation. The oligonucleotides are used as size standards in
 XX electrophoresis, and as internal controls allowing for calculation of
 XX relative amounts of material present. The present sequence represents a
 XX double stranded product DNA, which aids in outlining an approach to
 XX production of a single pattern characteristic of a sample, employing a
 XX type II restriction enzyme (FokI)
 XX Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 SQ Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1481 AAAAAAAAAAAAAA 1496
 Db |||||
 16 AAAAAAAAAAAAAA 1
 RESULT 255
 ADC84468/C
 ID ADC84468 standard; DNA; 17 BP.
 XX ADC84468;
 XX 01-JAN-2004 (first entry)
 XX PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 1.
 XX Plant blastogenesis; transformation; gene expression; tissue specific;
 XX PCR; primer, ss.
 XX Synthetic.
 XX JP2003159071-A.
 XX 03-JUN-2003.
 XX 22-NOV-2001; 2001JP-00358366.
 XX 22-NOV-2001; 2001JP-00358366.
 XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 XX WPI; 2003-818678/77.
 XX New naturally derived DNA specifically expressed during blastogenesis of
 XX a plant, useful for producing a transformed plant and for compulsive
 XX expression of a protein.
 XX Example 3; SEQ ID NO 1; 43pp; Japanese.
 XX The invention relates to naturally derived DNA specifically expressed
 XX during plant blastogenesis. The DNA of the invention is useful for
 XX producing a transformed plant. Methods of the invention are also useful
 XX for compulsive expression of this DNA. Methods of the invention are
 XX useful for plant tissue specific expression of genes. Also, the growth
 XX stage of a plant can be controlled specifically. The current sequence
 XX represents a PCR primer for amplifying a plant blastogenesis specific
 XX gene of the invention.
 XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

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Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1495
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 256
AAQ34110
ID AAQ34110 standard; DNA; 18 BP.
XX
AC AAQ34110;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX Sequence of a microsatellite from clone TGLA60B.
DE
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
XX
XX WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX Table 7; Page 375; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obt'd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 257
AAQ34110
ID AAQ34110 standard; DNA; 18 BP.
XX
AC AAQ34110;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX Sequence of a microsatellite from clone TGLA60B.
DE
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
XX
XX WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX Table 7; Page 375; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obt'd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

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AAQ75025/c
ID AAQ75025 standard; RNA; 18 BP.
XX
AC AAQ75025;
XX
DT 25-MAR-2003 (revised)
DT 03-AUG-1995 (first entry)
XX
XX PCR primer.
DE
XX
XX Synthetic oligo; solid phase immunoassay; ss.
XX
XX Synthetic.
XX
XX WO9426932-A1.
XX
PD 24-NOV-1994.
XX
PF 13-MAY-1994; 94WO-US005407.
XX
PR 13-MAY-1993; 93US-00061694.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Fields HA, Khudyakov YE;
XX
XX WPI; 1995-006819/01.
XX
XX Solid phase immunoassay using oligo:nucleotide as label - also new
PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT diagnosing hepatitis C or E virus infection.
XX
XX Example; Page 12; 34pp; English.
XX
XX AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC They are used in a method for detecting an antigen in a subject. The
CC method involves binding the antigen to a solid support and then reacting
CC it with an immunoreactive ligand (L) bound to an oligo; removing any
CC unreacted L, and then detecting the presence of the oligo. A similar
CC method can be used to detect Abs, in which case the ligand is an oligo-
CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC to be detected at very low levels. An exemplary oligo is AAQ75024 which
CC can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC a synthetic peptide. In the example, peptide AAR62941 was coupled to
CC oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to
CC contain HEV Abs were immobilised on plastic tubes or wells, then
CC incubated for 30-60 mins with the peptide-oligo product. The vessels were
CC washed; bound oligo was released with 0.2M glycine and amplified in a
CC separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR.
CC The amplification product - AAQ75031 - was treated with uracil DNA
CC glycosylase to remove the U18 fragment, and the product captured by
CC immobilised oligo-dT. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAAAAA 3

RESULT 258
AAQ94668/c
ID AAQ94668 standard; DNA; 18 BP.
XX
AC AAQ94668;
XX
XX 27-MAR-1998 (first entry)
XX
XX Anchored poly(T) oligonucleotide polyT-AnchC.

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XX Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
KW snapdragon; primer; ss.
XX Synthetic.
XX WO9732023-A1.
XX 04-SEP-1997.
XX 28-FEB-1997; 97WO-AU000124.
XX 01-MAR-1996; 96AU-00008386.
XX (FLOR-) FLORIGENE LTD.
XX Brugliera F, Holton TA, Michael MZ;
XX WPI; 1997-448691/41.
XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT. corresponding DNA, used in the manipulation of pigmentation in plants.
XX Example 15; Page 59; 234pp; English.
XX Anchored poly(T) oligonucleotides polyT-ancha (AAT94667), polyT-anchC
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC region of a polyadenylation sequence. They were used to prime cDNA
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC were also utilised in the PCR amplification of plant cytochrome P450
CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC flavonoid 3'-hydroxylase (see AAW35704) was isolated using a differential
CC display approach. This can be used to manipulate the pigmentation of
CC transgenic plants
XX
XX SQ Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 17 AAAAAAAAAAAAAA 2
RESULT 259
AAV54173/c
ID AAV54173 standard; cDNA; 18 BP.
XX AAV54173;
XX 21-DEC-1998 (first entry)
XX Nucleotide sequence PCR primer 10.
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX immunohistological staining.
XX Synthetic.
XX WO9839437-A1.
XX 11-SEP-1998.
XX 05-MAR-1998; 98WO-JP000905.
XX 05-MAR-1997; 97JP-00050302.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Sakaki Y;
XX WPI; 1998-495844/42.
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX Example 1; Page 47; 70pp; Japanese.
XX This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
XX SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAAAAAAAAA 1495
DB 17 TAAAAAAAAAAAAA 2
RESULT 260
AAV54164/c
ID AAV54164 standard; cDNA; 18 BP.
XX AAV54164;
XX 21-DEC-1998 (first entry)
XX Nucleotide sequence PCR primer 1.
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX immunohistological staining.
XX Synthetic.
XX WO9839437-A1.
XX 11-SEP-1998.
XX 05-MAR-1998; 98WO-JP000905.
XX 05-MAR-1997; 97JP-00050302.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Sakaki Y;
XX WPI; 1998-495844/42.
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX Example 1; Page 47; 70pp; Japanese.
XX This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
XX SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAAAAAAAAA 1495

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Db      17 TAAAAAAAAAAAAAAAAA 2
|||||
RESULT 261
AAV54167/c
ID   AAV54167 standard; cDNA; 18 BP.
XX
XX
AC   AAV54167;
XX
DT   21-DEC-1998 (first entry)
DE
DE   Nucleotide sequence PCR primer 4.
XX
XX   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX   immunohistological staining.
XX
XX   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
XX   05-MAR-1998; 98WO-JP000905.
XX
XX   05-MAR-1997; 97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX   Sakaki Y;
XX
XX   WPI; 1998-495844/42.
XX
XX   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
XX   Example 1; Page 48; 70pp; Japanese.
XX
XX   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
XX   Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
XX
Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAAAAAAAAAAAAA 1495
Db      17 TAAAAAAAAAAAAAAAAA 2
|||||
RESULT 262
AAV37712
ID   AAV37712 standard; cDNA; 18 BP.
XX
XX
AC   AAV37712;
XX
XX
DT   25-MAR-2003 (revised)
DT   07-SEP-1998 (first entry)
DE
DE   Human protein AQ2_1i 3'-portion and polyA tail.
XX
XX   Human; secreted protein; murine adult spleen; human foetal kidney; ovary;
XX   bone marrow; thymus; AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i;
XX   AQ2_1i; K433_1i; L256_1i; prevent; treat; ameliorate; medical; ds.
XX
XX   Homo sapiens.
XX

PN      WO9820130-A2.
XX
PD      14-MAY-1998.
XX
PF      31-OCT-1997; 97WO-US019857.
XX
XX      01-NOV-1996; 96US-00742973.
PR      29-OCT-1997; 97US-00960024.
XX
XX      (GEMY ) GENETICS INST INC.
XX
XX      Jacobs K, McCooy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI      Spaulding V, Agostino MJ;
XX
XX      WPI; 1998-286946/25.
XX
XX      New secreted proteins and associated polynucleotides - obtained from
PT      murine adult spleen, human foetal kidney, human ovary, murine bone marrow
PT      and murine adult thymus.
XX
XX      Disclosure; Page 58; 75pp; English.
XX
XX      The present invention describes novel proteins isolated from cDNA clones:
CC      AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i; AQ2_1i; K433_1i; or
CC      L256_1i, deposited as ATCC 98237. The present sequence represents the 3'-
CC      portion of AQ2_1i isolated from a human ovary cDNA library. The proteins
CC      from the present invention may be administered in a composition to
CC      prevent, treat or ameliorate a medical condition. The proteins may
CC      exhibit biological activities such as nutritional activity, cytokine and
CC      cell proliferation/differentiation activity, immune stimulating or
CC      suppressing activity, haematopoiesis regulating activity, tissue growth
CC      activity, activin/inhibin activity, chemotactic/chemokinetic activity,
CC      haemostatic and thrombotic activity, receptor/ligand activity, anti-
CC      inflammatory activity, cadherin/tumour invasion suppressor activity,
CC      tumour inhibition activity and other activities. (Updated on 25-MAR-2003
XX      to correct PR field.)
XX
XX      Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
Db      2 AAAAAAAAAAAAAAAAAA 17
|||||
RESULT 263
AAV07750
ID   AAV07750 standard; DNA; 18 BP.
XX
XX
AC   AAV07750;
XX
XX
DT   02-DEC-1998 (first entry)
DE
DE   Phosphorothioate oligodeoxynucleotide.
XX
XX
XX      phosphorothioate; electrospray ionisation-Fourier transform;
XX      mass spectrometry; off-resonance excitation; ss.
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
FH      misc_difference 1..18
FT      /tag= a
FT      /note= "phosphorothioate internucleotide linkages"
XX
XX      WO9840520-A1.
XX
XX      17-SEP-1998.
XX
XX      12-MAR-1998; 98WO-US004919.
XX

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XX 14-MAR-1997; 97US-0040717P.
XX (HYBR-) HYBRIDON INC.
XX Wang BH;
XX WPI; 1998-520830/44.
XX Determining the nucleotide sequence of a nucleic acid analyte - using
XX electro-spray ionisation.
XX Example 1; Fig 3A; 25pp; English.
XX The invention relates to an analytical method for determining the
XX nucleotide sequence of nucleic acid analytes, including chemically
XX modified oligonucleotides. This new method utilises electrospray
XX ionisation-Fourier transform mass spectrometry. The ions are excited by
XX sustained off-resonance excitation with single shot excitation, and the
XX target fragmented by collisionally activated dissociation by a neutral
XX gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation
XX can be nozzle skimmer dissociations. The method is used in molecular
XX biology and biomedical applications. The method, utilising electrospray
XX ionisation-Fourier transform ion cyclotron resonance mass spectrometry,
XX is extremely rapid and acts directly on the oligonucleotide. The method
XX is effective for a variety of nucleic acid analytes, particularly
XX chemically modified oligonucleotides which have not previously been
XX successfully sequenced. The present sequence represents a
XX phosphorothioate oligodeoxynucleotide
XX Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 1 AAAAAAAAAAAAAA 16

RESULT 264
AAV21970/C
ID AAV21970 standard; DNA; 18 BP.
XX AAV21970;
XX 14-JUL-1998 (first entry)
DE Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
XX Nuclease resistant; bacterial infection; antibiotic; target;
XX veterinary medicine; treatment; human; industrial process;
XX bacterial control; ss.
XX Synthetic.
XX WO9803533-A1.
XX 29-JAN-1998.
XX 23-JUL-1997; 97WO-US012961.
XX 24-JUL-1996; 96US-00685575.
XX (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX Arrow A, Dale RMK, Thompson TL;
XX WPI; 1998-120687/11.
XX Treating bacterial infections in humans or animals with
XX oligo:nucleotide(s) - resistant to nuclease and targeted to bacterial

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PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
XX with antibiotics.
XX Claim 49; Page 87; 163pp; English.
XX This antisense oligonucleotide is nuclease resistant and can be used in
XX the treatment of animals, including humans, having a bacterial infection.
XX The treatment comprises administration of such nuclease resistant
XX oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
XX and formulated with a carrier. A compound comprising this nuclease
XX resistant oligonucleotide can be covalently linked to an antibiotic. The
XX method is used to treat infections by a wide variety of Gram-positive and
XX Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
XX The methods are particularly used in immuno-compromised individuals (e.g.
XX patients with acquired immunodeficiency syndrome or those receiving
XX chemotherapy or radiation therapy). optionally in combination with, or
XX fused to, antiviral or other antimicrobial oligonucleotides. Apart from
XX therapeutic use, the oligonucleotides can be used to control bacteria in
XX laboratory cultures, foods, beverages and industrial processes. The
XX oligonucleotides are specific for bacteria, without affecting metabolism
XX in mammalian cells. They may also activate RNase H and have a general,
XX non-specific immune-stimulating effect. The oligonucleotides can be
XX administered orally, intranasally, rectally, topically or by injection,
XX optionally coupled to an agent (e.g. carbohydrate or polyamine) that
XX enhances cellular uptake
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 265
AAV19943/C
ID AAV19943 standard; DNA; 18 BP.
XX AAV19943;
XX 14-JUN-1999 (first entry)
DE Primer SEQ ID NO:3 from JP11075880.
XX Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX Synthetic.
XX JP11075880-A.
XX 23-MAR-1999.
XX 10-JUL-1998; 98JP-00195719.
XX 14-JUL-1997; 97JP-00205378.
XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX WPI; 1999-257710/22.
XX Labelling of an oligonucleotide - useful for detecting genes.
XX Example 1; Page 7; 10pp; Japanese.
XX A method has been developed for labelling an oligonucleotide having a
XX repeated sequence of (XY)n (where X and Y consists of a combination of
XX adenine and thymine or uracil or guanine and cytosine, and n is an
XX integer of 1 or more) at the 3'-terminal side in which the repeated
XX sequence is added and extended using a labelled body of the nucleotide
XX constituting the repeated sequence and a DNA polymerase lacked in 5' to

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CC 3' exonuclease activity. The method can be used for detecting a gene. The
 CC method can detect a gene in a sensitivity up to ten times higher than
 CC prior art methods. The present sequence represents a primer used in an
 CC example from the present invention

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 DB 18 AAAAAAAAAAAAAA 3

RESULT 266
 AAX19942
 ID AAX19942 standard; DNA; 18 BP.
 XX
 AC AAX19942;
 AC AAX19942;
 DT 14-JUN-1999 (First entry)
 XX
 DE Primer SEQ ID NO:2 from JP11075880.
 KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
 XX
 OS Synthetic.
 XX
 PN JP11075880-A.
 XX
 XX 23-MAR-1999.
 XX
 PF 10-JUL-1998; 98JP-00195719.
 PR
 PR 14-JUL-1997; 97JP-00205378.
 XX
 XX (KAGA) ZH KAGAKU & KESSHI RYOHO KENKYUSHO.
 XX
 DR WPI; 1999-257710/22.
 XX
 PT Labelling of an oligonucleotide - useful for detecting genes.
 XX
 PS Example 1; Page 7; 10pp; Japanese.
 XX
 CC A method has been developed for labelling an oligonucleotide having a
 CC repeated sequence of (XY)_n (where X and Y consists of a combination of
 CC adenine and thymine or uracil or guanine and cytosine, and n is an
 CC integer of 1 or more) at the 3'-terminal side in which the repeated
 CC sequence is added and extended using a labelled body of the nucleotide
 CC constituting the repeated sequence and a DNA polymerase lacked in 5' to
 CC 3' exonuclease activity. The method can be used for detecting a gene. The
 CC method can detect a gene in a sensitivity up to ten times higher than
 CC prior art methods. The present sequence represents a primer used in an
 CC example from the present invention

XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 SQ Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 DB 1 AAAAAAAAAAAAAA 16

RESULT 267
 AAA40563
 ID AAA40563 standard; cDNA; 18 BP.
 XX
 AC AAA40563;

XX 16-NOV-2000 (first entry)
 DT Human adult ovary cDNA fragment AQ2_1i #2.
 XX
 DE
 DE
 KW Secreted protein; cytostatic; immunostimulatory; antimicrobial;
 KW antiviral; immunosuppressive; antiinflammatory; vulnerrary; cytokine;
 KW cell proliferation; differentiation; regulator; treatment; tumor;
 KW autoimmune disease; inflammatory disorder; wound; microbial infection;
 KW viral disease; graft versus host reaction suppression; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200037630-A1.
 XX
 PD 29-JUN-2000.
 XX
 PF 22-DEC-1999; 99WO-US011005.
 XX
 PR 23-DEC-1998; 98US-00220876.
 XX
 XX (GEMY) GENETICS INST INC.
 PA
 XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR;
 XX
 DR WPI; 2000-442661/38.
 DR P-PSDB; AAB10274.
 XX
 PT Secreted human proteins AS296-1i and AS34-1i, useful for treating tumors,
 PT autoimmune diseases, inflammatory disorders, wounds, microbial infections
 PT and viral diseases.
 XX
 PS Disclosure; Page 269; 293pp; English.
 XX
 CC This invention describes novel secreted human proteins (I) which have
 CC cytostatic, immunostimulatory, antimicrobial, antiviral,
 CC immunosuppressive, antiinflammatory and vulnerrary activity and which act
 CC as cytokine, cell proliferation or differentiation regulators. (I) is
 CC useful for treating tumors, autoimmune diseases, inflammatory disorders,
 CC wounds, microbial infections and viral diseases. (I) is also useful for
 CC suppressing graft versus host reaction. AAA40490-A40580 represent cDNA
 CC fragments that encode the secreted proteins AAB10226-B10288 described in
 CC the method of the invention

XX Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
 SQ Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 DB 2 AAAAAAAAAAAAAA 17

RESULT 268
 AAZ90649/c
 ID AAZ90649 standard; DNA; 18 BP.
 XX
 AC AAZ90649;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 XX Human adipose tissue gene amplifying primer #10.
 DE
 XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2000037190-A.
 XX


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PD 08-FEB-2000.
PF 23-JUL-1998; 98JP-00225228.
PR 23-JUL-1998; 98JP-00225228.
XX (NIBS ) JAPAN TOBACCO INC.
XX WPI; 2000-306578/27.
XX
XX A physiologically active protein specifically derived from mammal tissue.
XX
XX Example 2; Page 18; 50pp; Japanese.
XX
XX The invention relates to identification of genes and proteins of adipose
XX tissue relating to obesity, particularly complications of visceral
XX obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
XX hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
XX proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
XX and treatment of adipose tissue related diseases. Sequences AAZ90640-51
XX represent PCR primers amplifying the human adipose tissue genes
XX
XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1480 TAAAAA 1495
XX 17 TAAAAA 2
XX
XX RESULT 269
XX AAZ90646/C
XX ID AAZ90646 standard; DNA; 18 BP.
XX
XX AC AAZ90646;
XX
XX DT 13-JUN-2000 (first entry)
XX
XX DE Human adipose tissue gene amplifying primer #7.
XX
XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN JP2000037190-A.
XX
XX PD 08-FEB-2000.
XX
XX PF 23-JUL-1998; 98JP-00225228.
XX
XX PR 23-JUL-1998; 98JP-00225228.
XX
XX (NIBS ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-306578/27.
XX
XX A physiologically active protein specifically derived from mammal tissue.
XX
XX Example 2; Page 18; 50pp; Japanese.
XX
XX The invention relates to identification of genes and proteins of adipose
XX tissue relating to obesity, particularly complications of visceral
XX obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
XX hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
XX proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
XX and treatment of adipose tissue related diseases. Sequences AAZ90640-51
XX represent PCR primers amplifying the human adipose tissue genes
XX
XX Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1480 TAAAAA 1495
XX 17 TAAAAA 2
XX
XX RESULT 269
XX AAZ90646/C
XX ID AAZ90646 standard; DNA; 18 BP.
XX
XX AC AAZ90646;
XX
XX DT 13-JUN-2000 (first entry)
XX
XX DE Human adipose tissue gene amplifying primer #7.
XX
XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN JP2000037190-A.
XX
XX PD 08-FEB-2000.
XX
XX PF 23-JUL-1998; 98JP-00225228.
XX
XX PR 23-JUL-1998; 98JP-00225228.
XX
XX (NIBS ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-306578/27.
XX
XX A physiologically active protein specifically derived from mammal tissue.
XX
XX Example 2; Page 18; 50pp; Japanese.
XX
XX The invention relates to identification of genes and proteins of adipose
XX tissue relating to obesity, particularly complications of visceral
XX obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
XX hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
XX proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
XX and treatment of adipose tissue related diseases. Sequences AAZ90640-51
XX represent PCR primers amplifying the human adipose tissue genes
XX
XX Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1480 TAAAAA 1495
XX 17 TAAAAA 2
XX
XX RESULT 271
XX AAZ87161
XX ID AAZ87161 standard; RNA; 18 BP.
XX
XX AC AAZ87161;
XX
XX DT 08-MAY-2000 (first entry)
XX
XX DE Oligoarabinonucleotide SEQ ID NO:2.
XX
XX KW Beta-D-arabinose; antisense; inhibition; transcription; expression;
XX reverse transcription; viral replication; RNase H cleavage;
XX triple helix formation; ss.

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XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..18
XX FT /*tag= a
XX FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX PN WO967378-A1.
XX PD 29-DEC-1999.
XX PF 17-JUN-1999; 99WO-CA000571.
XX PR 19-JUN-1998; 98CA-02241361.
XX PA (UYMC-) UNIV MCGILL.
XX PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX DR WPI; 2000-160584/14.
XX PT Therapeutic composition containing antisense oligonucleotides that
XX PT include arabinose sugars, particularly for inhibiting viral replication.
XX PS Example 1; Page 29; 91pp; English.
XX CC The invention relates to a new composition for selective, sequence-
XX CC specific inhibition of gene transcription and expression in a host. The
XX CC composition comprises oligonucleotides containing arabinose sugars that
XX CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
XX CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
XX CC helix, thereby inhibiting DNA replication and/or transcription. The
XX CC oligoarabinonucleotides are used for antisense inhibition of gene
XX CC expression or to prevent DNA replication, or reverse transcription of RNA
XX CC by retroviruses. The compositions are therefore particularly used to
XX CC inhibit retroviral replication. The oligoarabinonucleotides can also be
XX CC used, in combination with RNase H, as reagents for sequence-specific
XX CC cleavage or RNA mapping, and additionally for the study and control of
XX CC gene expression in cells. The oligoarabinonucleotides have excellent
XX CC affinity for RNA, increased resistance to nucleases and show little if
XX CC any non-specific binding to cellular or serum proteins. They target ss
XX CC RNA, but not complementary ss DNA, so may be useful for targeting
XX CC retroviral genomic RNA to inhibit the early stages of viral replication.
XX CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
XX CC with significantly higher thermal stability than those produced by normal
XX CC oligonucleotides. Sequences AAZ87160-287164 represent
XX CC oligoarabinonucleotides containing beta-D-arabinose used in an
XX CC exemplification of the present invention
XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 272
AAZ87162/c
ID AAZ87162 standard; RNA; 18 BP.
XX AC AAZ87162;
XX DT 08-MAY-2000 (first entry)
XX DE Oligoarabinonucleotide SEQ ID NO:3.
XX KW Beta-D-arabinose; antisense; inhibition; transcription; expression;
XX KW reverse transcription; viral replication; RNase H cleavage;

```

```

KW triple helix formation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..18
XX FT /*tag= a
XX FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX PN WO967378-A1.
XX PD 29-DEC-1999.
XX PF 17-JUN-1999; 99WO-CA000571.
XX PR 19-JUN-1998; 98CA-02241361.
XX PA (UYMC-) UNIV MCGILL.
XX PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX DR WPI; 2000-160584/14.
XX PT Therapeutic composition containing antisense oligonucleotides that
XX PT include arabinose sugars, particularly for inhibiting viral replication.
XX PS Example 1; Page 29; 91pp; English.
XX CC The invention relates to a new composition for selective, sequence-
XX CC specific inhibition of gene transcription and expression in a host. The
XX CC composition comprises oligonucleotides containing arabinose sugars that
XX CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
XX CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
XX CC helix, thereby inhibiting DNA replication and/or transcription. The
XX CC oligoarabinonucleotides are used for antisense inhibition of gene
XX CC expression or to prevent DNA replication, or reverse transcription of RNA
XX CC by retroviruses. The compositions are therefore particularly used to
XX CC inhibit retroviral replication. The oligoarabinonucleotides can also be
XX CC used, in combination with RNase H, as reagents for sequence-specific
XX CC cleavage or RNA mapping, and additionally for the study and control of
XX CC gene expression in cells. The oligoarabinonucleotides have excellent
XX CC affinity for RNA, increased resistance to nucleases and show little if
XX CC any non-specific binding to cellular or serum proteins. They target ss
XX CC RNA, but not complementary ss DNA, so may be useful for targeting
XX CC retroviral genomic RNA to inhibit the early stages of viral replication.
XX CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
XX CC with significantly higher thermal stability than those produced by normal
XX CC oligonucleotides. Sequences AAZ87160-287164 represent
XX CC oligoarabinonucleotides containing beta-D-arabinose used in an
XX CC exemplification of the present invention
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 273
AAZ87166/c
ID AAZ87166 standard; DNA; 18 BP.
XX AC AAZ87166;
XX DT 08-MAY-2000 (first entry)
XX DE Deoxyarabinonucleotide SEQ ID NO:7.
XX KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;

```

PR TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NING NO,
PI KAOKU OGAWA
PC C12N15/09, A61K31/00, A61K39/36, A61K45/00, C12Q1/68, C12N15/00 CC

FH Key Location/Qualifiers
FT source 1..17
/organism="Artificial Sequence".

FEATURES
source
1..17
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"

Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA1496
Db 17 TAAAAA1496

RESULT 58
AR187062/c
LOCUS AR187062 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2550 from patent US 6346398.
ACCESSION AR187062
VERSION AR187062.1 GI:20233027
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES
source
1..17
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA1496
Db 17 AAAAAA1496

RESULT 59
AR187063/c
LOCUS AR187063 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2551 from patent US 6346398.
ACCESSION AR187063
VERSION AR187063.1 GI:20233028
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2551 12-FEB-2002;
FEATURES
source
1..17
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA1496
Db 16 AAAAAA1496

RESULT 60
AR222463
LOCUS AR222463 17 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 23 from patent US 6429300.
ACCESSION AR222463
VERSION AR222463.1 GI:23329994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kurz, M., Lohse, P. and Wagner, R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 23 06-AUG-2002;
FEATURES
source
1..17
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA1496
Db 1 AAAAAA1496

RESULT 61
AR236087/c
LOCUS AR236087 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6462184.
ACCESSION AR236087
VERSION AR236087.1 GI:27279786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Manoharan, M. and Maier, M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6462184-A 5 08-OCT-2002;
FEATURES
source
1..17
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA1496
Db 17 AAAAAA1496

RESULT 62
AR266625/c
LOCUS AR266625 17 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 63 from patent US 6495319.
ACCESSION AR266625
VERSION AR266625.1 GI:29695689

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     McClelland,M., Welsh,J. and Trenkle,T.
TITLE       Reduced complexity nucleic acid targets and methods of using same
JOURNAL     Patent: US 6495319-A 63 17-DEC-2002;
FEATURES    Location/Qualifiers
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                /mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1495
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 63
AR323672/c
LOCUS      AR323672              17 bp    RNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 1074 from patent US 6566127.
ACCESSION  AR323672
VERSION    AR323672.1 GI:33709480
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Favco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 1074 20-MAY-2003;
FEATURES    Location/Qualifiers
            source
            1..17
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                /mol_type="unassigned RNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 64
AR323673/c
LOCUS      AR323673              17 bp    RNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 1075 from patent US 6566127.
ACCESSION  AR323673
VERSION    AR323673.1 GI:33709481
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Favco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 1075 20-MAY-2003;
FEATURES    Location/Qualifiers
            source
            1..17
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                /mol_type="unassigned RNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 65
AR323674/c
LOCUS      AR323674              17 bp    DNA      linear      PAT 15-FEB-2002
DEFINITION Sequence 24 from Patent WO0208461.
ACCESSION  AR323674
VERSION    AR323674.1 GI:18694225
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM   1
REFERENCE   1
AUTHORS     Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
TITLE       A method and an algorithm for mrna expression analysis
JOURNAL     Patent: WO 0208461-A 24 31-JAN-2002;
            Global Genomics AB (SE)
FEATURES    Location/Qualifiers
            source
            1..17
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Double-stranded product DNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 66
AX692525/c
LOCUS      AX692525              17 bp    DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5257 from Patent EP1281758.
ACCESSION  AX692525
VERSION    AX692525.1 GI:29415483
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5257 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..17
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 67
AX692526/c
LOCUS      AX692526              17 bp    DNA      linear      PAT 31-MAR-2003

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DEFINITION Sequence 5258 from Patent EP1281758.
ACCESSION AX692526
VERSION AX692526.1 GI:29415484
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5258 05-FEB-2003; Acomica, Inc. (US)
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
Query Match 1..17; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1
RESULT 68
AX814938/c
LOCUS AX814938
DEFINITION Sequence 24 from Patent WO03064691.
ACCESSION AX814938
VERSION AX814938.1 GI:39104076
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and Montelius,A.
TITLE Methods and means for manipulating nucleic acid
JOURNAL Patent: WO 03064691-A 24 07-AUG-2003; Global Genomics AB (SE)
FEATURES
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        /db_xref="taxon:32630"
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Query Match 1..17; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1
RESULT 69
BD011730/c
LOCUS BD011730
DEFINITION 795, a novel gene related to pollen allergy.
ACCESSION BD011730
VERSION BD011730.1 GI:22091919
KEYWORDS WO 0065050-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)

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AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi,A.
TITLE 795, a novel gene related to pollen allergy
JOURNAL Patent: WO 0065050-A 2 02-NOV-2000; GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI
COMMENT OS Artificial Sequence
    PN WO 0065050-A/2
    PD 02-NOV-2000
    PF 26-APR-2000 WO 2000JP002734
    PR 27-APR-1999 JP 99P 120494
    PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
    C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC A61P37/00
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FEATURES
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Query Match 1..17; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1480 TAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAA 2
RESULT 70
BD091742/c
LOCUS BD091742
DEFINITION 441, a novel gene related to pollen allergy.
ACCESSION BD091742
VERSION BD091742.1 GI:22637353
KEYWORDS WO 0073435-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
TITLE 441, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073435-A 2 07-DEC-2000; GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT OS Artificial Sequence
    PN WO 0073435-A/2
    PD 07-DEC-2000
    PF 18-MAY-2000 WO 2000JP003190
    PR 27-MAY-1999 JP 99P 148783
    PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
    PC C12N15/10,C12Q1/68,G01N33/15,G01N33/50
    CC Description of Artificial Sequence:Artificially Synthesized CC
FEATURES
    FH Key Location/Qualifiers
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        /mol_type="genomic DNA"

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA1495
Db 17 TAAAAA1495

RESULT 74
BD142808/c
LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD142808
VERSION BD142808.1 GI:23237753
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
Tsujimoto,G. and Takahashi,E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 2 28-MAR-2002;
GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
OS Artificial Sequence
PN WO 0224903-A/2
PD 28-MAR-2002
PE 21-SEP-2001 WO 2001JP008246
PF 25-SEP-2000 JP 00P 291318
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PC GOZO TSUJIMOTO, EIKI TAKAHASHI
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68, A01K67/027, A61K31/713, A61K45/00, A61P17/00, A61P37/08,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1.91), (C12P21/02, C12R1.91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
/organism='Artificial Sequence'.

FEATURES
source
QY 1480 TAAAAA1495
Db 17 TAAAAA1495

RESULT 75
BD143834/c
LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD143834
VERSION BD143834.1 GI:27849592
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and

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Tsujimoto,K.
Method of examining allergic disease
Patent: JP 2002095500-A 2 02-APR-2002;
GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
OS Artificial Sequence
PN JP 2002095500-A/2
PD 02-APR-2002
PF 25-SEP-2000 JP 2000291316
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PC KOZO TSUJIMOTO
PC C12Q1/68, A01K67/027, A61K31/7088, A61K31/711, A61K45/00, A61P37/08, PC
C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10 PC
C12N15/09, C12P21/02,
PC C12Q1/02, G01N33/15, G01N33/50//C12P21/08, C12N5/00, C12N5/00, PC
C12N15/00
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
/organism='Artificial Sequence'.

FEATURES
source
QY 1480 TAAAAA1495
Db 17 TAAAAA1495

RESULT 76
BD167835/c
LOCUS
DEFINITION Method for examination of allergosis.
ACCESSION BD167835
VERSION BD167835.1 GI:27873647
KEYWORDS WO 0233122-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
and Takahashi,E.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 0233122-A 2 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA, RYOICHI
HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
SAITO, EIKI TAKAHASHI
OS Artificial Sequence
PN WO 0233122-A/2
PD 25-APR-2002
PF 11-OCT-2001 WO 2001JP008937
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PC HIROHISA SAITO, EIKI TAKAHASHI
PC C12Q1/68, C12N15/09, G01N33/53, G01N33/50, C12Q1/02, A61K48/00, PC
A61K39/395,
PC A01K67/027//C07K16/18, C12N5/10
CC Description of Artificial Sequence:an artificially synthesized

CC anchor

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CC primer sequence      Location/Qualifiers
FH Key                  1..17
FT source               /organism='Artificial Sequence'.

FEATURES
  source               Location/Qualifiers
    1..17
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAA 2

RESULT 77
BD167907/c
LOCUS BD167907 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD167907
VERSION BD167907.1 GI:27873719
KEYWORDS WO 0226962-A/6.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 6 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI
SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0226962-A/6
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.

FEATURES
  source               Location/Qualifiers
    1..17
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAA 2

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RESULT 78
BD168111/c
LOCUS BD168111 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION BD168111
VERSION BD168111.1 GI:27873923
KEYWORDS WO 0233069-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0233069-A 18 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO
NATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0233069-A/18
PD 25-APR-2002
PF 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC
A61K39/395,
PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
CC Description of Artificial Sequence:an artificially synthesized

CC anchor
CC primer sequence
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.

FEATURES
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    /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAA 2

RESULT 79
BD171177/c
LOCUS BD171177 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD171177
VERSION BD171177.1 GI:27876989
KEYWORDS WO 0250269-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 2 27-JUN-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO
NATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU,
GOZO TSUJIMOTO
OS Artificial Sequence
PN WO 0250269-A/2

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PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
PI 21-DEC-2000 JP 00P 389476
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI
TAKESHI NAGASU,
PI GOZO TSUJIMOTO
PC C12N15/11.C07K16/18.A61K67/027.A61K31/711.A61K45/00.A61K48/00,
PC A61P37/08,
PC C12Q1/68.G01N33/50
CC Description of Artificial Sequence: 'GTL5A', an artificially
CC synthesized
CC primer sequence
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.
FEATURES
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1..17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAAAAAA 1495
Db
17 TAAAAAATAAAAAAAAAA 2
RESULT 80
AR034896/c
LOCUS AR034896 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5869643.
ACCESSION AR034896
VERSION AR034896.1 GI:5950501
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
tightly packed bed
JOURNAL Patent: US 5869643-A 12 09-FEB-1999;
FEATURES
source
1..18
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAAAAA 3
RESULT 81
AR034899
LOCUS AR034899 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 18 from patent US 5869643.
ACCESSION AR034899
VERSION AR034899.1 GI:5950504
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
tightly packed bed

JOURNAL Patent: US 5869643-A 18 09-FEB-1999;
FEATURES
source
1..18
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16
RESULT 82
AR058305
LOCUS AR058305 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5837820.
ACCESSION AR058305
VERSION AR058305.1 GI:5983882
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.
TITLE Seed specific biotinylated protein, SBP65, from leguminous plants
JOURNAL Patent: US 5837820-A 3 17-NOV-1998;
FEATURES
source
1..18
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16
RESULT 83
AR097579/c
LOCUS AR097579 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6071745.
ACCESSION AR097579
VERSION AR097579.1 GI:12806309
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to
preserve RNA and DNA contained in cells for use in molecular
biology experiments
JOURNAL Patent: US 6071745-A 9 06-JUN-2000;
FEATURES
source
1..18
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAAAAA 3

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RESULT 84
AR106506
LOCUS      AR106506      18 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 30 from patent US 6107060.
ACCESSION  AR106506
VERSION     AR106506.1 GI:12821036
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Keeling,P. and Guan,H.
TITLE       Starch encapsulation
JOURNAL     Patent: US 6107060-A 30 22-AUG-2000;
FEATURES    Location/Qualifiers
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            1..18
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                /mol_type="unassigned DNA"
            1.1% Score 16; DB 1; Length 18;
            Best Local Similarity 100.0%; Pred. No. 85;
            Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAA 16

RESULT 85
E28535
LOCUS      E28535      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION  E28535
VERSION     E28535.1 GI:13025387
KEYWORDS    JP 1999075880-A/2.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE       Method for labeling oligonucleotide and utilization thereof
JOURNAL     Patent: JP 1999075880-A 2 23-MAR-1999;
            CHERO SERO THERAPEUT RES INST
COMMENT     OS Unidentified
            EN JP 1999075880-A/2
            PD 23-MAR-1999
            PF 10-JUL-1998 JP 1998195719
            PR
            PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers
            FT source
                1..18
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                    /db_xref="taxon:32644"

QY 1481 AAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAA 16

RESULT 86
E28536/c
LOCUS      E28536      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION  E28536
VERSION     E28536.1 GI:13025388
KEYWORDS    JP 1999075880-A/3.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE       Method for labeling oligonucleotide and utilization thereof
JOURNAL     Patent: JP 1999075880-A 3 23-MAR-1999;
            CHERO SERO THERAPEUT RES INST
COMMENT     OS Unidentified
            EN JP 1999075880-A/3
            PD 23-MAR-1999
            PF 10-JUL-1998 JP 1998195719
            PR
            PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers
            FT source
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QY 1481 AAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAA 16

RESULT 86
E28536/c
LOCUS      E28536      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION  E28536
VERSION     E28536.1 GI:13025388
KEYWORDS    JP 1999075880-A/3.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE       Method for labeling oligonucleotide and utilization thereof
JOURNAL     Patent: JP 1999075880-A 3 23-MAR-1999;
            CHERO SERO THERAPEUT RES INST
COMMENT     OS Unidentified
            EN JP 1999075880-A/3
            PD 23-MAR-1999
            PF 10-JUL-1998 JP 1998195719
            PR
            PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers
            FT source
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                    /db_xref="taxon:32644"

QY 1481 AAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAA 16
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DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION  E28536
VERSION     E28536.1 GI:13025388
KEYWORDS    JP 1999075880-A/3.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE       Method for labeling oligonucleotide and utilization thereof
JOURNAL     Patent: JP 1999075880-A 3 23-MAR-1999;
            CHERO SERO THERAPEUT RES INST
COMMENT     OS Unidentified
            EN JP 1999075880-A/3
            PD 23-MAR-1999
            PF 10-JUL-1998 JP 1998195719
            PR
            PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers
            FT source
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                    /db_xref="taxon:32644"

QY 1481 AAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAA 3

RESULT 87
E32453/c
LOCUS      E32453      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32453
VERSION     E32453.1 GI:13018689
KEYWORDS    JP 2000037190-A/13.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Jun,N., Yuseke,N. and Toshihiro,T.
TITLE       Mammal-derived tissue specific physiologically active protein
JOURNAL     Patent: JP 2000037190-A 13 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS Artificial Sequence
            EN JP 2000037190-A/13
            PD 08-FEB-2000
            PF 23-JUL-1998 JP 1998225228
            PR
            PI JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10,PC
            C12N15/02
            PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC C12N15/00,
            CC C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            FH Key Location/Qualifiers
            FT primer_bind
                1..18
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

QY 1481 AAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAA 3

RESULT 87
E32453/c
LOCUS      E32453      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32453
VERSION     E32453.1 GI:13018689
KEYWORDS    JP 2000037190-A/13.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Jun,N., Yuseke,N. and Toshihiro,T.
TITLE       Mammal-derived tissue specific physiologically active protein
JOURNAL     Patent: JP 2000037190-A 13 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS Artificial Sequence
            EN JP 2000037190-A/13
            PD 08-FEB-2000
            PF 23-JUL-1998 JP 1998225228
            PR
            PI JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10,PC
            C12N15/02
            PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC C12N15/00,
            CC C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            FH Key Location/Qualifiers
            FT primer_bind
                1..18
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

QY 1481 AAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAA 3
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Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1480 TAAAAA... 1495
DB 17 TAAAAA... 2

RESULT 88
E32456/c
LOCUS      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32456
VERSION    E32456.1 GI:13018692
KEYWORDS  JP 2000037190-A/16.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Jun,N., Yusuken,N. and Toshihiro,T.
TITLE    Mammal-derived tissue specific physiologically active protein
JOURNAL  Patent: JP 2000037190-A 16 08-FEB-2000,
        JAPAN TOBACCO INC
COMMENT   OS Artificial Sequence
        PN JP 2000037190-A/16
        PD 08-FEB-2000
        PF 23-JUL-1998 JP 1998225228

PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC
FH Key      Location/Qualifiers
FT primer_bind (1)..(18).
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA... 1495
DB 17 TAAAAA... 2

RESULT 90
E32456/c
LOCUS      18 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5707807.
ACCESSION  I79509
VERSION    I79509.1 GI:3207799
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Kato,K.
TITLE    Molecular indexing for expressed gene analysis
JOURNAL  Patent: US 5707807-A 16 13-JAN-1998;
FEATURES  Location/Qualifiers
   source      1..18
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA... 1496
DB 18 AAAAAA... 3

RESULT 91
AR208426/c
LOCUS      18 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6383754.
ACCESSION  AR208426
VERSION    AR208426.1 GI:21509577
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE    Binary encoded sequence tags
JOURNAL  Patent: US 6383754-A 6 07-MAY-2002;
FEATURES  Location/Qualifiers
   source      1..18
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      1.1%; Score 16; DB 1; Length 18;
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Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1480 TAAAAA... 1495
DB 17 TAAAAA... 2

RESULT 88
E32456/c
LOCUS      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32456
VERSION    E32456.1 GI:13018692
KEYWORDS  JP 2000037190-A/16.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Jun,N., Yusuken,N. and Toshihiro,T.
TITLE    Mammal-derived tissue specific physiologically active protein
JOURNAL  Patent: JP 2000037190-A 16 08-FEB-2000,
        JAPAN TOBACCO INC
COMMENT   OS Artificial Sequence
        PN JP 2000037190-A/16
        PD 08-FEB-2000
        PF 23-JUL-1998 JP 1998225228

PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC
FH Key      Location/Qualifiers
FT primer_bind (1)..(18).
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA... 1495
DB 17 TAAAAA... 2

RESULT 89
E32459/c
LOCUS      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32459
VERSION    E32459.1 GI:13018695
KEYWORDS  JP 2000037190-A/19.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Jun,N., Yusuken,N. and Toshihiro,T.
TITLE    Mammal-derived tissue specific physiologically active protein
JOURNAL  Patent: JP 2000037190-A 19 08-FEB-2000;
        JAPAN TOBACCO INC
COMMENT   OS Artificial Sequence
        PN JP 2000037190-A/19
        PD 08-FEB-2000
        PF 23-JUL-1998 JP 1998225228
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Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 92
AR208427/c AR208427 18 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 7 from patent US 6383754.
DEFINITION AR208427
ACCESSION AR208427
VERSION AR208427.1 GI:21509578
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: US 6383754-A 7 07-MAY-2002;
FEATURES
    Location/Qualifiers
        source
            1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 93
AR215435/c AR215435 18 bp DNA linear PAT 25-SEP-2002
LOCUS Sequence 9 from patent US 6410321.
DEFINITION AR215435
ACCESSION AR215435
VERSION AR215435.1 GI:23313691
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to
    preserve RNA and DNA contained in cells for use in molecular
    biology experiments
JOURNAL Patent: US 6410321-A 9 25-JUN-2002;
FEATURES
    Location/Qualifiers
        source
            1..18
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 94
AR222464 AR222464 18 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 24 from patent US 6429300.
DEFINITION AR222464
ACCESSION AR222464
VERSION AR222464.1 GI:23329995
KEYWORDS

Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 96
AX004875/c AX004875 18 bp DNA linear PAT 24-AUG-2000
LOCUS Sequence 4 from Patent WO9910527.
DEFINITION AX004875
ACCESSION AX004875
VERSION AX004875.1 GI:9928275
KEYWORDS
SOURCE
ORGANISM synthetic construct
    artificial sequences.
REFERENCE 1
AUTHORS Bayer,E. and Schewitz,J.
TITLE Method for isolating anionic organic substances from aqueous
    systems using cationic polymer nanoparticles
JOURNAL Patent: WO 9910527-A 4 04-MAR-1999;
    SUEDEDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES
    Location/Qualifiers
        source
            1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="3' palmityl oligonucleotide"
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Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels
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RESULT 101
AX008123
LOCUS AX008123
DEFINITION Sequence 8 from Patent WO9967378.
ACCESSION AX008123
VERSION AX008123.1
KEYWORDS 18 bp DNA linear PAT 06-SEP-2000
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose
and its analogues
JOURNAL Patent: WO 9967378-A 8 29-DEC-1999;
(DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
(CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
BORKOW GADI (IL))
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Use as an oligomer"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 102
AX028844/c
LOCUS AX028844
DEFINITION Sequence 28 from Patent WO9732023.
ACCESSION AX028844
VERSION AX028844.1
KEYWORDS 18 bp DNA linear PAT 24-NOV-2000
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: WO 9732023-A 28 04-SEP-1997;
FLORIGENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY
ALBERT (AU); MICHAEL MICHAEL ZENON (AU)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 103
AX047271
LOCUS AX047271
DEFINITION Sequence 21 from Patent WO0068422.
ACCESSION AX047271
VERSION AX047271.1
KEYWORDS 18 bp DNA linear PAT 15-DEC-2000
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehleger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
Gumbiowski,K. and Zulauf,M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 21 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="second fragment of SEQ ID NO: 6"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 104
AX047273/c
LOCUS AX047273
DEFINITION Sequence 23 from Patent WO0068422.
ACCESSION AX047273
VERSION AX047273.1
KEYWORDS 18 bp DNA linear PAT 15-DEC-2000
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehleger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
Gumbiowski,K. and Zulauf,M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 23 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="second fragment of SEQ ID NO: 6"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 105
AX085252/c
LOCUS AX085252
DEFINITION Sequence 6 from Patent WO0112855.
ACCESSION AX085252
VERSION AX085252.1
KEYWORDS 18 bp DNA linear PAT 09-MAR-2001
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehleger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
Gumbiowski,K. and Zulauf,M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 21 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="second fragment of SEQ ID NO: 6"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

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REFERENCE
1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 6 22-FEB-2001;
YALE UNIVERSITY (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAAA 1

RESULT 106
AX085253/c
LOCUS AX085253 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 7 from Patent WO0112855.
ACCESSION AX085253
VERSION AX085253.1 GI:13275311
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 7 22-FEB-2001;
YALE UNIVERSITY (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAAA 1

RESULT 107
AX104721/c
LOCUS AX104721 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 913 from Patent WO0122972.
ACCESSION AX104721
VERSION AX104721.1 GI:13920918
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 913 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAAA 3

RESULT 108
AX104747/c
LOCUS AX104747 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 939 from Patent WO0122972.
ACCESSION AX104747
VERSION AX104747.1 GI:13920944
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 939 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAAA 3

RESULT 109
AX105651/c
LOCUS AX105651 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
Scios Inc. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="synthetic"

Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAAA 3

RESULT 110
AX105651/c
LOCUS AX105651 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
Scios Inc. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="synthetic"

Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAAA 3

RESULT 110

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AX108642/c
LOCUS AX108642 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123419.
ACCESSION AX108642
VERSION AX108642.1 GI:13923875
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Differentially expressed genes
JOURNAL Patent: WO 0123419-A 10 05-APR-2001;
SCIOS INC. (US)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1..18; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAA 3

RESULT 111
AX268883/c
LOCUS AX268883 18 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 84 from Patent WO0174901.
ACCESSION AX268883
VERSION AX268883.1 GI:16541910
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and White,R.T.
TITLE Secreted factors
JOURNAL Patent: WO 0174901-A 84 11-OCT-2001;
Scios Inc. (US)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligos corresponding to polylinker sequence."

Query Match 1..18; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAA 3

RESULT 112
AX355809/c
LOCUS AX355809 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 837 from Patent WO0197843.
ACCESSION AX355809
VERSION AX355809.1 GI:18620477
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.

```

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TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 837 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"

Query Match 1..18; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAA 3

RESULT 113
AX547774/c
LOCUS AX547774 18 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 913 from Patent WO02053141.
ACCESSION AX547774
VERSION AX547774.1 GI:25812918
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 913 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1..18; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAA 3

RESULT 114
AX547800/c
LOCUS AX547800 18 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 939 from Patent WO02053141.
ACCESSION AX547800
VERSION AX547800.1 GI:25812944
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 939 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

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Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 115
AX814716/c
LOCUS      AX814716      18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 1 from Patent WO03064441.
ACCESSION  AX814716
VERSION     AX814716.1 GI:39103916
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Damha, M.J. and Parniak, M.A.
TITLE       Oligonucleotides comprising alternating segments and uses thereof
JOURNAL     Patent: WO 03064441-A 1 07-AUG-2003;
            MCGILL UNIVERSITY (CA)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 116
AX814723/c
LOCUS      AX814723      18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 8 from Patent WO03064441.
ACCESSION  AX814723
VERSION     AX814723.1 GI:39103922
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Damha, M.J. and Parniak, M.A.
TITLE       Oligonucleotides comprising alternating segments and uses thereof
JOURNAL     Patent: WO 03064441-A 8 07-AUG-2003;
            MCGILL UNIVERSITY (CA)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"

misc_feature     1..17
                /notes="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                2'-O-methyl-D-uridine"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

```

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RESULT 117
AX814724/c
LOCUS      AX814724      18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 9 from Patent WO03064441.
ACCESSION  AX814724
VERSION     AX814724.1 GI:39103923
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Damha, M.J. and Parniak, M.A.
TITLE       Oligonucleotides comprising alternating segments and uses thereof
JOURNAL     Patent: WO 03064441-A 9 07-AUG-2003;
            MCGILL UNIVERSITY (CA)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"

misc_feature     1..15
                /notes="Residues 1-3, 7-9, and 13-15 are
                2'-O-methyl-D-uridine"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 118
AX814725/c
LOCUS      AX814725      18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 10 from Patent WO03064441.
ACCESSION  AX814725
VERSION     AX814725.1 GI:39103924
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Damha, M.J. and Parniak, M.A.
TITLE       Oligonucleotides comprising alternating segments and uses thereof
JOURNAL     Patent: WO 03064441-A 10 07-AUG-2003;
            MCGILL UNIVERSITY (CA)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"

misc_feature     1..18
                /notes="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 119
AX814736
LOCUS      AX814736      18 bp      RNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 21 from Patent WO03064441.

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ACCESSION AX814736
VERSION AX814736.1 GI:39103935
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Damha,M.J. and Patniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 21 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32830"
                /note="Target RNA oligonucleotide"
Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 120
LOCUS BD085545/c
DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085545
VERSION BD085545.1 GI:22631155
KEYWORDS JP 2001333800-A/2.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Shimada,K.
TITLE Method of comparison and detection of RNA amount and DNA amount
JOURNAL Patent: JP 2001333800-A 2 04-DEC-2001;
UNITECH CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2001333800-A/2
PD 04-DEC-2001
PF 30-MAY-2000 JP 2000160324
PI KAORI SHIMADA
PC C12Q1/68,C12N15/09,G01N33/50,C12N15/00
CC Method of comparison and detection of RNA amount and DNA CC
FH Key Location/Qualifiers
FT source 1..18
FT /organism="Homo sapiens"
FT /mol_type="genomic RNA"
FT /db_xref="taxon:9606"
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="Homo sapiens"
                /mol_type="genomic RNA"
                /db_xref="taxon:9606"
Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAAAAA 3

RESULT 121
LOCUS BD190553
DEFINITION Secretory proteins and polynucleotides encoding the same.

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ACCESSION BD190553
VERSION BD190553.1 GI:33000292
KEYWORDS JP 2002515753-A/12.
SOURCE Rattus
ORGANISM Rattus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jacobs,K., McCOY,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
Treacy,M., Spaulding,V. and Agostino,M.J.
TITLE Secretory proteins and polynucleotides encoding the same
JOURNAL Patent: JP 2002515753-A 12 28-MAY-2002;
GENETICS INSTITUTE INC
COMMENT PN JP 2002515753-A/12
PD 28-MAY-2002
PF 31-OCT-1997 JP 1998521609
PR 01-NOV-1996 US 08/724973
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
DAVID MERBERG,
PI MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC Strandedness:
Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
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        Location/Qualifiers
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                /db_xref="taxon:10114"
Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 2 AAAAAAAAAAAAAAAAAA 17

RESULT 122
LOCUS BD222596/c
DEFINITION Aminoxy-modified nucleoside compound and oligomer compound
produced therefrom.
ACCESSION BD222596
VERSION BD222596.1 GI:33032366
KEYWORDS JP 2002522447-A/14.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified nucleoside compound and oligomer compound
produced therefrom
JOURNAL Patent: JP 2002522447-A 14 23-JUL-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002522447-A/14
PD 23-JUL-2002
PF 09-AUG-1998 JP 2000563675
PR 07-AUG-1998 US 09/130973
PI MUTHIAH MANOHARAN,PHILIP DAN COOK,THAZHA P PRAKASH,ANDREW M
PI KAWASAKI
PC C07H19/167,C07H19/067,C07H19/10,C07H19/20,C07H21/02,C12N15/00,
C12N15/00
CC Description of Artificial Sequence: antisense sequence FH
Key Location/Qualifiers
FT source 1..18
FT /organism="Artificial Sequence".
FT Location/Qualifiers
    1..18
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        /mol_type="genomic DNA"
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="synthetic construct"
                /mol_type="genomic DNA"

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/db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 123
LOCUS BD233654/c
DEFINITION Two-color differential display as a method for detecting regulated
genes.
ACCESSION BD233654
VERSION BD233654.1 GI:33043424
KEYWORDS JP 2002524088-A/2.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kozian D. and Reuner, B.
TITLE Two-color differential display as a method for detecting regulated
JOURNAL Patent: JP 2002524088-A 2 06-AUG-2002;
COMMENT AVENTIS PHARMA DEUTSCHLAND GMBH
PN JP 2002524088-A/2
PD 06-AUG-2002
PF 26-AUG-1999 JP 2000569015
PR 07-SEP-1998 DE 198 40 731.9
PC DETLEF KOZIAN, BIRGIT REUNER
PC C12Q1/68, G01N33/58//A61K45/00, C12N15/09, C12N15/09, C12N15/00,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /note= 'M = A, C, G, N = A, C, G, T'
FH Key Location/Qualifiers
FT exon 1..17.
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1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      1.0%; Score 15.6; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
DB 16 KAAAAAAAAAAAAA 1

RESULT 124
LOCUS BD217905/c
DEFINITION Gene family encoding apoptosis-associated peptides, peptides
encoded thereby and method of using the same.
ACCESSION BD217905
VERSION BD217905.1 GI:33027675
KEYWORDS JP 2002516564-A/6.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Umansky S. and Melkonyan, H.
TITLE Gene family encoding apoptosis-associated peptides, peptides
JOURNAL Patent: JP 2002516564-A 6 04-JUN-2002;
COMMENT TANOX INC
OS Unidentified

PN JP 2002516564-A/6
PD 04-JUN-2002
PF 24-SEP-1997 JP 1998515877
PR 24-SEP-1996 US 60/026603, 11-OCT-1996 US 60/028363 PI
SAMUTL UMANSKY HOVSEP MELKONYAN
PC C12N15/12, C12N15/62, C07K14/47, C07K16/18, C12Q1/68, G01N33/53, PC
G01N33/68,
PC A61K38/17
CC Strandedness: Single;
CC Topology: Linear;
CC Gene family encoding apoptosis-associated peptides, peptides
CC thereby and method of using the same
FH Key Location/Qualifiers
FT source 1..17
/organism="Unidentified".
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/db_xref="taxon:32644"

Query Match      1.0%; Score 15.6; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 89;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAAAAA 1495
DB 17 SNAAAAAAAAAAAAAA 1

RESULT 125
LOCUS AX423222
DEFINITION Sequence 1558 from Patent WO0188124.
ACCESSION AX423222
VERSION AX423222.1 GI:21526604
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlwitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1558 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 CGCGCGCGCGCGCGCG 41
DB 1 CGCGCGCGCGCGCGCG 17

RESULT 126
LOCUS AX691936
DEFINITION Sequence 4668 from Patent EP1281758.
ACCESSION AX691936
VERSION AX691936.1 GI:29414877
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 4668 05-FEB-2003;
          Aeomica, Inc. (US)
FEATURES
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Query Match
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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 946 CTGAGGCCCGCAGCTC 962
Db 1 CTGAGGCCCGCAGCTC 17

RESULT 127
AX692527/c
LOCUS AX692527 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5259 from Patent EPI281758.
ACCESSION AX692527
VERSION AX692527.1 GI:29415485
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5259 05-FEB-2003;
          Aeomica, Inc. (US)
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Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAA 1496
Db 17 TCAAAAAAATAAAAAA 1

RESULT 128
AX692528/c
LOCUS AX692528 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5260 from Patent EPI281758.
ACCESSION AX692528
VERSION AX692528.1 GI:29415486
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5260 05-FEB-2003;
          Aeomica, Inc. (US)
FEATURES
source
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAA 1495
Db 18 CCAAAAAAATAAAAAA 2

RESULT 130
E32452/c
LOCUS E32452 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32452
VERSION E32452.1 GI:13018688
KEYWORDS JP 2000037190-A/12.
SOURCE synthetic construct
ORGANISM artificial sequences.
          1 (bases 1 to 18)
          Jun,N., Yusuke,N. and Toshihiro,T.
          Mammal-derived tissue specific physiologically active protein
          Patent: JP 2000037190-A 12 08-FEB-2000;
          JAPAN TOBACCO INC
          OS Artificial Sequence

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAA 1495
Db 18 CCAAAAAAATAAAAAA 2

RESULT 129
E32451/c
LOCUS E32451 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32451
VERSION E32451.1 GI:13018687
KEYWORDS JP 2000037190-A/11.
SOURCE synthetic construct
ORGANISM artificial sequences.
          1 (bases 1 to 18)
          Jun,N., Yusuke,N. and Toshihiro,T.
          Mammal-derived tissue specific physiologically active protein
          Patent: JP 2000037190-A 11 08-FEB-2000;
          JAPAN TOBACCO INC
          OS Artificial Sequence

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAA 1495
Db 17 CTCAAAAAATAAAAAA 1

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Key primer bind Location/Qualifiers
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PN JP 2000037190-A/12
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PI C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
PC C12N15/02,
PC C12P21/02, C12P21/08, C12N5/10, C12R1/91, (C12P21/08, C12R1/91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1/91)
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Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1495
DB 18 CGAAAAAAAAAAAAA 2

RESULT 131
E32457/c
LOCUS
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32457
VERSION E32457.1 GI:13018693
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Jun.N., Yusuke.N. and Toshihiro.T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 17 08-FEB-2000;
JAPAN TOBACCO INC
OS Artificial Sequence
PN JP 2000037190-A/17
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PI C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
PC C12N15/02,
PC C12P21/02, C12P21/08, C12N5/10, C12R1/91, (C12P21/08, C12R1/91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1/91)
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Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 18 TCAAAAAAAAAAAAAA 2

RESULT 132
E32460/c
LOCUS
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32460
VERSION E32460.1 GI:13018696
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Jun.N., Yusuke.N. and Toshihiro.T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 20 08-FEB-2000;
JAPAN TOBACCO INC
OS Artificial Sequence
PN JP 2000037190-A/20
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PI C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
PC C12N15/02,
PC C12P21/02, C12P21/08, C12N5/10, C12R1/91, (C12P21/08, C12R1/91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1/91)
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FT Key Location/Qualifiers
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Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 18 TCAAAAAAAAAAAAAA 2

RESULT 133
E32458/c
LOCUS
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32458
VERSION E32458.1 GI:13018694
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Jun.N., Yusuke.N. and Toshihiro.T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 18 08-FEB-2000;
JAPAN TOBACCO INC
OS Artificial Sequence
PN JP 2000037190-A/18
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PI C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
PC C12N15/02,
PC C12P21/02, C12P21/08, C12N5/10, C12R1/91, (C12P21/08, C12R1/91),
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PC C12N5/00, C12N15/00, (C12N5/00, C12R1/91)
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Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 18 TGAATAAAAAAAAAAAAA 2

RESULT 133
E32460/c
LOCUS
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32460
VERSION E32460.1 GI:13018696
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Jun.N., Yusuke.N. and Toshihiro.T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 20 08-FEB-2000;
JAPAN TOBACCO INC
OS Artificial Sequence
PN JP 2000037190-A/20
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PI C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
PC C12N15/02,
PC C12P21/02, C12P21/08, C12N5/10, C12R1/91, (C12P21/08, C12R1/91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1/91)
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CC
FT Key Location/Qualifiers
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Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 18 TGAATAAAAAAAAAAAAA 2

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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAA 1494
Db 18 GCAAAAAA 2

RESULT 134
AX838308
LOCUS AX838308 18 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 5432 from Patent EP1347046.
ACCESSION AX838308
VERSION AX838308.1 GI:39922000
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 5432 24-SEP-2003;
RESEARCH Association for Biotechnology (JP)
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synthesized primer se q"

Query Match
Best Local Similarity 1.0%; Score 15.4; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1459 AGAAGGACATCAGGC 1475
Db 1 AAGAGGACATCAGGC 17

RESULT 135
E52143/c
LOCUS E52143 16 bp DNA linear PAT 31-JAN-2002
DEFINITION TSA7005 gene.
ACCESSION E52143
VERSION E52143.1 GI:18629626
KEYWORDS JP 2001025389-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Ogawara,T., Suzuki,M. and Ozaki,K.
TITLE TSA7005 gene
JOURNAL Patent: JP 2001025389-A 3 30-JAN-2001;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Unknown
PN JP 2001025389-A/3
PD 30-JAN-2001
PE 15-JUL-1999 JP 1999201279
PR TSUYOSHI OGAWARA,MIKIO SUZUKI,KOICHI OZAKI
PI C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10//A61K31/00,
PC A61K38/00,A61K48/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC

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Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
Db 16 TAAAAA 1

RESULT 136
AR183909/c
LOCUS AR183909 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2 from patent US 6342376.
ACCESSION AR183909
VERSION AR183909.1 GI:20227878
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kozian,D. and Reuner,B.
TITLE Two-color differential display as a method for detecting regulated
genes
JOURNAL Patent: US 6342376-A 2 29-JAN-2002;
FEATURES
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/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 15.2; DB 1; Length 17;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
Db 16 BAAAAA 1

RESULT 137
AR429726/c
LOCUS AR429726 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6645741.
ACCESSION AR429726
VERSION AR429726.1 GI:40190064
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kozian,D. and Reuner,B.
TITLE Two-color differential display as a method for detecting regulated
genes
JOURNAL Patent: US 6645741-A 2 11-NOV-2003;
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.0%; Score 15.2; DB 1; Length 17;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
Db 16 BAAAAA 1
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[illegible]

<p>: </p>					
Db	16 BAAAAAAAAAAAAA 1				
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LOCUS	AR029402	Sequence 3 from patent US 5859233.	15 bp	DNA	linear
DEFINITION	AR029402	Sequence 3 from patent US 5859233.	15 bp	DNA	linear
ACCESSION	AR029402	Sequence 3 from patent US 5859233.	15 bp	DNA	linear
VERSION	AR029402.1	GI:5941375			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N., Nelson,J.S. and Schultz,R.G.				
TITLE	Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates				
JOURNAL	Patent: US 5859233-A 3 12-JAN-1999;				
FEATURES	Location/Qualifiers				
source	1..15				
Query Match	1.0%; Score 15; DB 1; Length 15;				
Best Local Similarity	100.0%; Pred. No. 86;				
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
<p>QY 1481 AAAAAAAAAAAAAA 1495</p>					
Db	15 AAAAAAAAAAAAAA 1				
<p>RESULT 139</p>					
AR029403	AR029403	Sequence 4 from patent US 5859233.	15 bp	DNA	linear
LOCUS	AR029403	Sequence 4 from patent US 5859233.	15 bp	DNA	linear
DEFINITION	AR029403	Sequence 4 from patent US 5859233.	15 bp	DNA	linear
ACCESSION	AR029403	Sequence 4 from patent US 5859233.	15 bp	DNA	linear
VERSION	AR029403.1	GI:5941376			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N., Nelson,J.S. and Schultz,R.G.				
TITLE	Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates				
JOURNAL	Patent: US 5859233-A 4 12-JAN-1999;				
FEATURES	Location/Qualifiers				
source	1..15				
Query Match	1.0%; Score 15; DB 1; Length 15;				
Best Local Similarity	100.0%; Pred. No. 86;				
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
<p>QY 1481 AAAAAAAAAAAAAA 1495</p>					
Db	15 AAAAAAAAAAAAAA 1				
<p>RESULT 140</p>					
AR034895/c	AR034895	Sequence 10 from patent US 5869643.	15 bp	DNA	linear
LOCUS	AR034895	Sequence 10 from patent US 5869643.	15 bp	DNA	linear
DEFINITION	AR034895	Sequence 10 from patent US 5869643.	15 bp	DNA	linear
ACCESSION	AR034895	Sequence 10 from patent US 5869643.	15 bp	DNA	linear
VERSION	AR034895.1	GI:5950500			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N., Nelson,J.S. and Schultz,R.G.				
TITLE	Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates				
JOURNAL	Patent: US 5859233-A 3 12-JAN-1999;				
FEATURES	Location/Qualifiers				
source	1..15				
Query Match	1.0%; Score 15; DB 1; Length 15;				
Best Local Similarity	100.0%; Pred. No. 86;				
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
<p>QY 1481 AAAAAAAAAAAAAA 1495</p>					
Db	1 AAAAAAAAAAAAAA 15				
<p>RESULT 141</p>					
AR034898	AR034898	Sequence 16 from patent US 5869643.	15 bp	DNA	linear
LOCUS	AR034898	Sequence 16 from patent US 5869643.	15 bp	DNA	linear
DEFINITION	AR034898	Sequence 16 from patent US 5869643.	15 bp	DNA	linear
ACCESSION	AR034898	Sequence 16 from patent US 5869643.	15 bp	DNA	linear
VERSION	AR034898.1	GI:5950503			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Chatelain,F. and Kumarev,V.				
TITLE	Process for preparing polynucleotides on a solid support in a tightly packed bed				
JOURNAL	Patent: US 5869643-A 16 09-FEB-1999;				
FEATURES	Location/Qualifiers				
source	1..15				
Query Match	1.0%; Score 15; DB 1; Length 15;				
Best Local Similarity	100.0%; Pred. No. 86;				
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
<p>QY 1481 AAAAAAAAAAAAAA 1495</p>					
Db	1 AAAAAAAAAAAAAA 15				
<p>RESULT 142</p>					
AR048768	AR048768	Sequence 2 from patent US 5821354.	15 bp	DNA	linear
LOCUS	AR048768	Sequence 2 from patent US 5821354.	15 bp	DNA	linear
DEFINITION	AR048768	Sequence 2 from patent US 5821354.	15 bp	DNA	linear
ACCESSION	AR048768	Sequence 2 from patent US 5821354.	15 bp	DNA	linear
VERSION	AR048768.1	GI:5971111			

RESULT 143	AR049970/c	AR049970	Sequence 3 from patent US 5824793.	15 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR049970	Sequence 3 from patent US 5824793.					
DEFINITION	AR049970	Sequence 3 from patent US 5824793.					
ACCESSION	AR049970.1	GI:5971962					
VERSION	AR049970.1	GI:5971962					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 15)						
AUTHORS	Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N., Nelson,J.S. and Schultz,R.G.						
TITLE	Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates						
JOURNAL	Patent: US 5824793-A 3 20-OCT-1998;						
FEATURES	Location/Qualifiers						
source	1. .15						
Query Match	1.0%; Score 15; DB 1; Length 15;						
Best Local Similarity	100.0%; Pred. No. 86;						
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1481 AAAAAAAAAAAAAA 1495						
Db	15 AAAAAAAAAAAAAA 1						
RESULT 144	AR049971	AR049971	Sequence 4 from patent US 5824793.	15 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR049971	Sequence 4 from patent US 5824793.					
DEFINITION	AR049971	Sequence 4 from patent US 5824793.					
ACCESSION	AR049971.1	GI:5971963					
VERSION	AR049971.1	GI:5971963					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 15)						
AUTHORS	Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N., Nelson,J.S. and Schultz,R.G.						
TITLE	Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates						
JOURNAL	Patent: US 5824793-A 4 20-OCT-1998;						
FEATURES	Location/Qualifiers						
source	1. .15						
Query Match	1.0%; Score 15; DB 1; Length 15;						
Best Local Similarity	100.0%; Pred. No. 86;						
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1481 AAAAAAAAAAAAAA 1495						
Db	15 AAAAAAAAAAAAAA 1						
RESULT 145	AR056157/c	AR056157	Sequence 361 from patent US 5837542.	15 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR056157/c	Sequence 361 from patent US 5837542.					
DEFINITION	AR056157	Sequence 361 from patent US 5837542.					
ACCESSION	AR056157	Sequence 361 from patent US 5837542.					
VERSION	AR056157.1	GI:5981734					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 15)						
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.						
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes						
JOURNAL	Patent: US 5837542-A 361 17-NOV-1998;						
FEATURES	Location/Qualifiers						
source	1. .15						
Query Match	1.0%; Score 15; DB 1; Length 15;						
Best Local Similarity	100.0%; Pred. No. 86;						
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1481 AAAAAAAAAAAAAA 1495						
Db	15 AAAAAAAAAAAAAA 1						
RESULT 146	AR056158/c	AR056158	Sequence 362 from patent US 5837542.	15 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR056158/c	Sequence 362 from patent US 5837542.					
DEFINITION	AR056158	Sequence 362 from patent US 5837542.					
ACCESSION	AR056158	Sequence 362 from patent US 5837542.					
VERSION	AR056158.1	GI:5981735					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 15)						
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.						
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes						
JOURNAL	Patent: US 5837542-A 362 17-NOV-1998;						
FEATURES	Location/Qualifiers						
source	1. .15						
Query Match	1.0%; Score 15; DB 1; Length 15;						
Best Local Similarity	100.0%; Pred. No. 86;					</	


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RESULT 148
AR084516
LOCUS          AR084516          15 bp      DNA          linear      PAT 01-SEP-2000
DEFINITION     Sequence 5 from patent US 5981185.
ACCESSION      AR084516
VERSION        AR084516.1  GI:10011287
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE         Oligonucleotide repeat arrays
JOURNAL       Patent: US 5981185-A 5 09-NOV-1999;
FEATURES      Location/Qualifiers
                source
                1. .15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 149
AR084520/c
LOCUS          AR084520          15 bp      DNA          linear      PAT 01-SEP-2000
DEFINITION     Sequence 9 from patent US 5981185.
ACCESSION      AR084520
VERSION        AR084520.1  GI:10011291
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE         Oligonucleotide repeat arrays
JOURNAL       Patent: US 5981185-A 9 09-NOV-1999;
FEATURES      Location/Qualifiers
                source
                1. .15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 150
AR105981/c
LOCUS          AR105981          15 bp      DNA          linear      PAT 14-FEB-2001
DEFINITION     Sequence 4 from patent US 6103474.
ACCESSION      AR105981
VERSION        AR105981.1  GI:12820046
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Dellinger,D.J., Dahm,S.C., Ilesley,D.D., Ach,R.A. and Troll,M.A.
TITLE         Hybridization assay signal enhancement
JOURNAL       Patent: US 6103474-A 4 15-AUG-2000;
FEATURES      Location/Qualifiers
                source
                1. .15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 1
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match    1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 151
AR113915/c
LOCUS          AR113915          15 bp      DNA          linear      PAT 16-MAY-2001
DEFINITION     Sequence 361 from patent US 6132967.
ACCESSION      AR113915
VERSION        AR113915.1  GI:14094237
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE         Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL       Patent: US 6132967-A 361 17-OCT-2000;
FEATURES      Location/Qualifiers
                source
                1. .15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 152
AR113916/c
LOCUS          AR113916          15 bp      DNA          linear      PAT 16-MAY-2001
DEFINITION     Sequence 362 from patent US 6132967.
ACCESSION      AR113916
VERSION        AR113916.1  GI:14094238
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE         Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL       Patent: US 6132967-A 362 17-OCT-2000;
FEATURES      Location/Qualifiers
                source
                1. .15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 153
AR105981/c
LOCUS          AR105981          15 bp      DNA          linear      PAT 14-FEB-2001
DEFINITION     Sequence 4 from patent US 6103474.
ACCESSION      AR105981
VERSION        AR105981.1  GI:12820046
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Dellinger,D.J., Dahm,S.C., Ilesley,D.D., Ach,R.A. and Troll,M.A.
TITLE         Hybridization assay signal enhancement
JOURNAL       Patent: US 6103474-A 4 15-AUG-2000;
FEATURES      Location/Qualifiers
                source
                1. .15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 153
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ARI170375      ARI170375      15 bp      DNA      linear      PAT 17-DEC-2001
LOCUS          Sequence 1 from patent US 6291438.
ACCESSION      ARI170375
VERSION        ARI170375.1 GI:117908334
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Wang,J.H.
TITLE        Antiviral anticancer poly-substituted phenyl derivatized
              oligoribonucleotides and methods for their use
JOURNAL        Patent: US 6291438-A 1 18-SEP-2001;
FEATURES      Location/Qualifiers
               source      1..15
                   /organism="unknown"
                   /mol_type="unassigned DNA"
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1481 AAAAAAAAAAAAAA 1495
Db      1 AAAAAAAAAAAAAA 15

RESULT 154
E08522/c
LOCUS          PCR primer.
DEFINITION      E08522.1 GI:2176637
ACCESSION      E08522.1 GI:2176637
VERSION        JP 1994335389-A/7.
KEYWORDS      unidentified
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,
              Tsubura,H., Tanaka,H. and Ishiguro,Y.
TITLE        S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
JOURNAL        Patent: JP 1994335389-A 7 06-DEC-1994;
              KAGOME CO LTD
COMMENT      OS None
              OC Artificial sequences.
              PN JP 1994335389-A/7
              PD 06-DEC-1994
              PF 27-MAY-1993 JP 1993126286
              PI TEI ITSUIRU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI
              OTA AKINORI,
              PI TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI
              PC C12N9/22,C12N15/52;
              CC strandedness: Single;
              CC topology: Linear;
              FH Key      Location/Qualifiers
              FT source      1..15
                  /organism='Artificial sequences'.
FEATURES      source      1..15
                  /organism="unidentified"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32644"
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1481 AAAAAAAAAAAAAA 1495
Db      15 AAAAAAAAAAAAAA 1

RESULT 155
E12591/c
LOCUS          PRIMER.
DEFINITION      E12591.1 GI:3251423
ACCESSION      E12591.1 GI:3251423
VERSION        JP 1997028381-A/8.
KEYWORDS      unidentified
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Tei,I., Minami,K. and Takagi,M.
TITLE        S- RIBONUCLEASE GENE AND PROMOTER SEQUENCE
JOURNAL        Patent: JP 1997028381-A 8 04-FEB-1997;
              TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI
FEATURES      OS None
              OC Artificial sequences.
              PN JP 1997028381-A/8
              PD 04-FEB-1997
              PF 24-JUL-1995 JP 1995187557
              PI TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI PC
              C12N15/09,C07H21/04,C12N1/21//A01H1/00,C12N5/10,C12N9/22, PC
              (C12N1/21,
              PC C12R1.19);
              CC strandedness: Single;
              CC topology: Linear;
              CC hypothetical: No;
              FH Key      Location/Qualifiers
              FT source      1..15
                  /organism='Artificial sequences'.
FEATURES      source      1..15
                  /organism="unidentified"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32644"
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1481 AAAAAAAAAAAAAA 1495
Db      15 AAAAAAAAAAAAAA 1

RESULT 156
I29068
LOCUS          Sequence 6 from patent US 5576427.
DEFINITION      I29068
ACCESSION      I29068
VERSION        I29068.1 GI:1819859
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Cook,P.D., Delecki,D.J. and Guinosso,C.
TITLE        Acyclic nucleoside analogs and oligonucleotide sequences containing
              them
JOURNAL        Patent: US 5576427-A 6 19-NOV-1996;
FEATURES      Location/Qualifiers
               source      1..15
                   /organism="unknown"
                   /mol_type="unassigned DNA"
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1481 AAAAAAAAAAAAAA 1495
Db      15 AAAAAAAAAAAAAA 1
```

Db 1 |||||AAAAAAAAAAAA 15
RESULT 157
LOCUS I38641/c I38641 15 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5614617.
ACCESSION I38641
VERSION I38641.1 GI:2084695
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cook, P.D. and Sanghvi, Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that
detect and modulate gene expression
JOURNAL Patent: US 5614617-A 1 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
RESULT 158
LOCUS AR180117 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 185 from patent US 633152.
ACCESSION AR180117
VERSION AR180117.1 GI:20222150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 633152-A 185 25-DEC-2001;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
RESULT 159
LOCUS AR180526 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 594 from patent US 633152.
ACCESSION AR180526
VERSION AR180526.1 GI:20222559
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W.

TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 633152-A 594 25-DEC-2001;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1390 CATGCACCTGTCCTT 1404
Db 1 CATGCACCTGTCCTT 15
RESULT 160
LOCUS AR180723 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 791 from patent US 633152.
ACCESSION AR180723
VERSION AR180723.1 GI:20222756
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 633152-A 791 25-DEC-2001;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1475 CATGCTAAAAAAA 1489
Db 1 CATGCTAAAAAAA 15
RESULT 161
LOCUS AR200476/c AR200476 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 19 from patent US 6357163.
ACCESSION AR200476
VERSION AR200476.1 GI:20251364
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt, O., Egholm, M., Nielsen, P.E. and Berg, R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical
procedures
JOURNAL Patent: US 6357163-A 19 19-MAR-2002;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

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RESULT 162
LOCUS AR200477 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 20 from patent US 6357163.
ACCESSION AR200477
VERSION AR200477.1 GI:20251365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical
JOURNAL procedures
FEATURES Patent: US 6357163-A 20 19-MAR-2002;
Location/Qualifiers
source
1. .15
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 163
LOCUS AR222461 15 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 21 from patent US 6429300.
ACCESSION AR222461
VERSION AR222461.1 GI:23329992
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 21 06-AUG-2002;
FEATURES Location/Qualifiers
source
1. .15
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 164
LOCUS AR266630/c 15 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 68 from patent US 6495319.
ACCESSION AR266630
VERSION AR266630.1 GI:29695694
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 68 17-DEC-2002;
FEATURES Location/Qualifiers
source
1. .15
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 165
LOCUS AR371280/c 15 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 17 from patent US 6395474.
ACCESSION AR371280
VERSION AR371280.1 GI:34608212
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 17 28-MAY-2002;
FEATURES Location/Qualifiers
source
1. .15
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 166
LOCUS AR371281 15 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 18 from patent US 6395474.
ACCESSION AR371281
VERSION AR371281.1 GI:34608213
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 18 28-MAY-2002;
FEATURES Location/Qualifiers
source
1. .15
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 167
LOCUS AR410213/c 15 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6635452.
ACCESSION AR410213
```

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VERSION AR410213.1 GI:40161460
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
TITLE Releasable nonvolatile mass label molecules
JOURNAL Patent: US 6635452-A 9 21-OCT-2003;
FEATURES
source
1. .15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 168
AX004877/c
LOCUS AX004877 15 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 6 from Patent WO9910527.
ACCESSION AX004877
VERSION AX004877.1 GI:9928277
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bayer,E. and Schewitz,J.
TITLE Method for isolating anionic organic substances from aqueous
systems using cationic polymer nanoparticles
JOURNAL Patent: WO 9910527-A 6 04-MAR-1999;
SUEDEDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' palmityl modified oligonucleotide"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 169
AX026066/c
LOCUS AX026066 15 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 4 from Patent WO0028046.
ACCESSION AX026066
VERSION AX026066.1 GI:10187502
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Marraccini,P. and Rogers,J.
TITLE Coffee arabica mannase
JOURNAL Patent: WO 0028046-A 4 18-MAY-2000;
NESTLE SA (CH); MARRACCINI PIERRE (FR); ROGERS JOHN (FR)
FEATURES
source
1. .15
/organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligo dA"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 170
AX048407/c
LOCUS AX048407 15 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 6 from Patent WO0071747.
ACCESSION AX048407
VERSION AX048407.1 GI:12225571
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Bургstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 6 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Region A"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 171
AX106973
LOCUS AX106973 15 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 26 from Patent WO0125442.
ACCESSION AX106973
VERSION AX106973.1 GI:13922522
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
TITLE Dna polymerase lambda and uses thereof
JOURNAL Patent: WO 0125442-A 26 12-APR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligo dA"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
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Db 1 AAAAAAAAAAAAAA 15

RESULT 172
AX127272/c
LOCUS AX127272 15 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 3 from Patent EP1111068.
ACCESSION AX127272
VERSION AX127272.1 GI:14133346
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
TITLE Branched compound for use in nucleic acid detection and analysis
JOURNAL reactions
        Patent: EP 1111068-A 3 27-JUN-2001;
        LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES
    source
        1..15
            Location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
    misc_structure 1
        /note="(NH2-C6-ttt)2-branch-"
    misc_feature 15
        /note="NH2
        kunstliche"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 173
AX127273/c
LOCUS AX127273 15 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 4 from Patent EP1111068.
ACCESSION AX127273
VERSION AX127273.1 GI:14133347
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
TITLE Branched compound for use in nucleic acid detection and analysis
JOURNAL reactions
        Patent: EP 1111068-A 4 27-JUN-2001;
        LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES
    source
        1..15
            Location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
    misc_structure 1
        /note="(dt-COOH)2-branch-"
    misc_feature 15
        /note="NH2
        kunstliche"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 174
AX180140/c
LOCUS AX180140 15 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 3 from Patent WO0146464.
ACCESSION AX180140
VERSION AX180140.1 GI:15132181
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
TITLE Branched compound for use in nucleic acid detection and analysis
JOURNAL reactions
        Patent: WO 0146464-A 3 28-JUN-2001;
        LION Bioscience AG (DE)
FEATURES
    Location/Qualifiers
        1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="stem of branched oligonucleotide - base 1
            modified-Modification is (NH2-C6-TTT)2-branch-"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 175
AX180141/c
LOCUS AX180141 15 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 4 from Patent WO0146464.
ACCESSION AX180141
VERSION AX180141.1 GI:15132182
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
TITLE Branched compound for use in nucleic acid detection and analysis
JOURNAL reactions
        Patent: WO 0146464-A 4 28-JUN-2001;
        LION Bioscience AG (DE)
FEATURES
    Location/Qualifiers
        1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="stem of branched oligonucleotide - base 1
            modified-Modification is (dt-COOH)2-branch-"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 176
AX429224/c
LOCUS AX429224 15 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 1 from Patent EP1201765.
ACCESSION AX429224
```

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VERSION AX429224.1 GI:21540537
SOURCE   synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS  Schubart,D., Habenberger,P., Stein-Cerlach,M. and Bevec,D.
TITLE    Cellular kinases involved in cytomagalovirus infection and their
          inhibition
JOURNAL  Patent: EP 1201765-A 1 02-MAY-2002;
          Axxima Pharmaceuticals Aktiengesellschaft (DE)
FEATURES Location/Qualifiers
          source
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="N/A"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 177
AX525141
LOCUS      AX525141
DEFINITION Sequence 1 from Patent WO02066675.
ACCESSION AX525141
VERSION   AX525141.1 GI:25170126
KEYWORDS  synthetic construct
          synthetic construct
          artificial sequences.
ORGANISM  1
REFERENCE 1
AUTHORS   Kahmann,S. and Mueller,O.
TITLE     Methods for detecting mutations
JOURNAL   Patent: WO 02066675-A 1 29-AUG-2002;
          Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES  Location/Qualifiers
          source
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="lys-Biotin"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 15

RESULT 178
AX525143
LOCUS      AX525143
DEFINITION Sequence 3 from Patent WO02066675.
ACCESSION AX525143
VERSION   AX525143.1 GI:25170128
KEYWORDS  synthetic construct
          synthetic construct
          artificial sequences.
ORGANISM  1
REFERENCE 1
AUTHORS   Kahmann,S. and Mueller,O.
TITLE     Methods for detecting mutations
JOURNAL   Patent: WO 02066675-A 3 29-AUG-2002;
          Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)

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FEATURES Location/Qualifiers
          source
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="lys-Digoxigenin"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 15

RESULT 179
AX633197/c
LOCUS      AX633197
DEFINITION Sequence 336 from Patent EP1260586.
ACCESSION AX633197
VERSION   AX633197.1 GI:28468811
KEYWORDS  unidentified
          unidentified
          unclassified.
ORGANISM  1
REFERENCE 1
AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
          Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
          Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
          Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
          Woolf,T.
TITLE     Method and reagent for inhibiting the expression of disease related
          genes
JOURNAL   Patent: EP 1260586-A 336 27-NOV-2002;
          RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES  Location/Qualifiers
          source
            1..15
            /organism="unidentified"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32644"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 180
AX633199/c
LOCUS      AX633199
DEFINITION Sequence 338 from Patent EP1260586.
ACCESSION AX633199
VERSION   AX633199.1 GI:28468813
KEYWORDS  unidentified
          unidentified
          unclassified.
ORGANISM  1
REFERENCE 1
AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
          Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
          Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
          Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
          Woolf,T.
TITLE     Method and reagent for inhibiting the expression of disease related
          genes
JOURNAL   Patent: EP 1260586-A 338 27-NOV-2002;
          RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES  Location/Qualifiers
          source
            1..15

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/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 181
AX696087/c
LOCUS      AX696087      15 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 6 from Patent WO03008643.
ACCESSION  AX696087
VERSION     AX696087.1 GI:29419249
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Hammonds,T.R.
TITLE       Method and polynukleotides for assaying the activity of a dna
            modifying enzyme
JOURNAL     Patent: WO 03008643-A 6 30-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES    Location/Qualifiers
            source          1..15
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Polynucleotide 6"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 182
AX711176
LOCUS      AX711176      15 bp      RNA      linear      PAT 11-APR-2003
DEFINITION Sequence 476 from Patent EP1288296.
ACCESSION  AX711176
VERSION     AX711176.1 GI:29787557
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Draper,K.G., Mcswiggen,J.A., Holecsek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
TITLE       Method and reagent for inhibiting HBV viral replication
JOURNAL     Patent: EP 1288296-A 476 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
            source          1..15
                        /organism="synthetic construct"
                        /mol_type="unassigned RNA"
                        /db_xref="taxon:32630"
                        /note="Polyadenylation region"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
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Db 1 AAAAAAAAAAAAAA 15

RESULT 183
BD074424/c
LOCUS      BD074424      15 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Polynucleotide encoding polypeptide having heparanase activity and
            expression of the polypeptide in induced cell.
ACCESSION  BD074424
VERSION     BD074424.1 GI:22620027
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Pecker,I., Vlodavsky,I. and Elena,F.
TITLE       Polynucleotide encoding polypeptide having heparanase activity and
            expression of the polypeptide in induced cell
JOURNAL     Patent: JP 2001514855-A 5 18-SEP-2001;
            INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
            & DEVELOPMENT LTD
COMMENT     OS Nucleic acid
            PN JP 2001514855-A/5
            PD 18-SEP-2001
            PF 31-AUG-1998 JP 2000508806
            PR 02-SEP-1997 US 08/922170,02-JUL-1998 US 09/109386 PI
            IRIS PECKER,ISRAEL VLODAVSKY,FEINSTEIN ELENA
            PC C12N15/09,A61K38/00,A61P17/00,A61P29/00,A61P35/00, PC
            A61P37/00,
            PC A61P43/00,C12N5/10,C12N9/24,C12Q1/68,G01N33/15,G01N33/50// PC
            A61K39/395,
            PC A61K39/395,C12N15/00,A61K37/02,C12N5/00
            CC Polynucleotide encoding polypeptide having
            heparanase activity
            CC expression of the polypeptide in induced cell FH Key
            FT source      1..15
                        /organism='Nucleic acid'.
                        Location/Qualifiers
                        1..15
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 184
BD084687/c
LOCUS      BD084687      15 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Releasable nonvolatile mass-label molecules.
ACCESSION  BD084687
VERSION     BD084687.1 GI:22630297
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Montforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
TITLE       Releasable nonvolatile mass-label molecules
JOURNAL     Patent: JP 2001524808-A 5 04-DEC-2001;
            GENETRACE SYSTEMS INC
COMMENT     OS Artificial Sequence
            PN JP 2001524808-A/5
            PD 04-DEC-2001
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```

PF 10-DEC-1997 JP 1998526924
PR 10-DEC-1996 US 60/033037,16-MAY-1997 US 60/046719 PI
JOSEPH A MONTFORT,CHRISTOPHER H BECKER,DANIEL J POLLART, PI
THOMAS A SHALAR
PC C12Q1/68,G01N15/06,G01N33/53,G01N33/542,C12P19/34,C12M1/00, PC
B01D59/44,
PC H01J49/00,C07H21/04,C07K15/26,C07K15/28
CC Description of Artificial Sequence: oligo dT15 primer FH Key
FT source 1..15
FT Location/Qualifiers
FEATURES
source
1..15
/organism="Artificial Sequence".
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
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Db 15 AAAAAAAAAAAAAA 1

BD184668 15 bp DNA linear PAT 17-JUN-2003
Method and detector for identifying subtypes of human papilloma
viruses.
ACCESSION BD184668
VERSION BD184668.1 GI:31876868
KEYWORDS JP 2002360271-A/647.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
Huang,C., Hau,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
TITLE Method and detector for identifying subtypes of human papilloma
JOURNAL Patent: JP 2002360271-A 647 17-DEC-2002;
KING CAR FOOD INDUSTRIAL CO LTD
OS Artificial Sequence
PN JP 2002360271-A/647
PD 17-DEC-2002
PF 28-NOV-2001 JP 2001362595
PR 04-MAY-2001 TW 90110785
PI CHING-FEE LING,RUEY-WEN LIN,ZHOU-MENG YOO,XIN-HSUAN HUANG,BOW-
PI HAENG LEE,
PI SHENG-HSIUNG LEE,YI-JU LIN,CI-CHUNG HUANG,HAN-CHANG HSU,CHA-
PI WEN SHI,
PI CHIH-XIN YEH,YI-PENG CAO,CHIH-LONG PAN
PC C12N15/09,C12N15/09,C12M1/34,C12Q1/04,C12Q1/42,C12Q1/68 PC
,C12Q1/70,G01N21/64,
PC G01N33/53,G01N33/574,G01N33/58,G01N37/00// (C12M1/34,C12R1:93),
PC C12Q1/70,C12R1:93,C12N15/00,C12N15/00
CC Added sequence for 3' end labeling of oligonucleic acid. FH
Key Location/Qualifiers
FT source 1..15
FT /organism="Artificial Sequence".
FEATURES
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

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Db 15 AAAAAAAAAAAAAA 1

RESULT 186
LOCUS BD206432/c
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD206432
VERSION BD206432.1 GI:33016202
KEYWORDS JP 2002512791-A/22.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 22 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/22
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
FT /organism="Hepatitis virus (hepatitis C virus)"
FEATURES
source
1..15
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 187
LOCUS BD209488/c
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD209488
VERSION BD209488.1 GI:33019258
KEYWORDS JP 2002512791-A/3078.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 3078 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/3078

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PD 08-MAY-2002
 PF 26-APR-1999 JP 2000545991
 PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
 25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
 LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
 PAVCO,
 PI DENNIS MACEJAK
 PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
 PC A61K37/66,
 PC C12N15/00
 CC Enzymatic nucleic acid treatment of diseases or conditions CC
 related to
 CC hepatitis C virus infection.
 FH Key Location/Qualifiers
 FT source 1..15
 FT /organism='Hepatitis virus (hepatitis C FT
 virus)'
 FEATURES
 source Location/Qualifiers
 1..15
 /organism='unidentified'
 /mol_type='genomic RNA'
 /db_xref='taxon:32644'
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1
 RESULT 188
 AR221693/c
 LOCUS 16 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 3 from patent US 6426408.
 ACCESSION AR221693
 VERSION AR221693.1 GI:23328765
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
 TITLE Covalently linked oligonucleotide minor groove binder conjugates
 JOURNAL Patent: US 6426408-A 3 30-JUL-2002;
 FEATURES Location/Qualifiers
 source 1..16
 /organism='unknown'
 /mol_type='genomic DNA'
 Query Match 1.0%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1
 RESULT 189
 AR221694/c
 LOCUS 16 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 4 from patent US 6426408.
 ACCESSION AR221694
 VERSION AR221694.1 GI:23328766
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
 TITLE Covalently linked oligonucleotide minor groove binder conjugates

JOURNAL Patent: US 6426408-A 4 30-JUL-2002;
 FEATURES Location/Qualifiers
 source 1..16
 /organism='unknown'
 /mol_type='genomic DNA'
 Query Match 1.0%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1
 RESULT 190
 AR221695/c
 LOCUS 16 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 5 from patent US 6426408.
 ACCESSION AR221695
 VERSION AR221695.1 GI:23328767
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
 TITLE Covalently linked oligonucleotide minor groove binder conjugates
 JOURNAL Patent: US 6426408-A 5 30-JUL-2002;
 FEATURES Location/Qualifiers
 source 1..16
 /organism='unknown'
 /mol_type='genomic DNA'
 Query Match 1.0%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1
 RESULT 191
 AR221696/c
 LOCUS 16 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 6 from patent US 6426408.
 ACCESSION AR221696
 VERSION AR221696.1 GI:23328768
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
 TITLE Covalently linked oligonucleotide minor groove binder conjugates
 JOURNAL Patent: US 6426408-A 6 30-JUL-2002;
 FEATURES Location/Qualifiers
 source 1..16
 /organism='unknown'
 /mol_type='genomic DNA'
 Query Match 1.0%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1
 RESULT 192
 AR221697/c
 LOCUS 16 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 7 from patent US 6426408.
 ACCESSION AR221697
 VERSION AR221697.1 GI:23328769
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
 TITLE Covalently linked oligonucleotide minor groove binder conjugates
 JOURNAL Patent: US 6426408-A 7 30-JUL-2002;
 FEATURES Location/Qualifiers
 source 1..16
 /organism='unknown'
 /mol_type='genomic DNA'

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LOCUS AR221697 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6426408.
ACCESSION AR221697
VERSION AR221697.1 GI:23328769
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 7 30-JUL-2002;
FEATURES
    Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 193
LOCUS AR221698 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 8 from patent US 6426408.
ACCESSION AR221698
VERSION AR221698.1 GI:23328770
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 8 30-JUL-2002;
FEATURES
    Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 194
LOCUS AR221699 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6486308.
ACCESSION AR221699
VERSION AR221699.1 GI:27307449
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 3 26-NOV-2002;
FEATURES
    Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 195
LOCUS AR257439 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 4 from patent US 6486308.
ACCESSION AR257439
VERSION AR257439.1 GI:27307450
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 4 26-NOV-2002;
FEATURES
    Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 196
LOCUS AR257440 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6486308.
ACCESSION AR257440
VERSION AR257440.1 GI:27307451
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 5 26-NOV-2002;
FEATURES
    Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 197
LOCUS AR257441 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 6 from patent US 6486308.
ACCESSION AR257441
VERSION AR257441.1 GI:27307452
KEYWORDS
SOURCE
ORGANISM
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LOCUS AR221697 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6426408.
ACCESSION AR221697
VERSION AR221697.1 GI:23328769
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 7 30-JUL-2002;
FEATURES
    Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 193
LOCUS AR221698 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 8 from patent US 6426408.
ACCESSION AR221698
VERSION AR221698.1 GI:23328770
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 8 30-JUL-2002;
FEATURES
    Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 194
LOCUS AR221699 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6486308.
ACCESSION AR221699
VERSION AR221699.1 GI:27307449
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 3 26-NOV-2002;
FEATURES
    Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 195
LOCUS AR257439 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 4 from patent US 6486308.
ACCESSION AR257439
VERSION AR257439.1 GI:27307450
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 4 26-NOV-2002;
FEATURES
    Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 196
LOCUS AR257440 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6486308.
ACCESSION AR257440
VERSION AR257440.1 GI:27307451
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 5 26-NOV-2002;
FEATURES
    Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 197
LOCUS AR257441 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 6 from patent US 6486308.
ACCESSION AR257441
VERSION AR257441.1 GI:27307452
KEYWORDS
SOURCE
ORGANISM
```

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 6 26-NOV-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 198
LOCUS AR257442/c 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 7 from patent US 6486308.
ACCESSION AR257442
VERSION AR257442.1 GI:27307453
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 7 26-NOV-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 199
LOCUS AR257443/c 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 8 from patent US 6486308.
ACCESSION AR257443
VERSION AR257443.1 GI:27307454
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 8 26-NOV-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 200
LOCUS AX494458 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 223 from Patent WO02059256.
ACCESSION AX494458
VERSION AX494458.1 GI:23340068
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tuijinder,M., Telerman,A., Anson,R. and Susini,L.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 02059256-A 223 01-AUG-2002;
FEATURES MOLECULAR ENGINEES LAB (PR)
source
1..16
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1477 TGCTAAAAAAAAAA 1491
|||||
DB 2 TGCTAAAAAAAAAA 16

RESULT 201
LOCUS E34259/c 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION E34259
VERSION E34259.1 GI:18624264
KEYWORDS JP 2000106879-A/3.
SOURCE synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE Pollinosis-associated gene
JOURNAL Patent: JP 2000106879-A 3 18-APR-2000;
COMMENT GENOX RESEARCH INC
OS Artificial Sequence
PN JP 2000106879-A/3
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NING NO,
PI KOURU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC
FH Key Location/Qualifiers
FT source 1..17
/organism='Artificial Sequence'.
FEATURES
source
1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 15; DB 1; Length 17;

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 202
E34260/c
LOCUS E34260 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Follinosis-associated gene.
ACCESSION E34260
VERSION E34260.1 GI:18624265
KEYWORDS JP 200106879-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No.N. and Ogawa,K.
TITLE Follinosis-associated gene
JOURNAL Patent: JP 200106879-A 4 18-APR-2000;
GENOX RESEARCH INC
COMMENT OS Artificial Sequence
PN JP 200106879-A/4
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NING NO,
PI KAORU OGAWA
PC C12N15/09.A61K31/00.A61K39/36.A61K45/00.C12Q1/68.C12N15/00 CC

FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.

FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 203
E59657/c
LOCUS E59657 17 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for preparing nucleic acid sample for analyzing minor gene,
nucleic acid sample thus prepared and method for analyzing nucleic
acid sample by using the same, and reagent kit and analysis service
for using the same.
E59657
ACCESSION E59657.1 GI:13019451
VERSION E59657.1 GI:13019451
KEYWORDS JP 2000037193-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Takamichi,M., Tsuyoshi,F., Masaharu,K., Takashi,I. and Kazunori,O.
TITLE Method for preparing nucleic acid sample for analyzing minor gene,
nucleic acid sample thus prepared and method for analyzing nucleic
acid sample by using the same, and reagent kit and analysis service
for using the same
JOURNAL Patent: JP 2000037193-A 3 08-FEB-2000;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 204
AR187061/c
LOCUS AR187061 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2549 from patent US 6346398.
ACCESSION AR187061
VERSION AR187061.1 GI:20233026
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 2549 12-FEB-2002;
JOURNAL Location/Qualifiers
FEATURES source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 17 AAAAAAAAAAAAAA 3

RESULT 205
AR187064/c
LOCUS AR187064 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2552 from patent US 6346398.
ACCESSION AR187064
VERSION AR187064.1 GI:20233029
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: JP 2000037193-A 3 08-FEB-2000;

HITACHI LTD
OS Unidentified
PN JP 200037193-A/3
PD 08-FEB-2000
PF 19-MAY-1999 JP 1999138051
PR TAKAMICHI MATSUMURA, TSUYOSHI FUJITA, MASAHARU KIYAMA, PI
TAKASHI IRIE,
PI KAZUNORI OKANO
PC C12N15/09.C12Q1/68.C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Unidentified'.

FEATURES
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1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 204
AR187061/c
LOCUS AR187061 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2549 from patent US 6346398.
ACCESSION AR187061
VERSION AR187061.1 GI:20233026
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 2549 12-FEB-2002;
JOURNAL Location/Qualifiers
FEATURES source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 17 AAAAAAAAAAAAAA 3

RESULT 205
AR187064/c
LOCUS AR187064 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2552 from patent US 6346398.
ACCESSION AR187064
VERSION AR187064.1 GI:20233029
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: JP 2000037193-A 3 08-FEB-2000;
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JOURNAL Patent: US 6346398-A 2552 12-FEB-2002;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 206
LOCUS AR241830/c 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 118 from patent US 6472154.
ACCESSION AR241830
VERSION AR241830.1 GI:27287642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 118 29-OCT-2002;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 207
LOCUS AR256849/c 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6485916.
ACCESSION AR256849
VERSION AR256849.1 GI:27306475
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Muramatsu,T., Fujita,T., Kiyama,M., Irie,T. and Okano,K.
TITLE Preparation method of nucleic acid sample for rare expressed genes and analyzing method using the prepared nucleic acid samples thereby

JOURNAL Patent: US 6485916-A 3 26-NOV-2002;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

JOURNAL Patent: US 6346398-A 2552 12-FEB-2002;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 208
LOCUS AR266626/c 17 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 64 from patent US 6495319.
ACCESSION AR266626
VERSION AR266626.1 GI:29695690
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 64 17-DEC-2002;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 209
LOCUS AR285950 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 322 from patent US 6528640.
ACCESSION AR285950
VERSION AR285950.1 GI:29723546
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 322 04-MAR-2003;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CCCCCGCGCCCGCGC 104
Db 3 CCCCCGCGCCCGCGC 17

RESULT 210
LOCUS AR323671/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1073 from patent US 6566127.
ACCESSION AR323671
VERSION AR323671.1 GI:33709479
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1073 20-MAY-2003;
FEATURES Location/Qualifiers

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source      1. .17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
Best Local Similarity 1.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 17 AAAAAAAAAAAAAA 3

RESULT 211
AR323674/c
LOCUS      AR323674      17 bp      RNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 1076 from patent US 6566127.
ACCESSION  AR323674
VERSION     AR323674.1 GI:33709482
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 1076 20-MAY-2003;
FEATURES
source     1. .17
           /organism="unknown"
           /mol_type="unassigned RNA"

Query Match
Best Local Similarity 1.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 212
AR397940
LOCUS      AR397940      17 bp      RNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 321 from patent US 6617438.
ACCESSION  AR397940
VERSION     AR397940.1 GI:40135343
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
           Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE      Oligoribonucleotides with enzymatic activity
JOURNAL    Patent: US 6617438-A 321 09-SEP-2003;
FEATURES
source     1. .17
           /organism="unknown"
           /mol_type="unassigned RNA"

Query Match
Best Local Similarity 1.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CCGCGCGCGCGCGC 104
Db 3 CCGCGCGCGCGCGC 17

RESULT 213
AX692524/c
LOCUS      AX692524      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5256 from Patent EP1281758.
ACCESSION  AX692524
VERSION     AX692524.1 GI:29415482
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
           mdz12
JOURNAL    Patent: EP 1281758-A 5256 05-FEB-2003;
           Aeomica, Inc. (US)
FEATURES
source     1. .17
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match
Best Local Similarity 1.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 17 AAAAAAAAAAAAAA 3

RESULT 214
BD011731/c
LOCUS      BD011731      17 bp      DNA      linear      PAT 02-AUG-2002
DEFINITION 795, a novel gene related to pollen allergy.
ACCESSION  BD011731
VERSION     BD011731.1 GI:22091920
KEYWORDS    WO 0065050-A/3.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
           Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
           Takahashi,E. and Yokoi,A.
TITLE      795, a novel gene related to pollen allergy
JOURNAL    Patent: WO 0065050-A 3 02-NOV-2000;
           GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
           TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,
           YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
           TAKAHASHI, AKIRA YOKOI
COMMENT    OS Artificial Sequence
           FN WO 0065050-A/3
           PD 02-NOV-2000
           PF 26-APR-2000 WO 2000JP002734
           PR 27-APR-1999 JP 99P 120494
           PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
           PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
           PI NEI YOSHIDA,
           PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI
           C12N15/12, C07K14/47, C07K16/18, C12Q1/68, G01N33/50//A61K31/00, PC
           A61P37/00
CC Description of Artificial Sequence:Artificially Synthesized CC
FEATURES
source     1. .17
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"

Query Match
Best Local Similarity 1.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 215
BD011732/c
LOCUS 17 bp DNA linear PAT 02-AUG-2002
DEFINITION 795, a novel gene related to pollen allergy.
ACCESSION BD011732
VERSION BD011732.1 GI:22091921
KEYWORDS WO 0065050-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE 795, a novel gene related to pollen allergy
JOURNAL Patent: WO 0065050-A 4 02-NOV-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
COMMENT OS Artificial Sequence
PN WO 0065050-A/4
PD 02-NOV-2000
PF 26-APR-2000 WO 2000JP002734
PR 27-APR-1999 JP 99P 120494
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C07K14/47, C07K16/18, C12Q1/68, G01N33/50//A61K31/00, PC
A61P37/00
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence Location/Qualifiers
FH Key 1.17
source /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 217
BD091744/c
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 441, a novel gene related to pollen allergy.
ACCESSION BD091744
VERSION BD091744.1 GI:22637355
KEYWORDS WO 0073435-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
TITLE 441, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073435-A 4 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI
COMMENT OS Artificial Sequence
PN WO 0073435-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003190
PR 27-MAY-1999 JP 99P 148783
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA, KEIKO MATSUI
PC C12N15/10, C12Q1/68, G01N33/15, G01N33/50
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence Location/Qualifiers
FH Key 1.17
source /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 216
BD091743/c
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 441, a novel gene related to pollen allergy.
ACCESSION BD091743
VERSION BD091743.1 GI:22637354
KEYWORDS WO 0073435-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
TITLE 441, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073435-A 3 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI

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RESULT 218
BD091751/c
LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 465, a novel gene related to pollen allergy.
ACCESSION  BD091751
VERSION     BD091751.1 GI:22637362
KEYWORDS   WO 0073439-A/3.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
TITLE       465, a novel gene related to pollen allergy
JOURNAL     Patent: WO 0073439-A 3 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS Artificial Sequence
            PN WO 0073439-A/3
            PD 07-DEC-2000
            PF 18-MAY-2000 WO 2000JP003191
            PR 27-MAY-1999 JP 99P 148784
            PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI NEI YOSHIDA,
            PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K45/00 CC Description
            of Artificial Sequence:Artificially Synthesized CC Primer
            Sequence
FEATURES             Location/Qualifiers
     FH   Key       Location/Qualifiers
     source          1..17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     Query Match     1.0%; Score 15; DB 1; Length 17;
     Best Local Similarity 100.0%; Pred. No. 1.2e+02;
     Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
     QY 1481 AAAAAAAAAAAAAA 1495
     DB 16 AAAAAAAAAAAAAA 2

RESULT 220
BD091774/c
LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 787, a novel gene related to pollen allergy.
ACCESSION  BD091774
VERSION     BD091774.1 GI:22637385
KEYWORDS   WO 0073440-A/3.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
TITLE       787, a novel gene related to pollen allergy
JOURNAL     Patent: WO 0073440-A 3 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS Artificial Sequence
            PN WO 0073440-A/3
            PD 07-DEC-2000
            PF 18-MAY-2000 WO 2000JP003192
            PR 27-MAY-1999 JP 99P 148785
            PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI NEI YOSHIDA,
            PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC Description of
            Artificial Sequence:Artificially Synthesized CC Primer Sequence
            Sequence
FEATURES             Location/Qualifiers
     FH   Key       Location/Qualifiers
     source          1..17
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     Query Match     1.0%; Score 15; DB 1; Length 17;
     Best Local Similarity 100.0%; Pred. No. 1.2e+02;
     Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
     QY 1481 AAAAAAAAAAAAAA 1495
     DB 16 AAAAAAAAAAAAAA 2

RESULT 219
BD091752/c
LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 465, a novel gene related to pollen allergy.
ACCESSION  BD091752
VERSION     BD091752.1 GI:22637363
KEYWORDS   WO 0073439-A/4.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
TITLE       465, a novel gene related to pollen allergy
JOURNAL     Patent: WO 0073439-A 4 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS Artificial Sequence
            PN WO 0073439-A/4
            PD 07-DEC-2000
            PF 18-MAY-2000 WO 2000JP003191

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LOCUS BD091775 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 787, a novel gene related to pollen allergy.
ACCESSION BD091775
VERSION BD091775.1 GI:22637386
KEYWORDS WO 0073440-A/4.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE 787, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073440-A 4 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
OS Artificial Sequence
PN WO 0073440-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
NEI YOSHIDA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, C12N5/06, C07K14/415 CC Description of
Artificial Sequence: Artificially Synthesized CC Primer Sequence
FH Key Location/Qualifiers
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/mol_type="genomic DNA"
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Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
RESULT 222
LOCUS BD097335/c 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for examination for allergosis.
ACCESSION BD097335
VERSION BD097335.1 GI:22642910
KEYWORDS WO 0165259-A/7.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0165259-A 7 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
OBAYASHI, KEIKO MATSUI, HIROHISA SAITO
OS Artificial Sequence
PN WO 0165259-A/7
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PR 02-MAR-2000 JP 00P 61832
PI TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI OBAYASHI, KEIKO MATSUI, PI
HIROHISA SAITO
PC GOIN33/53, C12Q1/68, C12N15/12, G01N33/15, A01K67/027, A61K39/395,
A61P37/08
CC Description of Artificial Sequence: Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
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source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
RESULT 224
LOCUS BD142809/c 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of examining allergic disease.
ACCESSION BD142809
VERSION BD142809.1 GI:23237754
KEYWORDS WO 0224903-A/3.

Primer Sequence
FH Key 1..17 Location/Qualifiers
FT source /organism='Artificial Sequence'.
FEATURES
source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
RESULT 223
LOCUS BD097336/c 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for examination for allergosis.
ACCESSION BD097336
VERSION BD097336.1 GI:22642910
KEYWORDS WO 0165259-A/7.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0165259-A 7 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
OBAYASHI, KEIKO MATSUI, HIROHISA SAITO
OS Artificial Sequence
PN WO 0165259-A/7
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PR 02-MAR-2000 JP 00P 61832
PI TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI OBAYASHI, KEIKO MATSUI, PI
HIROHISA SAITO
PC GOIN33/53, C12Q1/68, C12N15/12, G01N33/15, A01K67/027, A61K39/395,
A61P37/08
CC Description of Artificial Sequence: Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
FT source /organism='Artificial Sequence'.
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source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
RESULT 224
LOCUS BD142809/c 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of examining allergic disease.
ACCESSION BD142809
VERSION BD142809.1 GI:23237754
KEYWORDS WO 0224903-A/3.

SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
 Tsujimoto,G. and Takahashi,E.
 TITLE Method of examining allergic disease
 JOURNAL Patent: WO 0224903-A 3 28-MAR-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
 NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
 OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
 TAKAHASHI
 COMMENT OS Artificial Sequence
 PN WO 0224903-A/3
 PD 28-MAR-2002
 PF 21-SEP-2001 WO 2001JP008246
 PR 25-SEP-2000 JP 00P 291318
 PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
 TAKESHI NAGASU,
 PI GOZO TSUJIMOTO, EIKI TAKAHASHI
 PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
 C12Q1/68,
 PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
 PC G01N33/15,
 PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
 CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
 FH Key Location/Qualifiers
 FT source 1..17
 FEATURES Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
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Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2

RESULT 225
 BD142810/c
 LOCUS 17 bp DNA linear PAT 18-SEP-2002
 DEFINITION Method of examining allergic disease.
 ACCESSION BD142810
 VERSION BD142810.1 GI:23237755
 KEYWORDS WO 0224903-A/4.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
 Tsujimoto,G. and Takahashi,E.
 TITLE Method of examining allergic disease
 JOURNAL Patent: WO 0224903-A 4 28-MAR-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
 NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
 OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
 TAKAHASHI
 COMMENT OS Artificial Sequence
 PN WO 0224903-A/4
 PD 28-MAR-2002
 PF 21-SEP-2001 WO 2001JP008246
 PR 25-SEP-2000 JP 00P 291318
 PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
 TAKESHI NAGASU,

PI GOZO TSUJIMOTO, EIKI TAKAHASHI
 PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
 C12Q1/68,
 PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
 PC G01N33/15,
 PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
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CC sequence primer
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 FT source 1..17
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Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2

RESULT 226
 BD143835/c
 LOCUS 17 bp DNA linear PAT 17-JAN-2003
 DEFINITION Method of examining allergic disease.
 ACCESSION BD143835
 VERSION BD143835.1 GI:27849593
 KEYWORDS JP 2002095500-A/3.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
 Tsujimoto,K.
 TITLE Method of examining allergic disease
 JOURNAL Patent: JP 2002095500-A 3 02-APR-2002;
 GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
 COMMENT OS Artificial Sequence
 PN JP 2002095500-A/3
 PD 02-APR-2002
 PF 25-SEP-2000 JP 200291316
 PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
 TAKESHI NAGASU,
 PI KOZO TSUJIMOTO
 PC C12Q1/68, A01K67/027, A61K31/7088, A61K31/711, A61K45/00, A61P37/08, PC
 C07K14/47,
 PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10 PC
 C12N15/09, C12P21/02,
 PC C12Q1/02, G01N33/15, G01N33/50//C12P21/08, C12N5/00, C12N5/00, PC
 C12N15/00
 CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
 FH Key Location/Qualifiers
 FT source 1..17
 FEATURES Location/Qualifiers
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 /organism="synthetic construct"
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 /db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2

RESULT 227
 BD143836/c

LOCUS 17 bp DNA linear PAT 17-JAN-2003

DEFINITION Method of examining allergic disease.

ACCESSION BD143836

VERSION BD143836.1 GI:27849594

KEYWORDS JP 2002095500-A/4.

SOURCE synthetic construct

ORGANISM artificial construct

REFERENCE 1 (bases 1 to 17)

AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Teujimoto,K.

TITLE Method of examining allergic disease

JOURNAL GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL

COMMENT OS Artificial Sequence

PN JP 2002095500-A/4

PD 02-APR-2002

PF 25-SEP-2000 JP 2000291316

PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI TAKESHI NAGASU,

PI KOZO TSUJIMOTO

PC C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC C07K14/47,

PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC ,C12N15/09,C12P21/02,

PC C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC C12N15/00

CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer

CC key Location/Qualifiers

FT source 1..17

FT /organism='Artificial Sequence'.

FEATURES

source

1..17 Location/Qualifiers

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QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2

RESULT 228
 BD167836/c

LOCUS 17 bp DNA linear PAT 17-JAN-2003

DEFINITION Method for examination of allergosis.

ACCESSION BD167836

VERSION BD167836.1 GI:27873648

KEYWORDS WO 0233122-A/3.

SOURCE synthetic construct

ORGANISM artificial construct

REFERENCE 1 (bases 1 to 17)

AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H. and Takahashi,E.

TITLE Method for examination of allergosis

JOURNAL Patent: WO 0233122-A 3 25-APR-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO,EIKI TAKAHASHI

COMMENT OS Artificial Sequence

PN WO 0233122-A/3

PD 25-APR-2002

PF 11-OCT-2001 WO 2001JP008937

PR 13-OCT-2000 JP 00P 314093

PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI TAKESHI NAGASU,

PI HIROHISA SAITO,EIKI TAKAHASHI

PC C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC A61K39/395,

PC A01K67/027//C07K16/18,C12N5/10

CC Description of Artificial Sequence:an artificially synthesized

CC primer anchor

CC key Location/Qualifiers

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FT /organism='Artificial Sequence'.

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/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2

RESULT 229
 BD167837/c

LOCUS 17 bp DNA linear PAT 17-JAN-2003

DEFINITION Method for examination of allergosis.

ACCESSION BD167837

VERSION BD167837.1 GI:27873649

KEYWORDS WO 0233122-A/4.

SOURCE synthetic construct

ORGANISM artificial construct

REFERENCE 1 (bases 1 to 17)

AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H. and Takahashi,E.

TITLE Method for examination of allergosis

JOURNAL Patent: WO 0233122-A 4 25-APR-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO,EIKI TAKAHASHI

COMMENT OS Artificial Sequence

PN WO 0233122-A/4

PD 25-APR-2002

PF 11-OCT-2001 WO 2001JP008937

PR 13-OCT-2000 JP 00P 314093

PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI TAKESHI NAGASU,

PI HIROHISA SAITO,EIKI TAKAHASHI

PC C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC A61K39/395,

PC A01K67/027//C07K16/18,C12N5/10

CC Description of Artificial Sequence:an artificially synthesized

CC primer anchor

CC key Location/Qualifiers

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FT /organism='Artificial Sequence'.

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FT source 1..17 /organism='Artificial Sequence'.
FT Location/Qualifiers
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  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 230
BD167908/c
LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD167908
VERSION BD167908.1 GI:27873720
KEYWORDS WO 0226962-A/7.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.
TITLE Method of examining allergic disease
JOURNAL GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0226962-A/7
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC C12Q1/68.
PC A01K67/027, A61K31/713, A61K45/00, A61P17/00, A61P37/08, PC GOIN33/15,
PC GOIN33/50//C12P21/08, (C12N5/10, C12R1.91), (C12P21/02, C12R1.91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
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  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 232
BD168112/c
LOCUS
DEFINITION Method for examination for allergosis.
ACCESSION BD168112
VERSION BD168112.1 GI:27873924
KEYWORDS WO 0233069-A/19.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergosis
JOURNAL GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA ODAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0233069-A/19

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LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD167909
VERSION BD167909.1 GI:27873721
KEYWORDS WO 0226962-A/8.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.
TITLE Method of examining allergic disease
JOURNAL GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0226962-A/8
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC C12Q1/68.
PC A01K67/027, A61K31/713, A61K45/00, A61P17/00, A61P37/08, PC GOIN33/15,
PC GOIN33/50//C12P21/08, (C12N5/10, C12R1.91), (C12P21/02, C12R1.91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
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  /organism="synthetic construct"
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Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 232
BD168112/c
LOCUS
DEFINITION Method for examination for allergosis.
ACCESSION BD168112
VERSION BD168112.1 GI:27873924
KEYWORDS WO 0233069-A/19.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergosis
JOURNAL GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA ODAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0233069-A/19

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PD 25-APR-2002
 PF 28-SEP-2001 WO 2001JP008574
 PR 13-OCT-2000 JP ODP 314093
 PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBIYASHI, PI
 TAKESHI NAGASU,
 PI HIROHISA SAITO
 PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC
 A61K39/395,
 PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
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CC primer sequence anchor
 CC key Location/Qualifiers
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 Db |||||

16 AAAAAAAAAAAAAA 2

RESULT 233
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 DEFINITION
 ACCESSION BD168113
 VERSION WO 0233069-A/20.
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.

TITLE Method for examination for allergosis
 JOURNAL Patent: WO 0233069-A 20 25-APR-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBIYASHI, TAKESHI NAGASU, HIROHISA SAITO
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 PN WO 0233069-A/20
 PD 25-APR-2002
 PF 28-SEP-2001 WO 2001JP008574
 PR 13-OCT-2000 JP ODP 314093
 PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBIYASHI, PI
 TAKESHI NAGASU,
 PI HIROHISA SAITO
 PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC
 A61K39/395,
 PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
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16 AAAAAAAAAAAAAA 2

RESULT 234
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 LOCUS Method of examining allergic disease. 17 bp DNA linear PAT 17-JAN-2003
 DEFINITION
 ACCESSION BD171178
 VERSION WO 0250269-A/3.
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.

TITLE Method of examining allergic disease
 JOURNAL Patent: WO 0250269-A 3 27-JUN-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU,
 GOZO TSUJIMOTO
 OS Artificial Sequence
 PN WO 0250269-A/3
 PD 27-JUN-2002
 PF 21-DEC-2001 WO 2001JP011286
 PR 21-DEC-2000 JP ODP 389476
 PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI
 TAKESHI NAGASU,
 PI GOZO TSUJIMOTO
 PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00,
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FEATURES

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 Db |||||

16 AAAAAAAAAAAAAA 2

RESULT 235
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 LOCUS Method of examining allergic disease. 17 bp DNA linear PAT 17-JAN-2003
 DEFINITION
 ACCESSION BD171179
 VERSION BD171179.1 GI:27876991
 KEYWORDS WO 0250269-A/4.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and

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Tsujiimoto,C.
Method of examining allergic disease
Patent: WO 0250269-A 4 27-JUN-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO
MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUI SUGITA, TAKESHI NAGASU,
GOZO TSUJIMOTO
OS Artificial Sequence
FN WO 0250269-A/4
PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
PR 21-DEC-2000 JP OOP 389476
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUI SUGITA, PI
TAKESHI NAGASU,
PI GOZO TSUJIMOTO
PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00,
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QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 236
AR141562/C
LOCUS AR141562 16 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6146855.
ACCESSION AR141562
VERSION AR141562.1 GI:15101078
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Williams, K. Leslie., Vesey, G., Veal, D., Ashbolt, N. John. and
Dorsch, M.
TITLE Method for the detection of viable Cryptosporidium parvum oocysts
JOURNAL Patent: US 6146855-A 2 14-NOV-2000;
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1476 ATGCTAAAAAAAAA 1491
DB 16 ATACTAAAAAAAAA 1
RESULT 237
E53842/C
LOCUS E53842 16 bp DNA linear PAT 31-JAN-2002
DEFINITION LUNX gene and method for detecting micrometastasis of cancer.
ACCESSION E53842
Tsujimoto, C.
Method of examining allergic disease
Patent: WO 0250269-A 4 27-JUN-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO
MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUI SUGITA, TAKESHI NAGASU,
GOZO TSUJIMOTO
OS Artificial Sequence
FN WO 0250269-A/4
PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
PR 21-DEC-2000 JP OOP 389476
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUI SUGITA, PI
TAKESHI NAGASU,
PI GOZO TSUJIMOTO
PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00,
A61P37/08,
PC C12Q1/68, G01N33/50
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CC primer sequence
CC Key Location/Qualifiers
FT source 1..17
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Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 236
AR141562/C
LOCUS AR141562 16 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6146855.
ACCESSION AR141562
VERSION AR141562.1 GI:15101078
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Williams, K. Leslie., Vesey, G., Veal, D., Ashbolt, N. John. and
Dorsch, M.
TITLE Method for the detection of viable Cryptosporidium parvum oocysts
JOURNAL Patent: US 6146855-A 2 14-NOV-2000;
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1476 ATGCTAAAAAAAAA 1491
DB 16 ATACTAAAAAAAAA 1
RESULT 237
E53842/C
LOCUS E53842 16 bp DNA linear PAT 31-JAN-2002
DEFINITION LUNX gene and method for detecting micrometastasis of cancer.
ACCESSION E53842

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E53842.1 GI:18633612
JP 2001078772-A/3.
unidentified
SOURCE unclassified.
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS Kadota, M., Fujiwara, Y., Watanabe, R. and Ozaki, K.
TITLE LUNX gene and method for detecting micrometastasis of cancer
JOURNAL Patent: JP 2001078772-A 3 27-MAR-2001;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Unidentified
PN JP 2001078772-A/3
PD 27-MAR-2001
PD 07-SEP-1999 JP 1999253186
PR MORITO KADOTA, YOSHIYUKI FUJIWARA, RYUJI WATANABE, KOICHI OZAKI
PC C12N15/09, C07K14/82, C07K16/32, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10, C12Q1/68,
PC G01N33/15, G01N33/50, G01N33/566, G01N33/574//A61K31/713, PC
A61K35/12, A61K35/76,
PC A61K39/395, A61K39/395, A61K48/00, A61P35/00, A61P35/04, C12P21/08,
PC C12N15/00,
PC C12N5/00,
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/db_xref='taxon:32644'
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Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1480 TAAAAAAAAAAAAA 1495
DB 16 TAAAAAAAAAAAAA 1
RESULT 238
AR029886
LOCUS AR029886 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 75 from patent US 5861244.
ACCESSION AR029886
VERSION AR029886.1 GI:5943100
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Wang, C.-G. and Heppburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 75 19-JAN-1999;
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Location/Qualifiers
/organism='unknown'
/mol_type='unassigned DNA'
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
DB 1 AAAAAAAAAAAAAA 14
RESULT 239
AR029887/C
LOCUS AR029887 14 bp DNA linear PAT 29-SEP-1999

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Query Match	Sequence 76 from patent US 5861244.	0.9%; Score 14; DB 1; Length 14;	DB 1; Length 14;
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Matches	AR029887.1 GI:5943101	0; Mismatches 0; Indels 0; Gaps 0;	
LOCUS	Unknown.		
DEFINITION	Unclassified.		
AUTHORS	Wang, C.-G. and Hepburn, A.G.		
TITLE	Genetic sequence assay using DNA triple strand formation		
JOURNAL	Patent: US 5861244-A 76 19-JAN-1999;		
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AUTHORS	1 (bases 1 to 14)		
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Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
LOCUS	AR147961		
DEFINITION	Sequence 130 from patent US 6225054.		
AUTHORS	Frudakis, T.N., Smith, J.M. and Reed, S.G.		
TITLE	Compositions and methods for the treatment and diagnosis of breast cancer		
JOURNAL	Patent: US 6225054-A 130 01-MAY-2001;		
FEATURES	Location/Qualifiers		
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Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
LOCUS	AR174026		
DEFINITION	Sequence 16 from patent US 6306624.		
AUTHORS	Petkovich, F. Martin., White, J.A., Beckett, B.R. and Jones, G.		
TITLE	Retinoid metabolizing protein		
JOURNAL	Patent: US 6306624-A 16 23-OCT-2001;		
FEATURES	Location/Qualifiers		
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Best Local Similarity	100.0%; Pred. No. 1.2e+02;		
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
LOCUS	BD237031		
DEFINITION	Compounds for remedy and diagnosis of lung cancer and method for using the same.		
AUTHORS	Reed, S.G., Lodes, M.J., Frudakis, T.N. and Mohanath, R.		
TITLE	Compounds for remedy and diagnosis of lung cancer and method for using the same		
JOURNAL	Patent: JP 2002516659-A 32 11-JUN-2002;		
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	/mol_type="genomic DNA"		
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Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
LOCUS	BD237464		
DEFINITION	Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof.		
AUTHORS	Reed, S.G., Lodes, M.J., Frudakis, T.N. and Mohanath, R.		
TITLE	Compounds for remedy and diagnosis of lung cancer and method for using the same		
JOURNAL	Patent: JP 2002516659-A 32 11-JUN-2002;		
FEATURES	Location/Qualifiers		
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Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
LOCUS	BD237464		
DEFINITION	Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof.		
AUTHORS	Reed, S.G., Lodes, M.J., Frudakis, T.N. and Mohanath, R.		
TITLE	Compounds for remedy and diagnosis of lung cancer and method for using the same		
JOURNAL	Patent: JP 2002516659-A 32 11-JUN-2002;		
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DEFINITION	Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof.		
AUTHORS	Reed, S.G., Lodes, M.J., Frudakis, T.N. and Mohanath, R.		
TITLE	Compounds for remedy and diagnosis of lung cancer and method for using the same		
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DEFINITION	Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof.		
AUTHORS	Reed, S.G., Lodes, M.J., Frudakis, T.N. and Mohanath, R.		
TITLE	Compounds for remedy and diagnosis of lung cancer and method for using the same		
JOURNAL	Patent: JP 2002516659-A 32 11-JUN-2002;		
FEATURES	Location/Qualifiers		


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Db 14 CTAACAAAAA 1

RESULT 248
LOCUS AR364948 14 bp DNA PAT 03-SEP-2003
DEFINITION Sequence 4 from patent US 5453496.
ACCESSION AR364948
VERSION AR364948.1 GI:34428168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
TITLE Polynucleotide phosphorodithioate
JOURNAL Patent: US 5453496-A 4 26-SEP-1995;
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA 1494
Db 14 AAAAAA 1

RESULT 249
LOCUS AR364949 14 bp DNA PAT 03-SEP-2003
DEFINITION Sequence 5 from patent US 5453496.
ACCESSION AR364949
VERSION AR364949.1 GI:34428169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
TITLE Polynucleotide phosphorodithioate
JOURNAL Patent: US 5453496-A 5 26-SEP-1995;
FEATURES
    source
        Location/Qualifiers
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                /mol_type="genomic DNA"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA 1494
Db 14 AAAAAA 1

RESULT 250
LOCUS AR433159/c 14 bp DNA PAT 18-DEC-2003
DEFINITION Sequence 130 from patent US 6656480.
ACCESSION AR433159
VERSION AR433159.1 GI:40195941
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 14)
AUTHORS Retter,M.W. and Dillion,D.C.
TITLE Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6656480-A 130 02-DEC-2003;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1492
Db 14 CTAACAAAAA 1

RESULT 251
LOCUS AX048406/c 14 bp DNA PAT 12-JAN-2001
DEFINITION Sequence 5 from Patent WO0071747.
ACCESSION AX048406
VERSION AX048406.1 GI:12225570
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Bургstaller,P.
TITLE Detection system for separating constituents of a sample and production and use of the same
JOURNAL Patent: WO 0071747-A 5 30-NOV-2000;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
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QY 1481 AAAAAA 1494
Db 14 AAAAAA 1

RESULT 252
LOCUS AX316793/c 14 bp DNA PAT 14-DEC-2001
DEFINITION Sequence 130 from Patent WO0190152.
ACCESSION AX316793
VERSION AX316793.1 GI:17899884
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C., Retter,M.W., Wang,A., Skeiky,Y.A., Harlocker,S.L. and Day,C.H.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0190152-A 130 29-NOV-2001;
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QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 255
AX659631/c
LOCUS
DEFINITION Sequence 25 from Patent WO02103014.
ACCESSION AX659631
VERSION AX659631.1 GI:29161813
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Al-Mahmood,S.
TITLE Antisense oligonucleotides which can inhibit the formation of
JOURNAL capillary tubes by endothelial cells
FEATURES Patent: WO 02103014-A 25 27-DEC-2002;
source Al-Mahmood, Salman (FR)
1. .14 Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide anti-sens."

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 256
AX827014
LOCUS
DEFINITION Sequence 11 from Patent EP1344835.
ACCESSION AX827014
VERSION AX827014.1 GI:39837221
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
TITLE Real-time nucleic acid detection processes and compositions
JOURNAL Patent: EP 1344835-A 11 17-SEP-2003;
FEATURES Enzo Life Sciences, Inc. (US)
source Location/Qualifiers
1. .14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence: Primer"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
DB 1 AAAAAAAAAAAAAA 14

RESULT 257
AX839906
LOCUS

/db_xref="taxon:32630"
/notes="Primer"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 253
AX321516/c
LOCUS
DEFINITION Sequence 47 from Patent WO0172295.
ACCESSION AX321516
VERSION AX321516.1 GI:17905576
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Reed,S.G., Lodes,M.J., Mohamath,R., Secrist,H., Benson,D.R.,
FEATURES Indrias,C.Y., Henderson,R.A., Fling,S.P., Algate,P.A., Elliot,M.,
source Mannin,J. and Kalos,M.D.
1. .14 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 254
AX642209/c
LOCUS
DEFINITION Sequence 27 from Patent WO02061082.
ACCESSION AX642209
VERSION AX642209.1 GI:28474657
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Day,R.
TITLE Zis-br nucleic acid and amino acid sequences involved in the
JOURNAL regulated secretory pathway and/or the regulation of the
FEATURES neuroendocrine phenotype (nep)
source Patent: WO 02061082-A 27 08-AUG-2002;
1. .14 Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 255
AX642209/c
LOCUS
DEFINITION Sequence 27 from Patent WO02061082.
ACCESSION AX642209
VERSION AX642209.1 GI:28474657
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Day,R.
TITLE Zis-br nucleic acid and amino acid sequences involved in the
JOURNAL regulated secretory pathway and/or the regulation of the
FEATURES neuroendocrine phenotype (nep)
source Patent: WO 02061082-A 27 08-AUG-2002;
1. .14 Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 256
AX827014
LOCUS
DEFINITION Sequence 11 from Patent EP1344835.
ACCESSION AX827014
VERSION AX827014.1 GI:39837221
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
TITLE Real-time nucleic acid detection processes and compositions
JOURNAL Patent: EP 1344835-A 11 17-SEP-2003;
FEATURES Enzo Life Sciences, Inc. (US)
source Location/Qualifiers
1. .14
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence: Primer"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
DB 1 AAAAAAAAAAAAAA 14

RESULT 257
AX839906
LOCUS

/db_xref="taxon:32630"
/notes="Primer"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 253
AX321516/c
LOCUS
DEFINITION Sequence 47 from Patent WO0172295.
ACCESSION AX321516
VERSION AX321516.1 GI:17905576
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Reed,S.G., Lodes,M.J., Mohamath,R., Secrist,H., Benson,D.R.,
FEATURES Indrias,C.Y., Henderson,R.A., Fling,S.P., Algate,P.A., Elliot,M.,
source Mannin,J. and Kalos,M.D.
1. .14 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 254
AX642209/c
LOCUS
DEFINITION Sequence 27 from Patent WO02061082.
ACCESSION AX642209
VERSION AX642209.1 GI:28474657
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Day,R.
TITLE Zis-br nucleic acid and amino acid sequences involved in the
JOURNAL regulated secretory pathway and/or the regulation of the
FEATURES neuroendocrine phenotype (nep)
source Patent: WO 02061082-A 27 08-AUG-2002;
1. .14 Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 255
AX827014
LOCUS
DEFINITION Sequence 11 from Patent EP1344835.
ACCESSION AX827014
VERSION AX827014.1 GI:39837221
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
TITLE Real-time nucleic acid detection processes and compositions
JOURNAL Patent: EP 1344835-A 11 17-SEP-2003;
FEATURES Enzo Life Sciences, Inc. (US)
source Location/Qualifiers
1. .14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence: Primer"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
DB 1 AAAAAAAAAAAAAA 14

RESULT 257
AX839906
LOCUS

/db_xref="taxon:32630"
/notes="Primer"

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DEFINITION Sequence 11 from Patent EP1348713.
ACCESSION AX839906
VERSION AX839906.1 GI:39978437
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Stavrianopoulos,J.G. and Rabbani,E.
TITLE Labeling reagents and labeled targets, target labeling
        processes and other processes for using same in nucleic acid
        determinations and analyses
JOURNAL Patent: EP 1348713-A 11 01-OCT-2003;
        Enzo Life Sciences, Inc. (US)
FEATURES
    source
        1. .14
        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="Description of Artificial Sequence: Primer"
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
Db 1 AAAAAAAAAAAAAA 14

RESULT 258
BD073883/c
LOCUS BD073883 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION BD073883
VERSION BD073883.1 GI:22619486
KEYWORDS JP 2001512698-A/8.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 8 28-AUG-2001;
        UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
        PN JP 2001512698-A/8
        PD 28-AUG-2001
        PF 05-AUG-1998 JP 2000506375
        PR 08-AUG-1997 US 08/908873
        PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
        C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
        C12P21/02,
        PC C12P21/08,C12N15/00
        CC Strandedness: Single;
        CC Topology: Linear;
        CC Isolation of novel aging factor gene P23
        FH Key Location/Qualifiers
        FT source 1. .14
        FT /organism='Unidentified'.
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Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CTAATAAAAAAAAAA 14

DEFINITION Sequence 11 from Patent EP1348713.
ACCESSION AX839906
VERSION AX839906.1 GI:39978437
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Stavrianopoulos,J.G. and Rabbani,E.
TITLE Labeling reagents and labeled targets, target labeling
        processes and other processes for using same in nucleic acid
        determinations and analyses
JOURNAL Patent: EP 1348713-A 11 01-OCT-2003;
        Enzo Life Sciences, Inc. (US)
FEATURES
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        1. .14
        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="Description of Artificial Sequence: Primer"
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
Db 1 AAAAAAAAAAAAAA 14

RESULT 259
BD084127
LOCUS BD084127 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Polymorphisms and new genes in the region of the human
        hemochromatosis gene.
ACCESSION BD084127
VERSION BD084127.1 GI:22629737
KEYWORDS JP 2001525663-A/15.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 14)
AUTHORS Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
        Tsuchihashi,Z. and Wolff,R.K.
TITLE Polymorphisms and new genes in the region of the human
        hemochromatosis gene
JOURNAL Patent: JP 2001525663-A 15 11-DEC-2001;
        PROGENITOR INC
COMMENT OS Homo sapiens (human)
        PN JP 2001525663-A/15
        PD 11-DEC-2001
        PF 30-SEP-1997 JP 1998516815
        PR 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI
        JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
        WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
        C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
        and new genes in the region of the human CC hemochromatosis gene
        FH Key Location/Qualifiers
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Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
Db 1 AAAAAAAAAAAAAA 14

RESULT 260
BD084336/c
LOCUS BD084336 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Compositions and methods for the treatment and diagnosis of breast
        cancer.
ACCESSION BD084336
VERSION BD084336.1 GI:22629946
KEYWORDS JP 2001521384-A/129.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Fridakis,T.N., Smith,J.M. and Reed,S.G.
TITLE Compositions and methods for the treatment and diagnosis of breast
        cancer
JOURNAL Patent: JP 2001521384-A 129 06-NOV-2001;
        CORIXA CORP
COMMENT OS Unidentified
        PN JP 2001521384-A/129
        PD 06-NOV-2001
        PF 09-APR-1998 JP 1998543059
        PR 09-APR-1997 US 08/838762,11-DEC-1997 US 08/991789 PI
        TONY N FRIDAKIS,JOHN M SMITH,STEVEN G REED
        PC C07K14/47,C07K14/82,C07K14/15,C12Q1/68,G01N33/574,A61K38/17,
        PC A61K39/00

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CC Strandedness: Single;
CC Topology: Linear;
CC Compositions and methods for the treatment and diagnosis of
CC breast cancer
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Unidentified'.
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      /mol_type='genomic DNA'
      /db_xref='taxon:32644'
  Query Match 0.9%; Score 14; DB 1; Length 14;
  Best Local Similarity 100.0%; Pred. No. 1.2e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CTAATAAAAAAAAAA 1

RESULT 261
BD096963/c
LOCUS BD096963 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide for SNP detection.
ACCESSION BD096963
VERSION BD096963.1 GI:22642551
KEYWORDS JP 2001346579-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS KomiYama,M. and Asanuma,H.
TITLE Oligonucleotide for SNP detection
JOURNAL Patent: JP 2001346579-A 2 18-DEC-2001;
MAKOTO KOMIYAMA,HIROYUKI ASANUMA
OS Artificial Sequence
PN JP 2001346579-A/2
PD 18-DEC-2001
PF 02-JUN-2000 JP 2000165441
PI MAKOTO KOMIYAMA,HIROYUKI ASANUMA
PC C12N15/00,
PC C12N15/00
CC Oligonucleotide for SNP detection
FH Key Location/Qualifiers
FT modified base 1.
FT /organism='synthetic construct'
FT /mol_type='genomic DNA'
FT /db_xref='taxon:32630'

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    Best Local Similarity 100.0%; Pred. No. 1.2e+02;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 262
BD096965/c
LOCUS BD096965 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide for SNP detection.
ACCESSION BD096965
VERSION BD096965.1 GI:22642553
KEYWORDS JP 2001346579-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS KomiYama,M. and Asanuma,H.
TITLE Oligonucleotide for SNP detection
JOURNAL Patent: JP 2001346579-A 4 18-DEC-2001;
MAKOTO KOMIYAMA,HIROYUKI ASANUMA
OS Artificial Sequence
PN JP 2001346579-A/4
PD 18-DEC-2001
PF 02-JUN-2000 JP 2000165441
PI MAKOTO KOMIYAMA,HIROYUKI ASANUMA
PC C12N15/09,C12N15/09,C12Q1/68,G01N33/53,G01N33/566,
PC C12N15/00,
PC C12N15/00
CC Oligonucleotide for SNP detection
FH Key Location/Qualifiers
FT modified base 1.
FT /organism='synthetic construct'
FT /mol_type='genomic DNA'
FT /db_xref='taxon:32644'

FEATURES
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    0.9%; Score 14; DB 1; Length 14;
    Best Local Similarity 100.0%; Pred. No. 1.2e+02;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 263
BD132850/c
LOCUS BD132850 14 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods of nucleic acid detection.
ACCESSION BD132850
VERSION BD132850.1 GI:23227795
KEYWORDS JP 2002509443-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
TITLE Methods of nucleic acid detection
JOURNAL Patent: JP 2002509443-A 1 26-MAR-2002;
GEN PROBE INC
OS Artificial Sequence
PN JP 2002509443-A/1
PD 26-MAR-2002
PF 30-OCT-1998 JP 1999526687
PR 31-OCT-1997 US 60/063969
PI WILLIAM G WEISBURG,PAUL D STULL,MICHAEL R RESHATOFF PC
C12Q1/68
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FT modified base 1.
FT /organism='synthetic construct'
FT /mol_type='genomic DNA'
FT /db_xref='taxon:32630'

FEATURES
  source
    0.9%; Score 14; DB 1; Length 14;
    Best Local Similarity 100.0%; Pred. No. 1.2e+02;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 264
BD176795
LOCUS BD176795 14 bp DNA linear PAT 18-MAR-2003

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REFERENCE 1 (bases 1 to 14)
AUTHORS KomiYama,M. and Asanuma,H.
TITLE Oligonucleotide for SNP detection
JOURNAL Patent: JP 2001346579-A 4 18-DEC-2001;
MAKOTO KOMIYAMA,HIROYUKI ASANUMA
OS Artificial Sequence
PN JP 2001346579-A/4
PD 18-DEC-2001
PF 02-JUN-2000 JP 2000165441
PI MAKOTO KOMIYAMA,HIROYUKI ASANUMA
PC C12N15/09,C12N15/09,C12Q1/68,G01N33/53,G01N33/566,
PC C12N15/00,
PC C12N15/00
CC Oligonucleotide for SNP detection
FH Key Location/Qualifiers
FT modified base 1.
FT /organism='synthetic construct'
FT /mol_type='genomic DNA'
FT /db_xref='taxon:32630'

FEATURES
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    0.9%; Score 14; DB 1; Length 14;
    Best Local Similarity 100.0%; Pred. No. 1.2e+02;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 263
BD132850/c
LOCUS BD132850 14 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods of nucleic acid detection.
ACCESSION BD132850
VERSION BD132850.1 GI:23227795
KEYWORDS JP 2002509443-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
TITLE Methods of nucleic acid detection
JOURNAL Patent: JP 2002509443-A 1 26-MAR-2002;
GEN PROBE INC
OS Artificial Sequence
PN JP 2002509443-A/1
PD 26-MAR-2002
PF 30-OCT-1998 JP 1999526687
PR 31-OCT-1997 US 60/063969
PI WILLIAM G WEISBURG,PAUL D STULL,MICHAEL R RESHATOFF PC
C12Q1/68
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FT modified base 1.
FT /organism='synthetic construct'
FT /mol_type='genomic DNA'
FT /db_xref='taxon:32630'

FEATURES
  source
    0.9%; Score 14; DB 1; Length 14;
    Best Local Similarity 100.0%; Pred. No. 1.2e+02;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 264
BD176795
LOCUS BD176795 14 bp DNA linear PAT 18-MAR-2003

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DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176795
VERSION BD176795.1 GI:29122507
KEYWORDS WO 02074951-A/42.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 42 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT OS Artificial Sequence
PN WO 02074951-A/42
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14 /organism='Artificial Sequence'.
FEATURES
source 1..14 Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 265
BD176801/c
LOCUS BD176801
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176801
VERSION BD176801.1 GI:29122513
KEYWORDS WO 02074951-A/48.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 48 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT OS Artificial Sequence
PN WO 02074951-A/48
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14 /organism='Artificial Sequence'.
FEATURES
source 1..14 Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 266
BD176804/c
LOCUS BD176804
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176804
VERSION BD176804.1 GI:29122516
KEYWORDS WO 02074951-A/51.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 51 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT OS Artificial Sequence
PN WO 02074951-A/51
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14 /organism='Artificial Sequence'.
FEATURES
source 1..14 Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 267
AR056156/c
LOCUS AR056156
DEFINITION Sequence 360 from patent US 5837542.
ACCESSION AR056156
VERSION AR056156.1 GI:5981733
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 360 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..15

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/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAAAAAAAAA 1493
|||||
Db 14 TAAAAAAAAAAAAA 1

RESULT 266
BD176804/c
LOCUS BD176804
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176804
VERSION BD176804.1 GI:29122516
KEYWORDS WO 02074951-A/51.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 51 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT OS Artificial Sequence
PN WO 02074951-A/51
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14 /organism='Artificial Sequence'.
FEATURES
source 1..14 Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 267
AR056156/c
LOCUS AR056156
DEFINITION Sequence 360 from patent US 5837542.
ACCESSION AR056156
VERSION AR056156.1 GI:5981733
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 360 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..15

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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 15 AAAAAAAAAAAAAA 2

RESULT 268
AR056159/c
LOCUS          15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION    Sequence 363 from patent US 5837542.
ACCESSION    AR056159
VERSION      AR056159.1 GI:5981736
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL      Patent: US 5837542-A 363 17-NOV-1998;
FEATURES
  source
    1..15
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 269
AR113914/c
LOCUS          15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION    Sequence 360 from patent US 6132967.
ACCESSION    AR113914
VERSION      AR113914.1 GI:14094236
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL      Patent: US 6132967-A 360 17-OCT-2000;
FEATURES
  source
    1..15
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 15 AAAAAAAAAAAAAA 2

RESULT 270
AR113917/c
LOCUS          15 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION    Sequence 4 from patent US 5576427.
ACCESSION    I29066
VERSION      I29066.1 GI:1819857
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Cook,P.D., Delecki,D.J. and Guinosso,C.
TITLE        Acyclic nucleoside analogs and oligonucleotide sequences containing
              them
JOURNAL      Patent: US 5576427-A 4 19-NOV-1996;
FEATURES
  Location/Qualifiers
    source
      1..15
      /mol_type="unassigned DNA"

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LOCUS          15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION    Sequence 363 from patent US 6132967.
ACCESSION    AR113917
VERSION      AR113917.1 GI:14094239
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL      Patent: US 6132967-A 363 17-OCT-2000;
FEATURES
  Location/Qualifiers
    source
      1..15
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 271
I29065
LOCUS          15 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION    Sequence 3 from patent US 5576427.
ACCESSION    I29065
VERSION      I29065.1 GI:1819856
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Cook,P.D., Delecki,D.J. and Guinosso,C.
TITLE        Acyclic nucleoside analogs and oligonucleotide sequences containing
              them
JOURNAL      Patent: US 5576427-A 3 19-NOV-1996;
FEATURES
  Location/Qualifiers
    source
      1..15
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 272
I29066
LOCUS          15 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION    Sequence 4 from patent US 5576427.
ACCESSION    I29066
VERSION      I29066.1 GI:1819857
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Cook,P.D., Delecki,D.J. and Guinosso,C.
TITLE        Acyclic nucleoside analogs and oligonucleotide sequences containing
              them
JOURNAL      Patent: US 5576427-A 4 19-NOV-1996;
FEATURES
  Location/Qualifiers
    source
      1..15
      /mol_type="unassigned DNA"

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source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 273
AR241870/c
LOCUS AR241870 15 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 158 from patent US 6472154.
ACCESSION AR241870
VERSION AR241870.1 GI:27287682
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human Genes
JOURNAL Patent: US 6472154-A 158 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 274
AX633195/c
LOCUS AX633195 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 334 from Patent EPI260586.
ACCESSION AX633195
VERSION AX633195.1 GI:28468809
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 334 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 275
AX633201/c
LOCUS AX633201 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 340 from Patent EPI260586.
ACCESSION AX633201
VERSION AX633201.1 GI:28468815
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 340 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 276
AR002257/c
LOCUS AR002257 16 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 6 from patent US 5741643.
ACCESSION AR002257
VERSION AR002257.1 GI:3963811
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps
JOURNAL Patent: US 5741643-A 6 21-APR-1998;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 16 AAAAAAAAAAAAAA 3

RESULT 277
AR045207/c
LOCUS AR045207 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5817795.
ACCESSION AR045207
VERSION AR045207.1 GI:5966672
KEYWORDS
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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Gryaznov, S.M. and Lloyd, D.H.
TITLE        Oligonucleotide clamps having diagnostic and therapeutic
              applications
JOURNAL      Patent: US 5817795-A 6 06-OCT-1998;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 278
LOCUS      AR051238/c
DEFINITION Sequence 6 from patent US 5830658.
ACCESSION  AR051238
VERSION     AR051238.1 GI:5974602
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Gryaznov, S.M.
TITLE        Convergent synthesis of branched and multiply connected
              macromolecular structures
JOURNAL      Patent: US 5830658-A 6 03-NOV-1998;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 279
LOCUS      I16032/c
DEFINITION Sequence 6 from patent US 5473060.
ACCESSION  I16032
VERSION     I16032.1 GI:1250940
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Gryaznov, S.M. and Lloyd, D.H.
TITLE        Oligonucleotide clamps having diagnostic applications
JOURNAL      Patent: US 5473060-A 6 05-DEC-1995;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 280
LOCUS      I28367/c
DEFINITION Sequence 6 from patent US 5571677.
ACCESSION  I28367
VERSION     I28367.1 GI:1819143
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Gryaznov, S.M.
TITLE        Convergent synthesis of branched and multiply connected
              macromolecular structures
JOURNAL      Patent: US 5571677-A 6 05-NOV-1996;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 281
LOCUS      AX359760
DEFINITION Sequence 64 from Patent WO200691.
ACCESSION  AX359760
VERSION     AX359760.1 GI:18675467
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Vernet, C.A.; Tchernev, V.; Putturajan, M.; Malyankar, U.M.; Gusev, V.;
              Herrmann, J.L.; Macdougall, J.R.; Rastelli, L.; Zhong, H.; Spytek, K.A.;
              Shenoy, S.; Gerlach, V.L.; Gangolli, E.A.; Stone, D.J. and
              Smithson, G.
TITLE        Novel polynucleotides and polypeptides encoded thereby
JOURNAL      Patent: WO 0200691-A 64 03-JAN-2002;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 14

RESULT 282
LOCUS      A12730/c
DEFINITION Oligonucleotide.
ACCESSION  A12730

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QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 280
LOCUS      I28367/c
DEFINITION Sequence 6 from patent US 5571677.
ACCESSION  I28367
VERSION     I28367.1 GI:1819143
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Gryaznov, S.M.
TITLE        Convergent synthesis of branched and multiply connected
              macromolecular structures
JOURNAL      Patent: US 5571677-A 6 05-NOV-1996;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 281
LOCUS      AX359760
DEFINITION Sequence 64 from Patent WO200691.
ACCESSION  AX359760
VERSION     AX359760.1 GI:18675467
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Vernet, C.A.; Tchernev, V.; Putturajan, M.; Malyankar, U.M.; Gusev, V.;
              Herrmann, J.L.; Macdougall, J.R.; Rastelli, L.; Zhong, H.; Spytek, K.A.;
              Shenoy, S.; Gerlach, V.L.; Gangolli, E.A.; Stone, D.J. and
              Smithson, G.
TITLE        Novel polynucleotides and polypeptides encoded thereby
JOURNAL      Patent: WO 0200691-A 64 03-JAN-2002;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 14

RESULT 282
LOCUS      A12730/c
DEFINITION Oligonucleotide.
ACCESSION  A12730

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VERSION      A12730.1  GI:640594
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     synthetic construct
             artificial sequences.
REFERENCE    1 (bases 1 to 15)
AUTHORS      .
TITLE        PRODUCTION OF HUMAN SOMATOMEDIN C
JOURNAL      Patent: WO 8605810-A 9 09-OCT-1986;
FEATURES     Location/Qualifiers
             source
               1..15
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"

Query Match      0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1034 ATATAACGTTTCGG 1048
Db      15 ACATAACGTTTCGG 1

RESULT 283
A25390/c
LOCUS       A25390
DEFINITION Oligonucleotide.
ACCESSION  A25390
VERSION     A25390.1  GI:833580
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 15)
AUTHORS    .
TITLE      METHOD FOR SELECTING RECOMBINANT MICRO-ORGANISMS OF WHICH THE
JOURNAL    SURFACE COMPRISES AT LEAST ONE MOLECULE HAVING ENZYMAIC ACTIVITY
FEATURES   Patent: WO 9311242-A 4 10-JUN-1993;
             Location/Qualifiers
             source
               1..15
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"

Query Match      0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      298 CTTCTGGCTGGCTGG 312
Db      15 CTTCCGGCTGGCTGG 1

RESULT 284
AR041957
LOCUS       AR041957
DEFINITION Sequence 747 from patent US 5811300.
ACCESSION  AR041957
VERSION     AR041957.1  GI:5962453
KEYWORDS   .
SOURCE     Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Sullivan,S., Draper,K., Kisch,K., Stinchcomb,D.T. and McSwiggen,J.
TITLE      TNF- alpha. ribozymes
JOURNAL    Patent: US 5811300-A 747 22-SEP-1998;
FEATURES   Location/Qualifiers
             source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1479 CTAAAAA
Db      15 CTGAAAAA

RESULT 287
AR084518
LOCUS       AR084518
DEFINITION Sequence 7 from patent US 5981185.
ACCESSION  AR084518
VERSION     AR084518.1  GI:10011289
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Query Match      0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1334 ACCTTGTTCCCTCCT 1348
Db      1 ACCTTGTTGCCCTCCT 15

RESULT 285
AR056160/c
LOCUS       AR056160
DEFINITION Sequence 364 from patent US 5837542.
ACCESSION  AR056160
VERSION     AR056160.1  GI:5981737
KEYWORDS   .
SOURCE     Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
           Draper,K.G.
TITLE      Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL    Patent: US 5837542-A 364 17-NOV-1998;
FEATURES   Location/Qualifiers
             source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1480 TAAAAA
Db      15 TGA

RESULT 286
AR056161/c
LOCUS       AR056161
DEFINITION Sequence 365 from patent US 5837542.
ACCESSION  AR056161
VERSION     AR056161.1  GI:5981738
KEYWORDS   .
SOURCE     Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
           Draper,K.G.
TITLE      Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL    Patent: US 5837542-A 365 17-NOV-1998;
FEATURES   Location/Qualifiers
             source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1479 CTAAAAA
Db      15 CTGAAAAA

RESULT 287
AR084518
LOCUS       AR084518
DEFINITION Sequence 7 from patent US 5981185.
ACCESSION  AR084518
VERSION     AR084518.1  GI:10011289
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 7 09-NOV-1999;
FEATURES
    source
        1. .15
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 288
LOCUS AR084532 15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 21 from patent US 5981185.
ACCESSION AR084532
VERSION AR084532.1 GI:10011303
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 21 09-NOV-1999;
FEATURES
    source
        1. .15
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 GCGCGCGCGCGCGC 40
Db 1 GCGCGCGCGCGCGC 15

RESULT 289
LOCUS AR113918/c 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 364 from patent US 6132967.
ACCESSION AR113918
VERSION AR113918.1 GI:14094240
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 364 17-OCT-2000;
FEATURES
    source
        1. .15
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 365 17-OCT-2000;
FEATURES
    source
        1. .15
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1493
Db 15 CTGAAAAAAAAAAAAA 1

RESULT 291
LOCUS BD244856 15 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide primer capable of making the non-specific double strand formation unstable.
ACCESSION BD244856
VERSION BD244856.1 GI:33054626
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable
JOURNAL Patent: JP 2002532063-A 1 02-OCT-2002;
COMMENT MCGILL UNIVERSITY
OS Artificial Sequence
PN JP 2002532063-A/1
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1. .15
    Location/Qualifiers
    source 1. .15
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 365 17-OCT-2000;
FEATURES
    source
        1. .15
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAA 1494
Db 15 TGAATAAAAAATAAAAA 1

RESULT 290
LOCUS AR113919/c 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 365 from patent US 6132967.
ACCESSION AR113919
VERSION AR113919.1 GI:14094241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 365 17-OCT-2000;
FEATURES
    source
        1. .15
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 292
LOCUS AR241876 15 bp DNA PAT 20-DEC-2002
DEFINITION Sequence 164 from patent US 6472154.
ACCESSION AR241876
VERSION AR241876.1 GI:27287688
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 164 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 293
AR278935
LOCUS AR278935 15 bp DNA PAT 10-APR-2003
DEFINITION Sequence 13 from patent US 6514693.
ACCESSION AR278935
VERSION AR278935.1 GI:29713578
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Lansdorp,P.
TITLE Method for detecting multiple copies of a repeat sequence in a
nucleic acid molecule
JOURNAL Patent: US 6514693-A 13 04-FEB-2003;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 GGCGGCGCGCGCGC 40
Db 1 GGCGGCGCGCGCGC 15

RESULT 294
AX633203/c
LOCUS AX633203 15 bp RNA PAT 21-FEB-2003
DEFINITION Sequence 342 from Patent EP1260586.
ACCESSION AX633203
VERSION AX633203.1 GI:28468817
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 342 27-NOV-2002;
FEATURES Location/Qualifiers
source 1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1494
Db 15 TAAAAAAAAAAAAA 1

RESULT 295
AX633205/c
LOCUS AX633205 15 bp RNA PAT 21-FEB-2003
DEFINITION Sequence 344 from Patent EP1260586.
ACCESSION AX633205
VERSION AX633205.1 GI:28468819
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 344 27-NOV-2002;
FEATURES Location/Qualifiers
source 1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAAAAAAAA 1493
Db 15 CTAAAAAAAAAAAA 1

RESULT 296
AX637368
LOCUS AX637368 15 bp RNA PAT 21-FEB-2003
DEFINITION Sequence 4507 from Patent EP1260586.
ACCESSION AX637368
VERSION AX637368.1 GI:28472982
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
```

TITLE Karpinsky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J.,
McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M.,
Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
Wolfe, T.

JOURNAL Method and reagent for inhibiting the expression of disease related
genes

Patent: EP 1260586-A 4507 27-NOV-2002;

RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES Location/Qualifiers

1..15

/organism="unidentified"

/mol_type="unassigned RNA"

/db_xref="taxon:32644"

Query Match 0.9%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1334 ACCTGTTCCTCCT 1348

Db 1 ACCTGTTCCTCCT 15

RESULT 297

A52267/c

LOCUS

DEFINITION

Sequence 57 from Patent EP0705842.

Accession A52267

Version A52267.1 GI:2852045

Keywords

unidentified

Source

unclassified.

Reference 1

Authors

Title

Regulated genes by stimulation of chondrocytes with 1L-1beta

Journal Patent: EP 0705842-A 57 10-APR-1996;

Comment HOECHST AG (DE)

Other publication ZA 9508381 960424

Other publication JP 8191693 960730

Other publication CA 2159957 960407

Other publication AU 3308695 960418.

Features

Location/Qualifiers

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/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

Query Match 0.9%; Score 13.2; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.6e+02;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492

Db 14 CBAATAAAAAAAAAA 1

RESULT 298

AR064009/c

LOCUS

DEFINITION

Sequence 10 from patent US 5846773.

Accession AR064009

Version AR064009.1 GI:5993317

Keywords

Unknown.

Source

unclassified.

Reference 1 (bases 1 to 14)

Authors Lee, M.-E. and Hsieh, C.-M.

Title

Single gene encoding aortic-specific and striated-specific muscle

cell isoforms and uses thereof

Journal Patent: US 5846773-A 10 08-DEC-1998;

Features

Location/Qualifiers

source

1..14

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.2; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.6e+02;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492

Db 14 CBAATAAAAAAAAAA 1

RESULT 299

BD235627/c

LOCUS

DEFINITION

Single gene encoding aorta-specific muscular cell isoform and

striated muscle-specific isoform, regulatory sequence thereof and

utilization of the same.

Accession BD235627

Version BD235627.1 GI:33045397

Keywords JP 2002522074-A/3.

Source

synthetic construct

Organism

artificial construct

Reference 1 (bases 1 to 14)

Authors Lee, M.E. and Hsieh, C.M.

Title

Single gene encoding aorta-specific muscular cell isoform and

striated muscle-specific isoform, regulatory sequence thereof and

utilization of the same

Journal Patent: JP 2002522074-A 3 23-JUL-2002;

Comment PRESIDENT AND FELLOWS OF HARVARD COLLEGE

OS Artificial Sequence

PN JP 2002522074-A/3

PD 23-JUL-2002

PF 11-MAY-1999 JP 2000565124

PR 14-AUG-1998 US 09/134250, 30-APR-1999 US 09/303069 PI

MU EN LEE, CHUNG MING HSIEH

PC C12N15/09, C07K14/47, C12Q1/66, C12Q1/68, G01N33/15, G01N33/50, PC

G01N33/68,

PC C12N15/00

CC Synthetic Poly T Anchoring Primer

PH Key

FT source

1..14

/organism="Artificial Sequence".

Features

Location/Qualifiers

1..14

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 0.9%; Score 13.2; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.6e+02;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492

Db 14 CBAATAAAAAAAAAA 1

RESULT 300

E13664/c

LOCUS

DEFINITION

Primer.

Accession E13664

Version E13664.1 GI:3252441

Keywords JP 1997224671-A/2.

Source

unidentified

Organism

unclassified.

Reference 1 (bases 1 to 14)

Authors Shibata, D., Kato, T. and Ota, H.

Title

DNA CODING NEW CYTOCHROME P450

source

1..14

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.2; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.6e+02;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492

Db 14 CBAATAAAAAAAAAA 1

RESULT 299

BD235627/c

LOCUS

DEFINITION

Single gene encoding aorta-specific muscular cell isoform and

striated muscle-specific isoform, regulatory sequence thereof and

utilization of the same.

Accession BD235627

Version BD235627.1 GI:33045397

Keywords JP 2002522074-A/3.

Source

synthetic construct

Organism

artificial construct

Reference 1 (bases 1 to 14)

Authors Lee, M.E. and Hsieh, C.M.

Title

Single gene encoding aorta-specific muscular cell isoform and

striated muscle-specific isoform, regulatory sequence thereof and

utilization of the same

Journal Patent: JP 2002522074-A 3 23-JUL-2002;

Comment PRESIDENT AND FELLOWS OF HARVARD COLLEGE

OS Artificial Sequence

PN JP 2002522074-A/3

PD 23-JUL-2002

PF 11-MAY-1999 JP 2000565124

PR 14-AUG-1998 US 09/134250, 30-APR-1999 US 09/303069 PI

MU EN LEE, CHUNG MING HSIEH

PC C12N15/09, C07K14/47, C12Q1/66, C12Q1/68, G01N33/15, G01N33/50, PC

G01N33/68,

PC C12N15/00

CC Synthetic Poly T Anchoring Primer

PH Key

FT source

1..14

/organism="Artificial Sequence".

Features

Location/Qualifiers

1..14

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 0.9%; Score 13.2; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.6e+02;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492

Db 14 CBAATAAAAAAAAAA 1

RESULT 300

E13664/c

LOCUS

DEFINITION

Primer.

Accession E13664

Version E13664.1 GI:3252441

Keywords JP 1997224671-A/2.

Source

unidentified

Organism

unclassified.

Reference 1 (bases 1 to 14)

Authors Shibata, D., Kato, T. and Ota, H.

Title

DNA CODING NEW CYTOCHROME P450

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JOURNAL Patent: JP 1997224671-A 2 02-SEP-1997;
COMMENT MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
OS None
OC Artificial sequences.
PN JP 1997224671-A/2
PD 02-SEP-1997
PF 19-FEB-1996 JP 1996031075
PI SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
PC C12N15/09,C12N9/02,C12N9/02,C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key Location/Qualifiers
FH source 1..14
FH FT /organism='Artificial sequences'.
FT Location/Qualifiers
source 1..14
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1492
|:|||||
Db 14 CBAACAAAAA 1

RESULT 301
E13669/c
LOCUS AR212269 14 bp DNA linear PAT 27-APR-1998
DEFINITION Sequence 10 from patent US 6399753.
ACCESSION AR212269
VERSION AR212269.1 GI:3252446
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Lee,M.-E. and Ota,H.
TITLE DNA CODING NEW DNA-CONNECTED PROTEIN
JOURNAL Patent: JP 1997224672-A 2 02-SEP-1997;
COMMENT MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
OS None
OC Artificial sequences.
PN JP 1997224672-A/2
PD 02-SEP-1997
PF 21-FEB-1996 JP 1996033973
PI SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
PC C12N15/09,A01H5/00,C07H21/04,C07K14/415//C12N5/10,C12Q1/68, CC
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key Location/Qualifiers
FH source 1..14
FH FT /organism='Artificial sequences'.
FT Location/Qualifiers
source 1..14
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1492
|:|||||
Db 14 CBAACAAAAA 1

RESULT 302
E13669/c
LOCUS AR195060 14 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 10 from patent US 6350592.
ACCESSION AR195060
VERSION AR195060.1 GI:20244497
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Lee,M.-E. and Hsieh,C.-M.
TITLE Aortic-specific enhancer sequence and uses thereof
JOURNAL Patent: US 6350592-A 10 26-FEB-2002;
FEATURES
source 1..14
/organism='unassigned DNA'
/mol_type='unassigned DNA'

Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1492
|:|||||
Db 14 CBAACAAAAA 1

RESULT 303
E13669/c
LOCUS AR212269 14 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 10 from patent US 6399753.
ACCESSION AR212269
VERSION AR212269.1 GI:21515800
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Lee,M.-E. and Hsieh,C.-M.
TITLE Striated-specific muscle cell polypeptides
JOURNAL Patent: US 6399753-A 10 04-JUN-2002;
FEATURES
source 1..14
/organism='unassigned DNA'
/mol_type='unassigned DNA'

Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1492
|:|||||
Db 14 CBAACAAAAA 1

RESULT 304
E13669/c
LOCUS AR266627 14 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 65 from patent US 6495319.
ACCESSION AR266627
VERSION AR266627.1 GI:29695691
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 65 17-DEC-2002;
FEATURES
source 1..14
/organism='unassigned DNA'
/mol_type='unassigned DNA'
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source      1. .14
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAA 1493
Db 14 BAAAAAATAAAAAA 1

RESULT 305
BD057045/c
LOCUS      14 bp DNA linear PAT 27-AUG-2002
DEFINITION A single gene encoding aortic-specific and striated-specific muscle cell isoforms and uses thereof.
ACCESSION  BD057045
VERSION     BD057045.1 GI:22602651
KEYWORDS   JP 2001511016-A/3.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Lee,M.E. and Heieh,C.M.
TITLE     A single gene encoding aortic-specific and striated-specific muscle cell isoforms and uses thereof
JOURNAL   Patent: JP 2001511016-A 3 07-AUG-2001;
COMMENT   PRESIDENT AND FELLOWS OF HARVARD COLLEGE
          FN JP 2001511016-A/3
          PD 07-AUG-2001
          PF 06-FEB-1998 JP 1998534965
          PR 06-FEB-1997 US 08/795868
          PI MU EN LEE,CHUNG MING HSIEH
          PC C12N15/09,C07K14/47,C12N5/10,C12N15/00,C12N5/00 CC
          CC Topology: Linear;
          FH Key Location/Qualifiers.
FEATURES
source      1. .14
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAATAAAAAA 1492
Db 14 CBAATAAATAAAAAA 1

RESULT 306
E32457
LOCUS      18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32457
VERSION     E32457.1 GI:13018693
KEYWORDS   JP 2000037190-A/17.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
            1 (bases 1 to 18)
REFERENCE  Jun,N., Yusuke,N. and Toshihiro,T.
AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
TITLE     Mammal-derived tissue specific physiologically active protein
JOURNAL   Patent: JP 2000037190-A 17 08-FEB-2000;
COMMENT   JAPAN TOBACCO INC
          OS Artificial Sequence
          FN JP 2000037190-A/17
          PD 08-FEB-2000

PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
CC
FH Key Location/Qualifiers
FT primer bind (1)-(18).
   Location/Qualifiers
   1..18
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match      0.9%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1085 GTTTTCTTTTGTCTGA 1102
Db 1 GTTTTCTTTTGTCTGA 18

RESULT 307
AR012009/c
LOCUS      13 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 3 from patent US 5763183.
ACCESSION  AR012009
VERSION     AR012009.1 GI:3969999
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Pesonen,U., Koulu,M., Linnoila,M., Goldman,D. and Virkkunen,M.
TITLE     Allelic variation of the serotonin 5HT7 receptor
JOURNAL   Patent: US 5763183-A 3 09-JUN-1998;
FEATURES
source      1. .13
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAATAAAAAA 1493
Db 13 AAAAAAATAAAAAA 1

RESULT 308
AR012010/c
LOCUS      13 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5763183.
ACCESSION  AR012010
VERSION     AR012010.1 GI:3970000
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Pesonen,U., Koulu,M., Linnoila,M., Goldman,D. and Virkkunen,M.
TITLE     Allelic variation of the serotonin 5HT7 receptor
JOURNAL   Patent: US 5763183-A 4 09-JUN-1998;
FEATURES
source      1. .13
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 309
LOCUS AR145368 13 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6211354.
ACCESSION AR145368
VERSION AR145368.1 GI:15107235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Horie,R. and Ishiguro,T.
TITLE Optically active DNA probe having phosphonic diester linkage
JOURNAL Patent: US 6211354-A 1 03-APR-2001;
FEATURES
    source
        Location/Qualifiers
            1..13
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 310
LOCUS AR179431/c 13 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6 from patent US 6326175.
ACCESSION AR179431
VERSION AR179431.1 GI:20220986
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Guegler,K., Tan,R. and Rose,M.J.
TITLE Methods and compositions for producing full length cDNA libraries
JOURNAL Patent: US 6326175-A 6 04-DEC-2001;
FEATURES
    source
        Location/Qualifiers
            1..13
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 311
LOCUS E66853 13 bp DNA linear PAT 18-JUN-2001
DEFINITION DNA probe having optically active diphosphate bond.
ACCESSION E66853
VERSION E66853.1 GI:13018113
KEYWORDS JP 1999322783-A/1.
SOURCE synthetic construct

ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 13)
Ryuichi,H. and Takahiko,I.
DNA probe having optically active diphosphate bond
Patent: JP 1999322783-A 1 24-NOV-1999;
TOSOH CORP
OS Artificial Sequence
PN JP 1999322783-A/1
PD 24-NOV-1999
PF 06-MAY-1998 JP 1998123298
PR
PI RYUICHI HORIE,TAKAHIKO ISHIGURO
PC C07H21/04,C12N15/09,C12Q1/68,G01N21/78,G01N33/50, PC
G01N33/533,
PC G01N33/566,G01N33/58
CC
FH Key Location/Qualifiers
FT source 1..13 /organism='Artificial Sequence'.
FEATURES
    source
        Location/Qualifiers
            1..13
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 312
LOCUS E66854 13 bp DNA linear PAT 18-JUN-2001
DEFINITION DNA probe having optically active diphosphate bond.
ACCESSION E66854
VERSION E66854.1 GI:13018114
KEYWORDS JP 1999322783-A/2.
SOURCE synthetic construct
artificial sequences.
1 (bases 1 to 13)
Ryuichi,H. and Takahiko,I.
DNA probe having optically active diphosphate bond
Patent: JP 1999322783-A 2 24-NOV-1999;
TOSOH CORP
OS Artificial Sequence
PN JP 1999322783-A/2
PD 24-NOV-1999
PF 06-MAY-1998 JP 1998123298
PR
PI RYUICHI HORIE,TAKAHIKO ISHIGURO
PC C07H21/04,C12N15/09,C12Q1/68,G01N21/78,G01N33/50, PC
G01N33/533,
PC G01N33/566,G01N33/58
CC
FH Key Location/Qualifiers
FT source 1..13 /organism='Artificial Sequence'.
FEATURES
    source
        Location/Qualifiers
            1..13
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAA 13

RESULT 313
LOCUS AR205695 13 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6369199.
ACCESSION AR205695
VERSION AR205695.1 GI:21503343
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Guegler,K., Tan,R. and Rose,M.J.
TITLE Fusion protein comprising an eIF-4E domain and an eIF-4G domain
JOURNAL joined by a linker domain
FEATURES
    Patent: US 6369199-A 6 09-APR-2002;
    Location/Qualifiers
        source
            1..13
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

RESULT 316
LOCUS AX048405 13 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 4 from Patent WO0071747.
ACCESSION AX048405
VERSION AX048405.1 GI:12225569
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
JOURNAL Production and use of the same
FEATURES
    Patent: WO 0071747-A 4 30-NOV-2000;
    Aventis Research & Technologies GmbH & Co. KG (DE)
    Location/Qualifiers
        source
            1..13
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Region A"

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

RESULT 317
LOCUS AX104675 13 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 867 from Patent WO0122972.
ACCESSION AX104675
VERSION AX104675.1 GI:13920872
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 867 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
FEATURES
    GmbH (DE)
    Location/Qualifiers
        source
            1..13
                /organism="synthetic construct"

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QY 1481 AAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAA 13

RESULT 313
LOCUS AR205695 13 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6369199.
ACCESSION AR205695
VERSION AR205695.1 GI:21503343
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Guegler,K., Tan,R. and Rose,M.J.
TITLE Fusion protein comprising an eIF-4E domain and an eIF-4G domain
JOURNAL joined by a linker domain
FEATURES
    Patent: US 6369199-A 6 09-APR-2002;
    Location/Qualifiers
        source
            1..13
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

RESULT 314
LOCUS AR222459 13 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 19 from patent US 6429300.
ACCESSION AR222459
VERSION AR222459.1 GI:23329990
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 19 06-AUG-2002;
FEATURES
    Location/Qualifiers
        source
            1..13
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAA 13

RESULT 315
LOCUS AX021144 13 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 12 from Patent WO9929898.
ACCESSION AX021144
VERSION AX021144.1 GI:10044796
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
11_13
/notes="FITC moiety attached at 3' end of sequence.
Has phosphodiester backbone."
misc_feature
Query Match
Best Local Similarity 100.0%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 318
LOCUS AX104676/c
DEFINITION Sequence 868 from Patent WO0123972.
ACCESSION AX104676
VERSION AX104676.1 GI:13920873
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wang, J. and Herdewijn, P.
TITLE Cyclohexene nucleic acids
JOURNAL Patent: WO 0123972-A 868 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
GmbH (DE)
FEATURES
source
1. .13
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
11_13
/notes="Biotin moiety attached at 3' end of sequence.
Has phosphorothioate and phosphodiester chimeric backbone
with phosphodiester on 3' end."
misc_feature
Query Match
Best Local Similarity 100.0%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 319
AX235509/c
LOCUS AX235509
DEFINITION Sequence 25 from Patent WO0149687.
ACCESSION AX235509
VERSION AX235509.1 GI:15593971
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wang, J. and Herdewijn, P.
TITLE Cyclohexene nucleic acids
JOURNAL Patent: WO 0149687-A 25 12-JUL-2001;
UNIVERSITY OF IOWA RESEARCH & DEVELOPMENT (BE)
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
FEATURES
source
1. .13
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="DNA complement"
Query Match
0.9%; Score 13; DB 1; Length 13;
misc_feature 13
/notes="FITC labeled"
Query Match
0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 320
LOCUS AX235510/c
DEFINITION Sequence 26 from Patent WO0149687.
ACCESSION AX235510
VERSION AX235510.1 GI:15593972
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wang, J. and Herdewijn, P.
TITLE Cyclohexene nucleic acids
JOURNAL Patent: WO 0149687-A 26 12-JUL-2001;
UNIVERSITY OF IOWA RESEARCH & DEVELOPMENT (BE)
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
FEATURES
source
1. .13
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="oligomer used in this study"
Query Match
0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 321
AX355807/c
LOCUS AX355807
DEFINITION Sequence 835 from Patent WO0197843.
ACCESSION AX355807
VERSION AX355807.1 GI:18620475
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 835 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source
1. .13
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide-phosphodiester backbone"
misc_feature 13
/notes="FITC labeled"
Query Match
0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1
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RESULT 322
AX355808/c
LOCUS AX355808 13 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 836 from Patent WO0197843.
ACCESSION AX355808
VERSION AX355808.1 GI:18620476
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 867 11-JUL-2002;
FEATURES
source
Location/Qualifiers
1..13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide-chimeric
phosphorothioate/phosphodiester backbone with
phosphodiester on 3' end"
misc_difference 13
/notes="FITC labeled"

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 323
AX547728/c
LOCUS AX547728 13 bp DNA linear PAT 15-JAN-2003
DEFINITION Sequence 867 from Patent WO02053141.
ACCESSION AX547728
VERSION AX547728.1 GI:25812872
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 867 11-JUL-2002;
FEATURES
source
Location/Qualifiers
1..13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Has phosphodiester backbone."
misc_feature 11..13
/notes="Conjugated to FITC moiety."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 324
AX547729/c
LOCUS AX547729 13 bp DNA linear PAT 15-JAN-2003
DEFINITION Sequence 868 from Patent WO02053141.

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```

ACCESSION AX547729
VERSION AX547729.1 GI:25812873
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 868 11-JUL-2002;
FEATURES
source
Location/Qualifiers
1..13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Has phosphorothioate and phosphodiester chimeric
backbone with phosphodiester on 3' end."
misc_feature 11..13
/notes="Conjugated to biotin moiety."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 325
AR124885/c
LOCUS AR124885 14 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6172211.
ACCESSION AR124885
VERSION AR124885.1 GI:14110246
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Georgiev, G.P., Kiselev, S.L., Prokhorchouk, E.B. and Ostermann, E.
TITLE Nucleic acid encoding tsgr polypeptide
JOURNAL Patent: US 6172211-A 3 09-JAN-2001;
FEATURES
source
Location/Qualifiers
1..14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1492
Db 13 TAAAAAAAAAAAAA 1

RESULT 326
AR174027/c
LOCUS AR174027 14 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 17 from patent US 6306624.
ACCESSION AR174027
VERSION AR174027.1 GI:17914347
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Petkovich, P., Martin, J.A., Beckett, B.R. and Jones, G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 17 23-OCT-2001;
FEATURES
Location/Qualifiers

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source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAA 1492
|||||
Db 13 TAAAAAAAAAAAA 1

RESULT 327
AR174028/c
LOCUS AR174028 14 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 18 from patent US 6306624.
ACCESSION AR174028
VERSION AR174028.1 GI:17914348
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 18 23-OCT-2001;
FEATURES
Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAA 1492
|||||
Db 13 TAAAAAAAAAAAA 1

RESULT 328
AR174029/c
LOCUS AR174029 14 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 19 from patent US 6306624.
ACCESSION AR174029
VERSION AR174029.1 GI:17914349
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 19 23-OCT-2001;
FEATURES
Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAA 1492
|||||
Db 13 TAAAAAAAAAAAA 1

RESULT 329
AR228386
LOCUS AR228386 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 18 from patent US 6448039.
ACCESSION AR228386
VERSION AR228386.1 GI:27267215
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Nelson,P.J., Krensky,A.M. and Ortiz,B.D.
TITLE Enhancer sequences for late T cell expressed genes
JOURNAL Patent: US 6448039-A 18 10-SEP-2002;
FEATURES
Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 GACTGGAGGGCAG 1191
|||||
Db 1 GACTGGAGGGCAG 13

RESULT 330
AR241806/c
LOCUS AR241806 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 94 from patent US 6472154.
ACCESSION AR241806
VERSION AR241806.1 GI:27287618
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 94 29-OCT-2002;
FEATURES
Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAA 1

RESULT 331
AR349924/c
LOCUS AR349924 14 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 18 from patent US 6586204.
ACCESSION AR349924
VERSION AR349924.1 GI:33750834
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Lehar,S.M. and Guild,B.C.
TITLE Apoptosis gene BIZ4, compositions, and methods of use
JOURNAL Patent: US 6586204-A 18 01-JUL-2003;
FEATURES
Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAA 1
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Qy	1479	CTAAAAAAAAAAAAA	1492							
Db	14	CNAAAAAAAAAAAAA	1							

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RESULT_332      PAT    17-AUG-2003
AR349925/C     linear
LOCUS          14 bp   DNA
DEFINITION     Sequence 19 from patent US 6586204.
ACCESSION      AR349925
VERSION         AR349925.1 GI:33750835
KEYWORDS       .
SOURCE          Unknown.
ORGANISM       Unclassified.
REFERENCE       1 (bases 1 to 14)
AUTHORS        Lehar,S.M. and Guild,B.C.
TITLE           Apoptosis Gene Eir24, compositions, and methods of use
JOURNAL         Patent: US 6586204-A 19 01-JUL-2003;
FEATURES        Location/Qualifiers
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source          /organism="unknown"/
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Best Local Similarity	92.9%;	Pred. No. 1.8e+02;		
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QY	1480	TAAAAAAAAAAAAA	1493	
Db	14	TNAAAAAAAAAAAA	1	
RESULT 333				
AR349926/c				
LOCUS	AR349926		14 bp	DNA
DEFINITION	Sequence 20 from patent US 6586204.			
ACCESSION	AR349926			
VERSION	AR349926.1		GI:33750836	
KEYWORDS				
SOURCE				Unknown.

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REFERENCE          1 (bases 1 to 14)
AUTHORS            Lehar,S.M. and Guild,B.C.
TITLE              Apoptosis gene E124, compositions, and methods of use
JOURNAL            Patent: US 586204-A 20 01-JUL-2003;
FEATURES           Location/Qualifiers
                    1..14
                    /organism="unknown"
                    /mol_type="genomic DNA"

Query Match       0.9%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred.No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494
    | | | | | | | | | |
Db 14 ANAAAAAAAAAAAAAA 1

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RESULT 334	AX482598	14 bp	DNA	linear	PAT 16-AUG-2002
AX482598/c	Sequence	32 from Patent	WO02055547.		
LOCUS	AX482598				
DEFINITION	AX482598				
ACCESSION	AX482598.1	GI:22317052			
VERSION					
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
	artificial construct				
	artificial sequences.				

KEYWORDS
 SOURCE
 ORGANISM
 .
 synthetic construct
 synthetic construct
 artificial sequences.

```

REFERENCE
AUTHORS      Rubin,J.S., Uren,A., Horwood,N.J., Gillespie,M.T., Kay,B.K. and
               Weisblum,B.
TITLE        Sfrp and peptide motifs that interact with sfrp and methods of
               their use
JOURNAL      PATENT: WO 0205547-A 32 18-JUN-2002;
               THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US) ; St. Vincent's
               Institute of Medical Research (AU)
FEATURES
source       1. .14
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               /organism="synthetic construct"
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               /db_xref="taxon:32630"
               /note="Primer/Probe sequence"

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Query Match	0.9%;	Score 13;	DB 1;	Length 14;	
Best Local Similarity	92.9%;	Pred. No.	1.8e+02;		
Matches 13;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
Qy	1480	TAAAAAAAAAAAAA	1493		
Db	14	TNAAAAAAAAAAAA	1		
RESULT 335					
BD073880/c					
LOCUS	BD073880		14 bp	DNA	linear
DEFINITION	Isolation of novel aging factor gene P23.				
ACCESSION	BD073880				
VERSION	BD073880.1		GI:22619483		
KEYWORDS	JP 2001512698-A/5.				
SOURCE	unidentified				
ORGANISM	unclassified.				

REFERENCE	1 (bases 1 to 14)	
AUTHORS	Suishelm, K., Hosier, S. and Kubbies, M.	
TITLE	Isolation of novel aging factor gene P23	
JOURNAL	Patent: JP 2001512698-A 5 28-AUG-2001; UNIVERSITY OF WASHINGTON	
COMMENT	OS Unidentified	
	PN JP 2001512698-A/5	
	PD 28-AUG-2001	
	PF 05-AUG-1998 JP 2000506375	
	PR 08-AUG-1997 US 08/908873	
	PI KAREN SUISHELM, SUZANNE HOSIER, MANFRED KUBBIES PC	
	C12Q1/68, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N15/09, PC	
	C12P21/02.	
	PC C12P21/08, C12N15/00	
	CC Strandedness: Single;	
	CC Topology: Linear;	
	CC Isolation of novel aging factor gene P23	
	FF Key Location/Qualifiers	
	FT 1..14	
	FT /organism='Unidentified'.	

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FEATURES             source            Location/Qualifiers
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     /db_xref="taxon:32644"

Query Match          0.9%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1480 TAAAAAATAAAAAAA 1492
      ..||||||
Db      13 TAAAAAATAAAAAAA 1

RESULT 336
BD073886/c
LOCUS.          BD073886      14 bp      DNA      linear
DEFINITION      Isolation of novel aging factor gene p23.
PAT 27-AUG-2002

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ACCESSION BD073886
VERSION BD073886.1 GI:22619489
KEYWORDS JP 2001512698-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 11 28-AUG-2001;
UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
PN JP 2001512698-A/11
PD 28-AUG-2001
PP 05-AUG-1998 JP 2000506375
PR 08-AUG-1997 US 08/908873
PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
C12P21/02,
PC C12P21/08,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Isolation of novel aging factor gene P23
FH Key Location/Qualifiers
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/organism='Unidentified'.
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source
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/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.9%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA1492
Db 13 TAAAAA1

RESULT 338
BD073889/c
LOCUS
DEFINITION Isolation of novel aging factor gene P23
ACCESSION BD073889
KEYWORDS JP 2001512698-A/14.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 14 28-AUG-2001;
BOEHRINGER INGELHEIM INTERNATIONAL GMBH
COMMENT OS Unidentified
PN JP 2001509384-A/3
PD 24-JUL-2001
PP 10-JUL-1998 JP 2000502182
PR 11-JUL-1997 US 08/893764
PI GEORGII GEORGIEV,SERGEI KISELEV,EGOR PROKHORCHOUK,ELINBORG PI
OSTERMANN
PC C12N15/09,A61K35/76,A61K38/00,A61K48/00,A61P35/00,C07K14/525,
PC C07K16/24,
PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08 PC
,C12Q1/68,G01N33/53,
PC C12N15/00,A61K37/02,C12N5/00
CC Tumor proliferation inhibition- and apoptosis-associated gene
CC and
CC polypeptide and method of using the same
FH Key Location/Qualifiers
FT source 1..14
/organism='Unidentified'.
FEATURES
source
1..14
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.9%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA1492
Db 13 TAAAAA1

RESULT 339
BD084126/c
LOCUS
DEFINITION Polymorphisms and new genes in the region of the human
hemochromatosis gene.
ACCESSION BD084126
KEYWORDS JP 2001525663-A/14.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
   /organism="Artificial Sequence".
FEATURES
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        1..14
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        /db_xref="taxon:32630"
Query Match 0.9%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
   |||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 343
BD176802/c
LOCUS 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176802
VERSION BD176802.1 GI:29122514
KEYWORDS WO 02074951-A/49.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 14)
REFERENCE Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
AUTHORS Method of constructing cDNA tag for identifying expressed gene and
TITLE Method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 49 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/49
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
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        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match 0.9%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
   |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 344
BD176803/c
LOCUS 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176803
VERSION BD176803.1 GI:29122515

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KEYWORDS WO 02074951-A/50.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 14)
REFERENCE Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
AUTHORS Method of constructing cDNA tag for identifying expressed gene and
TITLE Method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 50 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/50
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 13-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
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Query Match 0.9%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
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Db 13 AAAAAAAAAAAAAA 1

RESULT 345
AR056155/c
LOCUS 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 359 from patent US 5837542.
ACCESSION AR056155
VERSION AR056155.1 GI:5981732
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 359 17-NOV-1998;
FEATURES
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Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
   |||||
Db 15 AAAAAAAAAAAAAA 3

RESULT 346
AR084519
LOCUS 15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 8 from patent US 5981185.
ACCESSION AR084519
VERSION AR084519.1 GI:10011290
KEYWORDS

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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 598185-A 8 09-NOV-1999;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1480 TAAAAAATAAAAA 1492
Db 3 TAAAAAATAAAAA 15

RESULT 347
AR095959/c
LOCUS AR095959 15 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 2 from patent US 6004939.
ACCESSION AR095959
VERSION AR095959.1 GI:10024324
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Chen,S.-F., Maine,I., Kerwin,S.M., Fletcher,T.M., Salazar,M.,
Mamiya,B., Wajima,M. and Windle,B.E.
TITLE Methods for modulation and inhibition of telomerase
JOURNAL Patent: US 6004939-A 2 21-DEC-1999;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1078 TTTTGGGGTTTG 1090
Db 13 TTTTGGGGTTTG 1

RESULT 348
AR104531/c
LOCUS AR104531 15 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 43 from patent US 6093809.
ACCESSION AR104531
VERSION AR104531.1 GI:12817239
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 43 25-JUL-2000;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1078 TTTTGGGGTTTG 1090
Db 13 TTTTGGGGTTTG 1

RESULT 349
AR104533/c
LOCUS AR104533 15 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 45 from patent US 6093809.
ACCESSION AR104533
VERSION AR104533.1 GI:12817241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 45 25-JUL-2000;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
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Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1078 TTTTGGGGTTTG 1090
Db 13 TTTTGGGGTTTG 1

RESULT 350
AR113913/c
LOCUS AR113913 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 359 from patent US 6132967.
ACCESSION AR113913
VERSION AR113913.1 GI:14094235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
JOURNAL intercellular adhesion molecule-1 (ICAM-1)
FEATURES Patent: US 6132967-A 359 17-OCT-2000;
Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1493
Db 15 AAAAAAAAAAAAA 3

RESULT 351
AR175792/c
LOCUS AR175792 15 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 43 from patent US 6309867.
ACCESSION AR175792
VERSION AR175792.1 GI:17917091
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 43 25-JUL-2000;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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REFERENCE 1 (bases 1 to 15)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 43 30-OCT-2001;
FEATURES
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    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match      0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGGTTTGG 1090
Db 13 TTTTGGGGTTTGG 1

RESULT 352
LOCUS AR175794 15 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 45 from patent US 6309867.
ACCESSION AR175794
VERSION AR175794.1 GI:17917093
KEYWORDS
SOURCE Unknown.
ORGANISM
    Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 45 30-OCT-2001;
FEATURES
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    /mol_type="unassigned DNA"

Query Match      0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGGTTTGG 1090
Db 13 TTTTGGGGTTTGG 1

RESULT 353
LOCUS E36806 15 bp DNA linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36806
VERSION E36806.1 GI:1302769
KEYWORDS JP 1999253177-A/14.
SOURCE unidentified
ORGANISM
    unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
        Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 14 21-SEP-1999;
        JERON CORP UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
        EN JP 1999253177-A/14
        PD 21-SEP-1999
        PF 15-OCT-1998 JP 1998320169
        PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
        25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
        09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
        14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503 PI THOMAS
        R SECHI, JOCHIMU RINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
        MORIN,
        PI CALVIN B HAREI, WILLIAM H ANDREWS

PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
PC C12Q1/02,
PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,C12N1/19, PC
C12R1:84),
PC (C12N1/21,C12R1:19), (C12N9/12,C12R1:19), (C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91), (C12N15/00,A61K37/64,C12N5/00 CC
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..15
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    /mol_type='genomic DNA'
    /db_xref='taxon:32644'

FEATURES
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Query Match      0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGGTTTGG 1090
Db 13 TTTTGGGGTTTGG 1

RESULT 354
LOCUS AR282617 15 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 13 from patent US 6521747.
ACCESSION AR282617
VERSION AR282617.1 GI:29719215
KEYWORDS
SOURCE Unknown.
ORGANISM
    Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Anastasio,A.E., Finkel,K., Koshy,B. and Lee,H.
TITLE Haplotypes of the AGTR1 gene
JOURNAL Patent: US 6521747-A 13 18-FEB-2003;
FEATURES
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Query Match      0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.1e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1106 TTCCTGTTTACCTTTT 1120
Db 15 TTCCTGTTTCTCTTTT 1

RESULT 355
LOCUS AR359628 15 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 2 from patent US 6593306.
ACCESSION AR359628
VERSION AR359628.1 GI:33766351
KEYWORDS
SOURCE Unknown.
ORGANISM
    Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Chen,S.-F., Maine,I., Kerwin,S.M., Fletcher,T.M., Salazar,M.,
        Mamiya,B., Wajima,M. and Windle,B.E.
TITLE Methods for modulation and inhibition of telomerase
JOURNAL Patent: US 6593306-A 2 15-JUL-2003;
FEATURES
    source      Location/Qualifiers
    1..15

```

```

/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTTC 1090
DB 13 TTTTGGGTTTTC 1

RESULT 356
LOCUS AR390483/C
DEFINITION Sequence 113 from patent US 6610839.
ACCESSION AR390483
VERSION AR390483.1 GI:40112407
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morin,G.B. and Andrews,W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 113 26-AUG-2003;
FEATURES
    Location/Qualifiers
    1..15
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTTC 1090
DB 13 TTTTGGGTTTTC 1

RESULT 357
LOCUS AR393097/C
DEFINITION Sequence 113 from patent US 6617110.
ACCESSION AR393097
VERSION AR393097.1 GI:40118374
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
        Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
        drug screening
JOURNAL Patent: US 6617110-A 113 09-SEP-2003;
FEATURES
    Location/Qualifiers
    1..15
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTTC 1090
DB 13 TTTTGGGTTTTC 1

RESULT 358
LOCUS AX033371/C
DEFINITION Sequence 3 from Patent WO0046601.
ACCESSION AX033371
VERSION AX033371.1 GI:10280145
KEYWORDS
SOURCE Unidentified.
ORGANISM Unidentified.
REFERENCE 1
AUTHORS Larsen,F. and Skaanseng,M.
TITLE Detecting telomerase activity
JOURNAL Patent: WO 0046601-A 3 10-AUG-2000;
        LARSEN FRANK (NO) ; SKAANSENG MARIANNE (NO)
FEATURES
    Location/Qualifiers
    1..15
    /organism="unidentified"
    /mol_type="unassigned RNA"
    /db_xref="taxon:32644"
    /note="Euplotes"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTTC 1090
DB 13 TTTTGGGTTTTC 1

RESULT 359
LOCUS AX033372/C
DEFINITION Sequence 4 from Patent WO0046601.
ACCESSION AX033372
VERSION AX033372.1 GI:10280146
KEYWORDS
SOURCE Oxytricha sp.
ORGANISM Oxytricha sp.
REFERENCE 1
AUTHORS Larsen,F. and Skaanseng,M.
TITLE Detecting telomerase activity
JOURNAL Patent: WO 0046601-A 4 10-AUG-2000;
        LARSEN FRANK (NO) ; SKAANSENG MARIANNE (NO)
FEATURES
    Location/Qualifiers
    1..15
    /organism="Oxytricha sp."
    /mol_type="unassigned RNA"
    /db_xref="taxon:99928"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTTC 1090
DB 13 TTTTGGGTTTTC 1

RESULT 360
LOCUS AX391450/C
DEFINITION Sequence 13 from Patent EP1184456.
ACCESSION AX391450
VERSION AX391450.1 GI:19700060
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Anastasio,A.E., Koshy,B., Finkel,K. and Lee,H.H.
TITLE Haplotypes of the agt1 gene

```

JOURNAL Patent: EP 1184456-A 13 06-MAR-2002;
Genaisance Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..15
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.1e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1106 TTCCTGTTACCTTT 1120
|:|||||
Db 15 TVCCTGTTCCCTTT 1

RESULT 361
AX633193/c
LOCUS AX633193 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 332 from Patent EP1260586.
ACCESSION AX633193
VERSION AX633193.1 GI:28468807
KEYWORDS
SOURCE unclassified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulich-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweidger,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Wolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes

JOURNAL Patent: EP 1260586-A 332 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1493
|:|||||
Db 15 AAAAAAAAAA 3

RESULT 362
AX810148/c
LOCUS AX810148 15 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 113 from Patent EP1333094.
ACCESSION AX810148
VERSION AX810148.1 GI:38523876
KEYWORDS
SOURCE unclassified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: EP 1333094-A 113 06-AUG-2003;
Geron Corporation (US) ; University Technology Corporation (US)

FEATURES Location/Qualifiers
source 1..15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTCGGGTTTG 1090
|:|||||
Db 13 TTTTCGGGTTTG 1

RESULT 363
BD011057/c
LOCUS BD011057 15 bp DNA linear PAT 31-JAN-2002
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011057
VERSION BD011057.1 GI:18639430
KEYWORDS JP 2001081042-A/14.
SOURCE unclassified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 14 27-MAR-2001;
GERON CORP. UNIVERSITY TECHNOLOGY CORP
KEYWORDS OS Unidentified
COMMENT PN JP 2001081042-A/14

PF 27-MAR-2001
PD 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HARLEY, WILLIAM H ANDREWS
PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
PC C07K5/10,
PC C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
C12N15/09,
PC C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
G01N33/53,
PC G01N33/56,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..15
FT /organism="Unidentified".
FT /organism="Unidentified".
FT Location/Qualifiers

FEATURES source
1..15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTCGGGTTTG 1090
|:|||||
Db 13 TTTTCGGGTTTG 1

Search completed: April 21, 2004, 10:38:31
Job time : 7 secs

XX 10-NOV-1999; 99US-0164596P.
XX (GLAX) GLAXO GROUP LTD.
XX (AFFY-) AFFYMETRIX INC.
XX Au K, Chen J, Patil N, Thomas D;
XX WPI; 2001-335945/35.
XX New polymorphic sites derived from the human genome are useful to
PT determine sites correlating with phenotypic traits, particularly disease,
PT and also in forensics and paternity testing.
XX Claim 37; Page 9; 43pp; English.
XX The present invention relates to human oligonucleotides comprising a
CC single nucleotide polymorphic site (SNP: AAH89219). The present
CC sequence is one such oligonucleotide. The oligonucleotides can be used in
CC forensics, paternity testing, correlation of polymorphisms with
CC phenotypic traits, genetic mapping of phenotypic traits and marker
CC assisted breeding of animals and crop plants
XX Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
XX Query Match 1.4%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 23;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 979 TGCAGTGGCCCTAAGTGACC 999
XX 1 TGCAGTGGCCCTAAGTGACC 21
XX
XX RESULT 13
XX AAH8906
XX ID AAH8906 standard; DNA; 21 BP.
XX AC AAH8906;
XX DT 27-FEB-2002 (first entry)
XX DE Human polymorphic oligonucleotide AC003693 fragment #2.
XX Human; single nucleotide polymorphic; SNP; forensic science;
XX paternity testing; phenotypic trait; genetic mapping; animal breeding;
XX plant breeding; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Variation replace(11,t)
XX /tag= a
XX /standard_name= "single nucleotide polymorphism"
XX
XX W0200134840-A2.
XX
XX 17-MAY-2001.
XX 10-NOV-2000; 2000WO-US030766.
XX 10-NOV-1999; 99US-0164596P.
XX (GLAX) GLAXO GROUP LTD.
XX (AFFY-) AFFYMETRIX INC.
XX Au K, Chen J, Patil N, Thomas D;
XX WPI; 2001-335945/35.
XX New polymorphic sites derived from the human genome are useful to
PT determine sites correlating with phenotypic traits, particularly disease,
PT and also in forensics and paternity testing.

XX Claim 37; Page 9; 43pp; English.
XX The present invention relates to human oligonucleotides comprising a
CC single nucleotide polymorphic site (SNP: AAH89219). The present
CC sequence is one such oligonucleotide. The oligonucleotides can be used in
CC forensics, paternity testing, correlation of polymorphisms with
CC phenotypic traits, genetic mapping of phenotypic traits and marker
CC assisted breeding of animals and crop plants
XX Sequence 21 BP; 5 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
XX Query Match 1.4%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 23;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1036 ATACGTTTCGGTATTACTC 1056
XX 1 ATACGTTTCGGTATTACTC 21
XX
XX RESULT 14
XX ACC78663
XX ID ACC78663 standard; DNA; 21 BP.
XX AC ACC78663;
XX DT 02-SEP-2003 (first entry)
XX DE Nucleotide sequence of a PCR primer CD81_F.
XX KW Cardiopathy; nucleic acid marker; therapy; human; primer; ss.
XX OS Homo sapiens.
XX PN W02003040407-A2.
XX PD 15-MAY-2003.
XX PF 08-NOV-2002; 2002WO-BP012522.
XX PR 09-NOV-2001; 2001EP-00126800.
XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX PI Ruiz P, Grzeskowiak R, Drungowski M, Witt H, Osterziel KJ;
XX PI Perrot A, Saleh A;
XX DR WPI; 2003-430678/40.
XX
XX New diagnostic composition comprising at least one nucleic acid molecule
PT that is capable of specifically hybridizing to the mRNA of the gene,
PT useful for diagnosing cardiopathy, e.g. cardiomyopathy or dilated
PT cardiomyopathy.
XX
XX Example 1; Page 21; 82pp; English.
XX The invention relates to a diagnostic composition comprising at least one
CC nucleic acid molecule listed in the specification that is capable of
CC specifically hybridizing to the mRNA of at least one of the genes given
CC in the specification. The diagnostic composition and nucleic acid
CC molecules are useful for diagnosing cardiopathy or a disposition to
CC cardiopathy, e.g. cardiomyopathy or dilated cardiomyopathy. The method
CC involves contacting a target sample with the nucleic acid molecule cited
CC above, and comparing the concentration of the individual mRNA(s) with the
CC concentration of the corresponding mRNAs from at least one of the healthy
CC donor. The nucleic acids are also useful for the isolation and
CC development of a compound useful for therapy or prevention of a
CC cardiopathy. Sequences ACC78653-700 represent primers used in real-time
CC quantitative PCR for amplifying human genes, during the course of the
XX invention
XX Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

12/10/2001

```

DT 05-FEB-2003 (first entry)
DE CD81 forward PCR primer.
XX
XX
KW CD81; tetraspanin; human; dendritic cell; cell culture; cancer;
KW immunotherapy; cell therapy; cytostatic; antitumour; vaccine; PCR;
KW primer; ss.
XX
XX
OS Homo sapiens.
XX
XX WO200244338-A2.
PN
XX
XX 06-JUN-2002.
PD
XX
XX 30-NOV-2001; 2001WO-US045099.
PF
XX
XX 30-NOV-2000; 2000US-00726883.
PR
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
PA
XX
XX Harris PE, Hesdorffer C;
PI
XX
XX WPI; 2003-058273/05.
DR
XX
XX Reproducibly generating dendritic cells comprises loading blood
PT mononuclear cells into cell culture container containing microcarrier
PT beads, incubating the container, separating non-adherent cells and cells
PT adhered to beads.
XX
XX Example 2; Page 24; 79pp; English.
PS
XX
XX The present sequence is that of a forward primer, designated CD81-F, for
XX the human tetraspanin molecule, CD81. Semi-quantitative PCR was used to
XX determine the level of expression of 4 genes (CD37, CD81, CD53 and BCL-6)
XX in mature and immature dendritic cells (DCs). Abundant accumulation of
XX CD81 mRNA was detected in immature DCs, whereas significantly lower
XX levels of CD81 transcripts were detected following DC maturation,
XX indicating differential expression. The invention provides good
XX manufacturing procedure (GMP)-compatible culture methods for the
XX production of DCs to be used in cancer immunotherapy. These involve
XX loading blood mononuclear cells into a cell culture container, e.g. a gas
XX permeable cell culture bag containing sterile plastic microcarrier
XX beads, incubating the tissue culture, and separating non-adherent cells
XX from cells adhered to the microcarrier beads. The method can be adapted
XX for growth of other adherence-dependent haematopoietic cells
XX
XX Sequence 24 BP; 5 A; 9 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 398 GCGCCCAACACCTTCTATGTAGGC 421
DB 1 GCGCCCAACACCTTCTATGTAGGC 24
RESULT 11
ABV75839/C
ID ABV75839 standard; DNA; 24 BP.
XX
XX
AC ABV75839;
XX
XX
DT 05-FEB-2003 (first entry)
DE
DE CD81 reverse PCR primer.
XX
XX CD81; tetraspanin; human; dendritic cell; cell culture; cancer;
KW immunotherapy; cell therapy; cytostatic; antitumour; vaccine; PCR;
KW primer; ss.
XX
XX Homo sapiens.
OS
XX
XX Sequence 24 BP; 5 A; 9 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 398 GCGCCCAACACCTTCTATGTAGGC 421
DB 1 GCGCCCAACACCTTCTATGTAGGC 24

```

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PN WO200244338-A2.
XX
XX 06-JUN-2002.
PD
XX
XX 30-NOV-2001; 2001WO-US045099.
PF
XX
XX 30-NOV-2000; 2000US-00726883.
PR
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
PA
XX
XX Harris PE, Hesdorffer C;
PI
XX
XX WPI; 2003-058273/05.
DR
XX
XX Reproducibly generating dendritic cells comprises loading blood
PT mononuclear cells into cell culture container containing microcarrier
PT beads, incubating the container, separating non-adherent cells and cells
PT adhered to beads.
XX
XX Example 2; Page 24; 79pp; English.
PS
XX
XX The present sequence is that of a reverse primer, designated CD81-R, for
XX the human tetraspanin molecule, CD81. Semi-quantitative PCR was used to
XX determine the level of expression of 4 genes (CD37, CD81, CD53 and BCL-6)
XX in mature and immature dendritic cells (DCs). Abundant accumulation of
XX CD81 mRNA was detected in immature DCs, whereas significantly lower
XX levels of CD81 transcripts were detected following DC maturation,
XX indicating differential expression. The invention provides good
XX manufacturing procedure (GMP)-compatible culture methods for the
XX production of DCs to be used in cancer immunotherapy. These involve
XX loading blood mononuclear cells into a cell culture container, e.g. a gas
XX permeable cell culture bag containing sterile plastic microcarrier
XX beads, incubating the tissue culture, and separating non-adherent cells
XX from cells adhered to the microcarrier beads. The method can be adapted
XX for growth of other adherence-dependent haematopoietic cells
XX
XX Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 892 CGAGATGATCCTGAGCATGCTGCT 915
DB 24 CGAGATGATCCTGAGCATGCTGCT 1
RESULT 12
AAH88905
ID AAH88905 standard; DNA; 21 BP.
XX
XX
AC AAH88905;
XX
XX
DT 27-FEB-2002 (first entry)
DE
DE Human polymorphic oligonucleotide AC003693 fragment #1.
XX
XX Human; single nucleotide polymorphic; SNP; forensic science;
KW paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW plant breeding; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Variation replace(11,g)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200134840-A2.
PN
XX
XX 17-MAY-2001.
PD
XX
XX 10-NOV-2000; 2000WO-US030766.
PF

```

CC The invention relates to a novel method for screening substances
 CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
 CC antibody having an affinity for the protein. The novel method comprises:
 CC contacting the protein with any of the antibodies selected, from those
 CC described in the specification, in the presence or absence of a test
 CC substance; and comparing the binding results. Compositions comprising the
 CC (recombinant) antibodies are useful as antivirals and are especially
 CC useful in preventing or treating HCV (hepatitis C) infections. This
 CC polynucleotide sequence represents a PCR primer relating to the novel HCV
 CC therapy method of the invention
 XX
 SQ Sequence 26 BP; 3 A; 7 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 1.7%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 GCGCCGCCATGGAGTGGAGGGCTGC 256
 Db 1 GCGCCGCCATGGAGTGGAGGGCTGC 26

RESULT 8

AAH74674/C
 ID AAH74674 standard; DNA; 24 BP.

XX AC AAH74674;

XX 29-OCT-2001 (first entry)

XX PCR primer used to amplify DNA encoding a HCV protein.

XX Complementarity determining region; CDR; single chain antibody; ScFv;
 KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
 KW envelope glycoprotein; PCR primer; ss.

XX Hepatitis C virus.

XX WO200159459-A1.

XX 16-AUG-2001.

XX 13-FEB-2001; 2001WO-JP000967.

XX 14-FEB-2000; 2000JP-00034906.

XX (MITS-) MITSUBISHI-TOKYO PHARM INC.

XX Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;

XX WPI; 2001-496986/54.

XX Remedies for hepatitis C containing substances with antiviral effects
 PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
 PT compounds, by inhibiting binding of hepatitis C virus envelope
 PT glycoprotein or CD81.

XX Example 1; Page 27; 138pp; Japanese.

XX PCR primers AAH74673-74 were used to amplify DNA encoding a hepatitis C
 CC virus (HCV) protein. The amplified fragment was used in the course of the
 CC invention. The specification describes a substance which inhibits the
 CC binding between hepatitis C virus (HCV) and cells with potential HCV
 CC infection, cells with expression of CD81, or CD81. This substance is
 CC especially an antibody with affinity towards HCV E2/NS1 protein,
 CC containing amino acid sequences based on the complementarity determining
 CC region (CDR) 1, CDR2 and CDR3 of the H and L chain variable regions. The
 CC antibody inhibits the viral envelope glycoprotein. It is also a CD81
 CC inhibitor. The antibodies and drugs are used for treatment and/or
 CC prevention of hepatitis C, or for diagnosis of hepatitis C

XX Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TCCGGAACAGCTCCGTGTACTGAG 950
 Db 24 TCCGGAACAGCTCCGTGTACTGAG 1

RESULT 9

ABT34329/C
 ID ABT34329 standard; DNA; 24 BP.

XX AC ABT34329;

XX 12-JUN-2003 (first entry)

XX Hepatitis C virus treatment related PCR primer SEQ ID No 41.

XX Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
 KW antibody; recombinant; antiviral; infection; PCR; primer; ss.

XX Unidentified.

XX WO2003014728-A1.

XX 20-FEB-2003.

XX 09-AUG-2002; 2002WO-JP008175.

XX 10-AUG-2001; 2001JP-00243947.

XX (MITS-) MITSUBISHI PHARMA CORP.

PA (NINA-) JAPAN AGENCY NAT INST HEALTH.

XX Itami S, Seki M, Kito M, Matsuura Y, Miyamura T;

XX WPI; 2003-248334/24.

XX Pharmaceutical compositions for hepatitis C containing screened
 PT inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
 PT antibody, useful in preventing or treating HCV infections.

XX Example 2; Page 24; 136pp; Japanese.

XX The invention relates to a novel method for screening substances
 CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
 CC antibody having an affinity for the protein. The novel method comprises:
 CC contacting the protein with any of the antibodies selected, from those
 CC described in the specification, in the presence or absence of a test
 CC substance; and comparing the binding results. Compositions comprising the
 CC (recombinant) antibodies are useful as antivirals and are especially
 CC useful in preventing or treating HCV (hepatitis C) infections. This
 CC polynucleotide sequence represents a PCR primer relating to the novel HCV
 CC therapy method of the invention

XX Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TCCGGAACAGCTCCGTGTACTGAG 950
 Db 24 TCCGGAACAGCTCCGTGTACTGAG 1

RESULT 10

ABV75838
 ID ABV75838 standard; DNA; 24 BP.

XX AC ABV75838;

XX

QY 1385 GCCTTCATGCACTGTCCCTTTCTAAACAGTCGCGCTTCAACTGTGAATCACA 1434
 |||
 Db 1 GCCTTCATGCACTGTCCCTTTCTAAACAGTCGCGCTTCAACTGTGAATCACA 50

RESULT 3
 ACDC44032
 ID ACDC44032 standard; DNA; 31 BP.
 XX
 AC ACDC44032;
 XX
 DT 09-SEP-2003 (first entry)
 XX
 DE Human gene single nucleotide polymorphism region #466.
 XX
 KW Human; single nucleotide polymorphism; SNP; forensic; paternity testing;
 KW genetic mapping of phenotypic trait; ds.
 XX
 OS Homo sapiens.
 XX
 PN US2003039973-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 24-JUL-2001; 2001US-00912263.
 XX
 PR 24-JUL-2000; 2000US-0220315P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2003-492161/46.
 XX
 CC New nucleic acids comprising single nucleotide polymorphisms, useful in
 PT forensics (e.g. to identify an individual), paternity testing,
 PT correlating polymorphisms with phenotypic traits, and genetic mapping of
 PT phenotypic traits.
 XX
 PS Example; Page 40; 48pp; English.

XX The invention describes a nucleic acid molecule comprising one of 525 31
 CC nucleotide sequences, given in the specification, or at least 10
 CC nucleotides in length, and comprising a polymorphic site, where the
 CC nucleotide at the polymorphic site is different from a nucleotide at the
 CC polymorphic site in a corresponding reference allele. The nucleic acids
 CC comprising a single nucleotide polymorphism are useful in forensics (e.g.
 CC to identify an individual), in paternity testing, in correlating
 CC polymorphisms with phenotypic traits, and in genetic mapping of
 CC of a gene and a phenotype can be used in the diagnosis of that phenotype,
 CC as well as in the development of treatments for the phenotype. This
 CC sequence represents a fragment of a human gene found to containing a
 CC single nucleotide polymorphism following re-sequencing. The regions can
 CC be used to develop primers and probes for use in detect the SNP regions
 CC in individuals
 XX
 SQ Sequence 31 BP; 5 A; 10 C; 7 G; 8 T; 0 U; 1 Other;

Query Match 2.0%; Score 30.6; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 0.65;
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 820 CGATGACCTTCTTCGGGAAGCTGTACCTC 850
 |||
 Db 1 CGATGACCTTCTTCGGGAAGCTGTACCTC 31

RESULT 4
 ACDC44033
 ID ACDC44033 standard; DNA; 31 BP.
 XX

AC ACDC44033;
 XX
 DT 09-SEP-2003 (first entry)
 XX
 DE Human gene single nucleotide polymorphism region #467.
 XX
 KW Human; single nucleotide polymorphism; SNP; forensic; paternity testing;
 KW genetic mapping of phenotypic trait; ds.
 XX
 OS Homo sapiens.
 XX
 PN US2003039973-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 24-JUL-2001; 2001US-00912263.
 XX
 PR 24-JUL-2000; 2000US-0220315P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2003-492161/46.
 XX
 CC New nucleic acids comprising single nucleotide polymorphisms, useful in
 PT forensics (e.g. to identify an individual), paternity testing,
 PT correlating polymorphisms with phenotypic traits, and genetic mapping of
 PT phenotypic traits.
 XX
 PS Example; Page 40; 48pp; English.

XX The invention describes a nucleic acid molecule comprising one of 525 31
 CC nucleotide sequences, given in the specification, or at least 10
 CC nucleotides in length, and comprising a polymorphic site, where the
 CC nucleotide at the polymorphic site is different from a nucleotide at the
 CC polymorphic site in a corresponding reference allele. The nucleic acids
 CC comprising a single nucleotide polymorphism are useful in forensics (e.g.
 CC to identify an individual), in paternity testing, in correlating
 CC polymorphisms with phenotypic traits, and in genetic mapping of
 CC of a gene and a phenotype can be used in the diagnosis of that phenotype,
 CC as well as in the development of treatments for the phenotype. This
 CC sequence represents a fragment of a human gene found to containing a
 CC single nucleotide polymorphism following re-sequencing. The regions can
 CC be used to develop primers and probes for use in detect the SNP regions
 CC in individuals
 XX
 SQ Sequence 31 BP; 4 A; 8 C; 8 G; 10 T; 0 U; 1 Other;

Query Match 2.0%; Score 30.6; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 0.65;
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 862 TGCCATCGTGGTCGCTGTCATCATGATCTTC 892
 |||
 Db 1 TGCCATCGTGGTCGCTGTCATCATGATCTTC 31

RESULT 5
 ACDC35534
 ID ACDC35534 standard; DNA; 28 BP.
 XX
 AC ACDC35534;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 RT-PCR probe.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection; PCR; probe; RT-PCR; reverse transcriptase PCR;

545 13.4 0.9 15 1 AAF52139 IGF-1 oligonucleot
 546 13.4 0.9 15 1 AAF51849 IGF-1 oligonucleot
 547 13.4 0.9 15 1 AAF53315 IGF-1 oligonucleot
 548 13.4 0.9 15 1 AAF46582 IGF-1 oligonucleot
 549 13.4 0.9 15 1 AAF49043 IGF-1 oligonucleot
 550 13.4 0.9 15 1 AAF49042 IGF-1 oligonucleot
 551 13.4 0.9 15 1 AAF80919 PTGS2 allele speci
 552 13.4 0.9 15 1 AAF69483 Human IL4Ralpha ge
 553 13.4 0.9 15 1 ABA97405 Nucleotide sequenc
 554 13.4 0.9 15 1 ABK98166 Triple helix formi
 555 13.4 0.9 15 1 ABK98185 Triple helix formi
 556 13.4 0.9 15 1 ABZ95518 Human chymase anti
 557 13.4 0.9 15 1 ABX79839 EST polymorphic DN
 558 13.4 0.9 15 1 ADB68522 Single-base mismat
 559 13.2 0.9 14 1 AAV48216 3' poly-A-anchori
 560 13.2 0.9 14 1 AA251049 3' poly-A-anchori
 561 13.2 0.9 14 1 AA236741 Anchored oligo(dT)
 562 13.2 0.9 14 1 AAD44142 Oligo-dT PCR prime
 563 13.2 0.9 14 1 AAD44148 Oligo-dT PCR prime
 564 13.2 0.9 14 1 ADC51416 Rat LIRF protein-r
 565 13.2 0.9 15 1 AAX18386 RT-PCR primer of t

ALIGNMENTS

RESULT 1
 ABZ04679 standard; DNA; 50 BP.
 ID ABZ04679 standard; DNA; 50 BP.
 AC ABZ04679;
 XX
 DT 09-JAN-2003 (first entry)
 DE Human leukocyte gene expression profiling probe SEQ ID NO 4670.
 XX
 KW T7; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200257414-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 22-OCT-2001; 2001WO-US047856.
 XX
 PR 20-OCT-2000; 2000US-0241994P.
 PR 08-JUN-2001; 2001US-0296764P.
 XX
 PA (BIOC-) BIOCARDIA INC.
 XX
 PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 PI Ly N, Woodward R, Quertermous T, Johnson F;
 XX
 DR WPI; 2002-636525/68.
 XX
 PT New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.
 XX
 PS Claim 1; Page 477; Opp; English.
 XX
 CC The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 XX
 SQ Sequence 50 BP; 11 A; 18 C; 6 G; 15 T; 0 U; 0 Other;
 Query Match 3.3%; Score 50; DB 1; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 XX
 SQ Sequence 50 BP; 13 A; 17 C; 5 G; 15 T; 0 U; 0 Other;
 Query Match 3.3%; Score 50; DB 1; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1404 TTCTAACAGTCGCTTCAACTGTAATCAACATCCTGACTCCGTCATT 1453
 Db 1 TTCTAACAGTCGCTTCAACTGTAATCAACATCCTGACTCCGTCATT 50
 RESULT 2
 ABZ00175 standard; DNA; 50 BP.
 ID ABZ00175 standard; DNA; 50 BP.
 XX
 AC ABZ00175;
 XX
 DT 09-JAN-2003 (first entry)
 DE Human leukocyte gene expression profiling probe SEQ ID NO 166.
 XX
 KW T7; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200257414-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 22-OCT-2001; 2001WO-US047856.
 XX
 PR 20-OCT-2000; 2000US-0241994P.
 PR 08-JUN-2001; 2001US-0296764P.
 XX
 PA (BIOC-) BIOCARDIA INC.
 XX
 PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 PI Ly N, Woodward R, Quertermous T, Johnson F;
 XX
 DR WPI; 2002-636525/68.
 XX
 PT New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.
 XX
 PS Claim 1; Page 332; Opp; English.
 XX
 CC The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 XX
 SQ Sequence 50 BP; 11 A; 18 C; 6 G; 15 T; 0 U; 0 Other;
 Query Match 3.3%; Score 50; DB 1; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C 399	1.0	15	1	ABL57056	Hydrazide phosphor	C 472	14.4	1.0	16	1	AA183367	RT-PCR primer of t
C 400	1.0	15	1	ABL57060	Hydrazide precursor	C 473	14.4	1.0	16	1	AA183368	RT-PCR primer of t
C 401	1.0	15	1	ABK98141	Triple helix formi	C 474	14.4	1.0	16	1	AA27758	Primer used in hum
C 402	1.0	15	1	ABK98184	Triple helix formi	C 475	14.4	1.0	16	1	AAD44143	Oligo-dT PCR prime
C 403	1.0	15	1	AB275501	Oligonucleotide SE	C 476	14.4	1.0	16	1	AD86353	Human pTPN11 PCR p
C 404	1.0	15	1	ABV74142	5' End of CDNA lib	C 477	14.2	0.9	15	1	AA47676	Oligo d(T) primer
C 405	1.0	15	1	ABV74141	Oligonucleotide us	C 478	14.2	0.9	15	1	AAD41150	Oligo-AT PCR prime
C 406	1.0	15	1	ABV75865	Oligonucleotide u	C 479	14.2	0.9	16	1	AA183387	RT-PCR primer of t
C 407	1.0	15	1	ADA14836	Hairpin target seq	C 480	14	0.9	14	1	AAQ33508	Sequence of micros
C 408	1.0	15	1	ADB68520	Single-base mismat	C 481	14	0.9	14	1	AAT36896	Candida albicans 1
C 409	1.0	15	1	ADC18592	Annealing control	C 482	14	0.9	14	1	AAT75017	Breast tumour CDNA
C 410	1.0	15	1	AA183369	RT-PCR primer of t	C 483	14	0.9	14	1	AA833329	Breast cancer tumo
C 411	1.0	16	1	AA157075	Molecular beacon t	C 484	14	0.9	14	1	AAV09229	3' poly(T) primer
C 412	1.0	16	1	ABQ94572	Tumour suppression	C 485	14	0.9	14	1	AAV12221	Poly(T) oligonucle
C 413	1.0	16	1	AAQ94572	Tumour suppression	C 486	14	0.9	14	1	AAV69039	Human breast tumou
C 414	1.0	16	1	AAQ94572	Tumour suppression	C 487	14	0.9	14	1	AAQ02695	Barley HPPD primer
C 415	1.0	16	1	AAQ94572	Tumour suppression	C 488	14	0.9	14	1	AAQ02695	Triple helix third
C 416	1.0	17	1	AAQ94572	Tumour suppression	C 489	14	0.9	14	1	AAQ14689	Triple helix third
C 417	1.0	17	1	AAQ94572	Tumour suppression	C 490	14	0.9	14	1	AAQ14688	Triple helix third
C 418	1.0	17	1	AAQ94572	Tumour suppression	C 491	14	0.9	14	1	AAQ14688	Triple helix third
C 419	1.0	17	1	AAQ94572	Tumour suppression	C 492	14	0.9	14	1	AAQ14688	Triple helix third
C 420	1.0	17	1	AAQ94572	Tumour suppression	C 493	14	0.9	14	1	AAQ14688	Triple helix third
C 421	1.0	17	1	AAQ94572	Tumour suppression	C 494	14	0.9	14	1	AAQ14688	Triple helix third
C 422	1.0	17	1	AAQ94572	Tumour suppression	C 495	14	0.9	14	1	AAQ14688	Triple helix third
C 423	1.0	17	1	AAQ94572	Tumour suppression	C 496	14	0.9	14	1	AAQ14688	Triple helix third
C 424	1.0	17	1	AAQ94572	Tumour suppression	C 497	14	0.9	14	1	AAQ14688	Triple helix third
C 425	1.0	17	1	AAQ94572	Tumour suppression	C 498	14	0.9	14	1	AAQ14688	Triple helix third
C 426	1.0	17	1	AAQ94572	Tumour suppression	C 499	14	0.9	14	1	AAQ14688	Triple helix third
C 427	1.0	17	1	AAQ94572	Tumour suppression	C 500	14	0.9	14	1	AAQ14688	Triple helix third
C 428	1.0	17	1	AAQ94572	Tumour suppression	C 501	14	0.9	14	1	AAQ14688	Triple helix third
C 429	1.0	17	1	AAQ94572	Tumour suppression	C 502	14	0.9	14	1	AAQ14688	Triple helix third
C 430	1.0	17	1	AAQ94572	Tumour suppression	C 503	14	0.9	14	1	AAQ14688	Triple helix third
C 431	1.0	17	1	AAQ94572	Tumour suppression	C 504	14	0.9	14	1	AAQ14688	Triple helix third
C 432	1.0	17	1	AAQ94572	Tumour suppression	C 505	14	0.9	14	1	AAQ14688	Triple helix third
C 433	1.0	17	1	AAQ94572	Tumour suppression	C 506	14	0.9	14	1	AAQ14688	Triple helix third
C 434	1.0	17	1	AAQ94572	Tumour suppression	C 507	14	0.9	14	1	AAQ14688	Triple helix third
C 435	1.0	17	1	AAQ94572	Tumour suppression	C 508	14	0.9	14	1	AAQ14688	Triple helix third
C 436	1.0	17	1	AAQ94572	Tumour suppression	C 509	14	0.9	14	1	AAQ14688	Triple helix third
C 437	1.0	17	1	AAQ94572	Tumour suppression	C 510	14	0.9	14	1	AAQ14688	Triple helix third
C 438	1.0	17	1	AAQ94572	Tumour suppression	C 511	14	0.9	14	1	AAQ14688	Triple helix third
C 439	1.0	17	1	AAQ94572	Tumour suppression	C 512	14	0.9	14	1	AAQ14688	Triple helix third
C 440	1.0	17	1	AAQ94572	Tumour suppression	C 513	14	0.9	14	1	AAQ14688	Triple helix third
C 441	1.0	17	1	AAQ94572	Tumour suppression	C 514	14	0.9	14	1	AAQ14688	Triple helix third
C 442	1.0	17	1	AAQ94572	Tumour suppression	C 515	14	0.9	14	1	AAQ14688	Triple helix third
C 443	1.0	17	1	AAQ94572	Tumour suppression	C 516	14	0.9	14	1	AAQ14688	Triple helix third
C 444	1.0	17	1	AAQ94572	Tumour suppression	C 517	14	0.9	14	1	AAQ14688	Triple helix third
C 445	1.0	17	1	AAQ94572	Tumour suppression	C 518	14	0.9	14	1	AAQ14688	Triple helix third
C 446	1.0	17	1	AAQ94572	Tumour suppression	C 519	14	0.9	14	1	AAQ14688	Triple helix third
C 447	1.0	17	1	AAQ94572	Tumour suppression	C 520	14	0.9	14	1	AAQ14688	Triple helix third
C 448	1.0	17	1	AAQ94572	Tumour suppression	C 521	14	0.9	14	1	AAQ14688	Triple helix third
C 449	1.0	17	1	AAQ94572	Tumour suppression	C 522	14	0.9	14	1	AAQ14688	Triple helix third
C 450	1.0	17	1	AAQ94572	Tumour suppression	C 523	14	0.9	14	1	AAQ14688	Triple helix third
C 451	1.0	17	1	AAQ94572	Tumour suppression	C 524	14	0.9	14	1	AAQ14688	Triple helix third
C 452	1.0	17	1	AAQ94572	Tumour suppression	C 525	13.8	0.9	18	1	AAQ14688	Triple helix third
C 453	1.0	17	1	AAQ94572	Tumour suppression	C 526	13.6	0.9	15	1	AAQ14688	Triple helix third
C 454	1.0	17	1	AAQ94572	Tumour suppression	C 527	13.6	0.9	50	1	AAQ14688	Triple helix third
C 455	1.0	17	1	AAQ94572	Tumour suppression	C 528	13.4	0.9	15	1	AAQ14688	Triple helix third
C 456	1.0	17	1	AAQ94572	Tumour suppression	C 529	13.4	0.9	15	1	AAQ14688	Triple helix third
C 457	1.0	17	1	AAQ94572	Tumour suppression	C 530	13.4	0.9	15	1	AAQ14688	Triple helix third
C 458	1.0	17	1	AAQ94572	Tumour suppression	C 531	13.4	0.9	15	1	AAQ14688	Triple helix third
C 459	1.0	17	1	AAQ94572	Tumour suppression	C 532	13.4	0.9	15	1	AAQ14688	Triple helix third
C 460	1.0	17	1	AAQ94572	Tumour suppression	C 533	13.4	0.9	15	1	AAQ14688	Triple helix third
C 461	1.0	17	1	AAQ94572	Tumour suppression	C 534	13.4	0.9	15	1	AAQ14688	Triple helix third
C 462	1.0	17	1	AAQ94572	Tumour suppression	C 535	13.4	0.9	15	1	AAQ14688	Triple helix third
C 463	1.0	17	1	AAQ94572	Tumour suppression	C 536	13.4	0.9	15	1	AAQ14688	Triple helix third
C 464	1.0	17	1	AAQ94572	Tumour suppression	C 537	13.4	0.9	15	1	AAQ14688	Triple helix third
C 465	1.0	17	1	AAQ94572	Tumour suppression	C 538	13.4	0.9	15	1	AAQ14688	Triple helix third
C 466	1.0	17	1	AAQ94572	Tumour suppression	C 539	13.4	0.9	15	1	AAQ14688	Triple helix third
C 467	1.0	17	1	AAQ94572	Tumour suppression	C 540	13.4	0.9	15	1	AAQ14688	Triple helix third
C 468	1.0	17	1	AAQ94572	Tumour suppression	C 541	13.4	0.9	15	1	AAQ14688	Triple helix third
C 469	1.0	17	1	AAQ94572	Tumour suppression	C 542	13.4	0.9	15	1	AAQ14688	Triple helix third
C 470	1.0	17	1	AAQ94572	Tumour suppression	C 543	13.4	0.9	15	1	AAQ14688	Triple helix third
C 471	1.0	17	1	AAQ94572	Tumour suppression	C 544	13.4	0.9	15	1	AAQ14688	Triple helix third

C 253	1.1	17	1	ACF36345	Nucleotide sequenc	C 326	15.4	1.0	18	1	AAZ90641	Human adipose tiss
C 254	1.1	17	1	ACF36370	Nucleotide sequenc	C 327	15.4	1.0	18	1	AAZ90650	Human adipose tiss
C 255	1.1	17	1	ADC84468	PCR primer for amp	C 328	15.4	1.0	18	1	AAZ90647	Human adipose tiss
C 256	1.1	18	1	AAQ34110	Sequence of a micr	C 329	15.4	1.0	18	1	AAF85699	Multiple repeated
C 257	1.1	18	1	AAQ5025	PCR primer. Synth	C 330	15.4	1.0	18	1	ADA27361	Human microsatelli
C 258	1.1	18	1	AAQ94668	Anchored poly(T) o	C 331	15.4	1.0	18	1	ADC26385	NOV protein-relate
C 259	1.1	18	1	AAV54173	Nucleotide sequenc	C 332	15.2	1.0	16	1	AAQ82119	Human TSA7005 gene
C 260	1.1	18	1	AAV54164	Nucleotide sequenc	C 333	15.2	1.0	17	1	AAQ82119	RT-PCR primer of t
C 261	1.1	18	1	AAV54167	Nucleotide sequenc	C 334	15.2	1.0	17	1	AAQ82119	Modified Poly-T Pr
C 262	1.1	18	1	AAV37712	Human protein AQ2	C 335	15	1.0	15	1	AAQ79185	Nuclease resistant
C 263	1.1	18	1	AAV07750	Phosphorothioate o	C 336	15	1.0	15	1	AAQ79184	Nuclease resistant
C 264	1.1	18	1	AAV21970	Nuclease resistant	C 337	15	1.0	15	1	AAQ79184	Human ICAM hammerh
C 265	1.1	18	1	AAV19943	Primer SEQ ID NO:3	C 338	15	1.0	15	1	AAQ79184	Human ICAM hammerh
C 266	1.1	18	1	AAV19942	Primer SEQ ID NO:2	C 339	15	1.0	15	1	AAQ79184	Oligonucleotide co
C 267	1.1	18	1	AAA40563	Human adult ovary	C 340	15	1.0	15	1	AAV01604	Oligonucleotide co
C 268	1.1	18	1	AAZ90643	Human adipose tiss	C 341	15	1.0	15	1	AAV01603	Oligonucleotide co
C 269	1.1	18	1	AAZ90646	Human adipose tiss	C 342	15	1.0	15	1	AAV01603	Synthetic peptide-
C 270	1.1	18	1	AAZ90643	Human adipose tiss	C 343	15	1.0	15	1	AAQ86675	Oligonucleotide li
C 271	1.1	18	1	AAZ87161	Oligoarabinonucleo	C 344	15	1.0	15	1	AAQ86675	Oligonucleotide se
C 272	1.1	18	1	AAZ87162	Deoxyarabinonucleo	C 345	15	1.0	15	1	AAQ86675	Transcript tag seq
C 273	1.1	18	1	AAZ87166	Deoxyarabinonucleo	C 346	15	1.0	15	1	AAQ86675	Tag sequence of a
C 274	1.1	18	1	AAZ87167	Deoxyarabinonucleo	C 347	15	1.0	15	1	AAQ86675	Tag sequence of a
C 275	1.1	18	1	AAQ03565	Oligonucleotide #6	C 348	15	1.0	15	1	AAQ00787	N3-P5 phosphoramid
C 276	1.1	18	1	AAQ17014	Oligonucleotide A1	C 349	15	1.0	15	1	AAQ00787	N3-P5 phosphoramid
C 277	1.1	18	1	AAQ17014	Binary encoded seq	C 350	15	1.0	15	1	AAQ00787	HCV 3', non core re
C 278	1.1	18	1	AAQ75597	Binary encoded seq	C 351	15	1.0	15	1	AAQ00787	Substrate for HH r
C 279	1.1	18	1	AAQ75597	mRNA fragment used	C 352	15	1.0	15	1	AAQ00787	PCR primer used to
C 280	1.1	18	1	AAQ99708	Immunostimulatory	C 353	15	1.0	15	1	AAQ00787	Primer used to rev
C 281	1.1	18	1	AAQ99734	Immunostimulatory	C 354	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 282	1.1	18	1	AAQ92472	Phagemid vector pC	C 355	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 283	1.1	18	1	AAQ51158	Human cytomegalovi	C 356	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 284	1.1	18	1	AAQ51158	Human cytomegalovi	C 357	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 285	1.1	18	1	AAQ51158	Human cytomegalovi	C 358	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 286	1.1	18	1	AAQ51158	Human cytomegalovi	C 359	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 287	1.1	18	1	AAQ51158	Human cytomegalovi	C 360	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 288	1.1	18	1	AAQ51158	Human cytomegalovi	C 361	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 289	1.1	18	1	AAQ51158	Human cytomegalovi	C 362	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 290	1.1	18	1	AAQ51158	Human cytomegalovi	C 363	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 291	1.1	18	1	AAQ51158	Human cytomegalovi	C 364	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 292	1.1	18	1	AAQ51158	Human cytomegalovi	C 365	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 293	1.1	18	1	AAQ51158	Human cytomegalovi	C 366	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 294	1.1	18	1	AAQ51158	Human cytomegalovi	C 367	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 295	1.1	18	1	AAQ51158	Human cytomegalovi	C 368	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 296	1.1	18	1	AAQ51158	Human cytomegalovi	C 369	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 297	1.1	18	1	AAQ51158	Human cytomegalovi	C 370	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 298	1.1	18	1	AAQ51158	Human cytomegalovi	C 371	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 299	1.1	18	1	AAQ51158	Human cytomegalovi	C 372	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 300	1.1	18	1	AAQ51158	Human cytomegalovi	C 373	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 301	1.1	18	1	AAQ51158	Human cytomegalovi	C 374	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 302	1.1	18	1	AAQ51158	Human cytomegalovi	C 375	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 303	1.1	18	1	AAQ51158	Human cytomegalovi	C 376	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 304	1.1	18	1	AAQ51158	Human cytomegalovi	C 377	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 305	1.1	18	1	AAQ51158	Human cytomegalovi	C 378	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 306	1.1	18	1	AAQ51158	Human cytomegalovi	C 379	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 307	1.1	18	1	AAQ51158	Human cytomegalovi	C 380	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 308	1.1	18	1	AAQ51158	Human cytomegalovi	C 381	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 309	1.1	18	1	AAQ51158	Human cytomegalovi	C 382	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 310	1.1	18	1	AAQ51158	Human cytomegalovi	C 383	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 311	1.1	18	1	AAQ51158	Human cytomegalovi	C 384	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 312	1.1	18	1	AAQ51158	Human cytomegalovi	C 385	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 313	1.1	18	1	AAQ51158	Human cytomegalovi	C 386	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 314	1.1	18	1	AAQ51158	Human cytomegalovi	C 387	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 315	1.1	18	1	AAQ51158	Human cytomegalovi	C 388	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 316	1.1	18	1	AAQ51158	Human cytomegalovi	C 389	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 317	1.1	18	1	AAQ51158	Human cytomegalovi	C 390	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 318	1.1	18	1	AAQ51158	Human cytomegalovi	C 391	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 319	1.1	18	1	AAQ51158	Human cytomegalovi	C 392	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 320	1.1	18	1	AAQ51158	Human cytomegalovi	C 393	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 321	1.1	18	1	AAQ51158	Human cytomegalovi	C 394	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 322	1.1	18	1	AAQ51158	Human cytomegalovi	C 395	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 323	1.1	18	1	AAQ51158	Human cytomegalovi	C 396	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 324	1.1	18	1	AAQ51158	Human cytomegalovi	C 397	15	1.0	15	1	AAQ00787	Nucleic acid sequ
C 325	1.1	18	1	AAQ51158	Human cytomegalovi	C 398	15	1.0	15	1	AAQ00787	Nucleic acid sequ

C 107	18	1.2	19	1	AAQ75551	Reverse transcript	C 180	16.4	1.1	18	1	ACF36339	Nucleotide sequenc
C 108	18	1.2	20	1	AAQ75575	Reverse transcript	C 181	16.4	1.1	18	1	ACF36364	Nucleotide sequenc
C 109	18	1.2	20	1	AAQ75577	Reverse transcript	C 182	16.4	1.1	19	1	AAQ75549	Reverse transcript
C 110	18	1.2	20	1	AAQ75576	Reverse transcript	C 183	16.4	1.1	19	1	AAQ75548	Reverse transcript
C 111	18	1.2	20	1	AAT04916	Mammalian stem cel	C 184	16.4	1.1	19	1	AAQ75547	Reverse transcript
C 112	18	1.2	20	1	AAH13753	Stem cell factor u	C 185	16.4	1.1	19	1	AAQ75555	Reverse transcript
C 113	18	1.2	20	1	AAH41332	Universal stem cel	C 186	16.2	1.1	18	1	AAH18389	RT-PCR primer of t
C 114	18	1.2	20	1	AAH41332	Universal stem cel	C 187	16.2	1.1	19	1	AAH18389	RT-PCR primer of t
C 115	18	1.2	20	1	AAH41332	Universal stem cel	C 188	16.2	1.1	19	1	AAH18390	RT-PCR primer of t
C 116	18	1.2	20	1	AAH23890	Human SCF (stem ce	C 189	16.2	1.1	19	1	AAH06572	(-)-limonene-6-hyd
C 117	18	1.2	20	1	AAH04213	Human SCF (stem ce	C 190	16.2	1.1	19	1	AAZ99489	Primer HOOK for CD
C 118	18	1.2	20	1	AAH10448	Human stem cell fa	C 191	16.2	1.1	19	1	AAZ15201	3' sequencing prim
C 119	18	1.2	20	1	AAH35465	Rat SCF 5' cDNA am	C 192	16.2	1.1	19	1	AAH21968	Mouse total gene è
C 120	18	1.2	20	1	ABH73849	SCF universal olig	C 193	16.2	1.1	19	1	AAH76617	Spearmint (-)-limo
C 121	18	1.2	20	1	ABA05917	Hepatitis B virus	C 194	16.2	1.1	19	1	AAH06525	Mouse microglia an
C 122	18	1.2	20	1	ABZ89240	Human oligonucleot	C 195	16.2	1.1	19	1	ABK71509	CNS related 3' seq
C 123	18	1.2	20	1	ADH52461	Stem cell factor (C 196	16.2	1.1	19	1	ABK71231	Rabbit atheroscler
C 124	18	1.2	21	1	AAQ75713	Reverse transcript	C 197	16.2	1.1	19	1	ABK71231	PCR primer #4 used
C 125	18	1.2	21	1	AAQ75703	Reverse transcript	C 198	16.2	1.1	19	1	AAH34663	HOOK PCR primer us
C 126	18	1.2	21	1	AAQ75714	Reverse transcript	C 199	16.2	1.1	19	1	ABZ40279	Reverse transcript
C 127	18	1.2	21	1	AAQ75705	Reverse transcript	C 200	16.2	1.1	19	1	ABZ68389	Reverse transcript
C 128	18	1.2	21	1	AAQ75706	Reverse transcript	C 201	16.2	1.1	19	1	ACF79402	M13 sequencing pri
C 129	18	1.2	21	1	AAQ75707	Reverse transcript	C 202	16.2	1.1	19	1	AAH49149	3' sequencing prim
C 130	18	1.2	21	1	AAQ75710	Reverse transcript	C 203	16.2	1.1	19	1	ADH50267	3' sequencing prim
C 131	18	1.2	21	1	AAQ75709	Reverse transcript	C 204	16.2	1.1	19	1	ADH21495	Human PRDI-BF1 RT-
C 132	18	1.2	21	1	AAQ75711	Reverse transcript	C 205	16.2	1.1	16	1	AAH18368	RT-PCR primer of t
C 133	17.4	1.2	19	1	AAQ75550	Reverse transcript	C 206	16.2	1.1	16	1	AAH07568	Homo sapiens fetal
C 134	17.4	1.2	20	1	AAQ75574	Reverse transcript	C 207	16.2	1.1	16	1	AAH06068	DNA chip primer #4
C 135	17.4	1.2	20	1	AAQ75586	Reverse transcript	C 208	16.2	1.1	16	1	ABH04585	Oligonucleotide #5
C 136	17.4	1.2	20	1	AAQ75594	Reverse transcript	C 209	16.2	1.1	16	1	AAH30895	Oligonucleotide-mi
C 137	17.4	1.2	20	1	AAQ75562	Reverse transcript	C 210	16.2	1.1	16	1	AAH30880	Oligonucleotide po
C 138	17.4	1.2	20	1	AAQ75573	Reverse transcript	C 211	16.2	1.1	16	1	ABH42481	Oligonucleotide us
C 139	17.4	1.2	20	1	AAQ75590	Reverse transcript	C 212	16.2	1.1	16	1	ABH97402	Nucleotide sequenc
C 140	17.4	1.2	20	1	AAQ75582	Reverse transcript	C 213	16.2	1.1	16	1	AAH56451	2' F-ANA antisense
C 141	17.4	1.2	20	1	AAQ75571	Reverse transcript	C 214	16.2	1.1	16	1	AAH54078	Oligo-homodeoxyrib
C 142	17.4	1.2	20	1	AAH83128	Cell cycle regulat	C 215	16.2	1.1	16	1	ADH68519	DNA hybridisation
C 143	17.4	1.2	20	1	AAH69679	Hepatitis E virus	C 216	16.2	1.1	17	1	AAH98800	Human flt1 VEGF re
C 144	17.4	1.2	20	1	AAH69675	Hepatitis E virus	C 217	16.2	1.1	17	1	AAH98801	Human flt1 VEGF re
C 145	17.4	1.2	20	1	ABZ85532	Human oligonucleot	C 218	16.2	1.1	17	1	AAH49503	Human eosinophil c
C 146	17	1.1	18	1	AAH94667	Anchored poly(T) o	C 219	16.2	1.1	17	1	AAH18371	RT-PCR primer of t
C 147	17	1.1	18	1	AAH54170	Nucleotide sequenc	C 220	16.2	1.1	17	1	AAH18370	PCR primer GT15A u
C 148	17	1.1	18	1	AAH16008	PCR primer D-R use	C 221	16.2	1.1	17	1	AAH30179	Human IGA nephropa
C 149	17	1.1	18	1	AAH18373	RT-PCR primer of t	C 222	16.2	1.1	17	1	AAH82720	Anchored oligo(dr)
C 150	17	1.1	18	1	AAH18372	RT-PCR primer of t	C 223	16.2	1.1	17	1	AAH36739	Oestrogen receptor
C 151	17	1.1	18	1	AAZ90640	Human adipose ties	C 224	16.2	1.1	17	1	AAH25450	Oestrogen receptor
C 152	17	1.1	18	1	AAZ43267	Murine Sox3 gene p	C 225	16.2	1.1	17	1	AAH25449	Oestrogen receptor
C 153	17	1.1	18	1	AAH03252	PCR primer D-R use	C 226	16.2	1.1	17	1	AAH98232	Human retrovirus H
C 154	17	1.1	19	1	AAQ75552	Reverse transcript	C 227	16.2	1.1	17	1	AAH50197	2'-Methoxyethoxy-m
C 155	17	1.1	19	1	AAQ75553	Reverse transcript	C 228	16.2	1.1	17	1	AAH64202	PCR anchor primer,
C 156	17	1.1	19	1	AAQ75554	Reverse transcript	C 229	16.2	1.1	17	1	AAH64181	PCR anchor primer,
C 157	17	1.1	20	1	AAQ75584	Reverse transcript	C 230	16.2	1.1	17	1	AAH64171	PCR anchor primer,
C 158	17	1.1	20	1	AAQ75585	Reverse transcript	C 231	16.2	1.1	17	1	AAH64161	PCR anchor primer,
C 159	17	1.1	20	1	AAQ75579	Reverse transcript	C 232	16.2	1.1	17	1	AAH64213	PCR anchor primer,
C 160	17	1.1	20	1	AAQ75589	Reverse transcript	C 233	16.2	1.1	17	1	AAH64230	PCR anchor primer,
C 161	17	1.1	20	1	AAQ75588	Reverse transcript	C 234	16.2	1.1	17	1	AAH92292	Human pollinosis-a
C 162	17	1.1	20	1	AAQ75581	Reverse transcript	C 235	16.2	1.1	17	1	AAH91719	PCR anchor primer,
C 163	17	1.1	20	1	AAQ75583	Reverse transcript	C 236	16.2	1.1	17	1	AAH28874	Human pollinosis-a
C 164	17	1.1	20	1	AAQ75580	Reverse transcript	C 237	16.2	1.1	17	1	AAH47126	Nucleotide sequenc
C 165	17	1.1	20	1	AAQ75587	Reverse transcript	C 238	16.2	1.1	17	1	ABK13941	5'-PCR primer used
C 166	17	1.1	20	1	AAH07752	Phosphorothioate o	C 239	16.2	1.1	17	1	ABK49634	Human Acetyltransf
C 167	17	1.1	20	1	ABZ89546	Human oligonucleot	C 240	16.2	1.1	17	1	ABH59038	Nucleotide sequenc
C 168	17	1.1	20	1	ABZ88880	Human oligonucleot	C 241	16.2	1.1	17	1	ABH99829	Human allergic dis
C 169	17	1.1	20	1	ABZ89179	Human oligonucleot	C 242	16.2	1.1	17	1	AAH49948	Human B1153 expres
C 170	17	1.1	20	1	ABZ92865	Human oligonucleot	C 243	16.2	1.1	17	1	AAH47234	Allergic disease e
C 171	17	1.1	20	1	ABZ89703	Human oligonucleot	C 244	16.2	1.1	17	1	ABK49756	Human atopic derma
C 172	17	1.1	20	1	ABZ88694	Human oligonucleot	C 245	16.2	1.1	17	1	ABH04271	Human MD27 scanlin
C 173	17	1.1	20	1	ABZ89014	Human oligonucleot	C 246	16.2	1.1	17	1	ABH04272	Human MD27 scanlin
C 174	17	1.1	20	1	ABZ89014	Human oligonucleot	C 247	16.2	1.1	17	1	ABZ70578	Primer. Synthetic
C 175	16.6	1.1	18	1	ADH44128	PCR primer #3 deat	C 248	16.2	1.1	17	1	AAH56441	Antisense oligo #2
C 176	16.6	1.1	19	1	AAH69640	Telomerase Oligo-d	C 249	16.2	1.1	17	1	AAH56448	2' F-ANA antisense
C 177	16.4	1.1	18	1	AAH30173	Sequence derived f	C 250	16.2	1.1	17	1	AAH56449	2' F-ANA antisense
C 178	16.4	1.1	18	1	AAH94669	Anchored poly(T) o	C 251	16.2	1.1	17	1	AAH56447	2' F-ANA antisense
C 179	16.4	1.1	18	1	ABK13935	5'-PCR primer used	C 252	16.2	1.1	17	1	AAH56450	2' F-ANA antisense

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OM nucleic - nucleic search, using sw model

Run on: April 21, 2004, 10:48:45 ; Search time 8 seconds
(without alignments)

3.711 Million cell updates/sec

Title: \ us-10-006-430-3

Perfect score: 1496

Sequence: 1 ccattgtgtggaaggcgc.....tgctaaaaaataaaaaaa 1496

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 562 seqs, 9922 residues

Total number of hits satisfying chosen parameters: 1124

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 565 summaries

Database : rng3.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	3.3	50	1	ABZ004679
2	50	3.3	50	1	Human leukocyte ge
3	30.6	2.0	31	1	ACD44032
4	30.6	2.0	31	1	Human gene single
5	28	1.9	28	1	Human gene single
6	26	1.7	26	1	Human CD81/TAPA-1
7	26	1.7	26	1	PCR primer used to
8	24	1.6	24	1	Hepatitis C virus
9	24	1.6	24	1	PCR primer used to
10	24	1.6	24	1	Hepatitis C virus
11	24	1.6	24	1	CD81 forward PCR p
12	21	1.4	21	1	CD81 reverse PCR p
13	21	1.4	21	1	Human polymorphic
14	21	1.4	21	1	Human polymorphic
15	20	1.3	20	1	Nucleotide sequenc
16	20	1.3	20	1	Nucleotide sequenc
17	20	1.3	20	1	Human CD81/TAPA-1
18	20	1.3	20	1	Human CD81/TAPA-1
19	20	1.3	20	1	Human CD81/TAPA-1
20	20	1.3	20	1	Human CD81/TAPA-1
21	20	1.3	20	1	Human CD81/TAPA-1
22	20	1.3	20	1	Human CD81/TAPA-1
23	20	1.3	20	1	Human CD81/TAPA-1
24	20	1.3	20	1	Human CD81/TAPA-1
25	20	1.3	20	1	Human CD81/TAPA-1
26	20	1.3	20	1	Human CD81/TAPA-1
27	20	1.3	20	1	Human CD81/TAPA-1
28	20	1.3	20	1	Human CD81/TAPA-1
29	20	1.3	20	1	Human CD81/TAPA-1
30	20	1.3	20	1	Human CD81/TAPA-1
31	20	1.3	20	1	Human CD81/TAPA-1
32	20	1.3	20	1	Human CD81/TAPA-1
33	20	1.3	20	1	Human CD81/TAPA-1

Human	CD81/TAPA-1	1	ADC35597	20	1.3	20	C 34
Human	CD81/TAPA-1	1	ADC35544	20	1.3	20	C 35
Human	CD81/TAPA-1	1	ADC35558	20	1.3	20	C 36
Human	CD81/TAPA-1	1	ADC35572	20	1.3	20	C 37
Human	CD81/TAPA-1	1	ADC35617	20	1.3	20	C 38
Human	CD81/TAPA-1	1	ADC35577	20	1.3	20	C 39
Human	CD81/TAPA-1	1	ADC35590	20	1.3	20	C 40
Human	CD81/TAPA-1	1	ADC35605	20	1.3	20	C 41
Human	CD81/TAPA-1	1	ADC35554	20	1.3	20	C 42
Human	CD81/TAPA-1	1	ADC35566	20	1.3	20	C 43
Human	CD81/TAPA-1	1	ADC35579	20	1.3	20	C 44
Human	CD81/TAPA-1	1	ADC35587	20	1.3	20	C 45
Human	CD81/TAPA-1	1	ADC35589	20	1.3	20	C 46
Human	CD81/TAPA-1	1	ADC35581	20	1.3	20	C 47
Human	CD81/TAPA-1	1	ADC35582	20	1.3	20	C 48
Human	CD81/TAPA-1	1	ADC35598	20	1.3	20	C 49
Human	CD81/TAPA-1	1	ADC35550	20	1.3	20	C 50
Human	CD81/TAPA-1	1	ADC35552	20	1.3	20	C 51
Human	CD81/TAPA-1	1	ADC35555	20	1.3	20	C 52
Human	CD81/TAPA-1	1	ADC35569	20	1.3	20	C 53
Human	CD81/TAPA-1	1	ADC35593	20	1.3	20	C 54
Human	CD81/TAPA-1	1	ADC35560	20	1.3	20	C 55
Human	CD81/TAPA-1	1	ADC35588	20	1.3	20	C 56
Human	CD81/TAPA-1	1	ADC35594	20	1.3	20	C 57
Human	CD81/TAPA-1	1	ADC35602	20	1.3	20	C 58
Human	CD81/TAPA-1	1	ADC35542	20	1.3	20	C 59
Human	CD81/TAPA-1	1	ADC35553	20	1.3	20	C 60
Human	CD81/TAPA-1	1	ADC35576	20	1.3	20	C 61
Human	CD81/TAPA-1	1	ADC35596	20	1.3	20	C 62
Human	CD81/TAPA-1	1	ADC35541	20	1.3	20	C 63
Human	CD81/TAPA-1	1	ADC35546	20	1.3	20	C 64
Human	CD81/TAPA-1	1	ADC35559	20	1.3	20	C 65
Human	CD81/TAPA-1	1	ADC35601	20	1.3	20	C 66
Human	CD81/TAPA-1	1	ADC35604	20	1.3	20	C 67
Human	CD81/TAPA-1	1	ADC35532	20	1.3	20	C 68
Human	CD81/TAPA-1	1	ADC35573	20	1.3	20	C 69
Human	CD81/TAPA-1	1	ADC35562	20	1.3	20	C 70
Human	CD81/TAPA-1	1	ADC35565	20	1.3	20	C 71
Human	CD81/TAPA-1	1	ADC35578	20	1.3	20	C 72
Human	CD81/TAPA-1	1	ADC35580	20	1.3	20	C 73
Human	CD81/TAPA-1	1	ADC35603	20	1.3	20	C 74
Human	CD81/TAPA-1	1	ADC35606	20	1.3	20	C 75
Human	CD81/TAPA-1	1	ADC35547	20	1.3	20	C 76
Human	CD81/TAPA-1	1	ADC35549	20	1.3	20	C 77
Human	CD81/TAPA-1	1	ADC35561	20	1.3	20	C 78
Human	CD81/TAPA-1	1	ADC35563	20	1.3	20	C 79
Human	CD81/TAPA-1	1	ADC35570	20	1.3	20	C 80
Human	CD81/TAPA-1	1	ADC35575	20	1.3	20	C 81
Human	CD81/TAPA-1	1	ADC35583	20	1.3	20	C 82
Human	CD81/TAPA-1	1	ADC35592	20	1.3	20	C 83
Human	CD81/TAPA-1	1	ADC35600	20	1.3	20	C 84
Reverse transcript			AAQ75716	21	1.3	20	C 85
Reverse transcript			AAQ75661	21	1.3	20	C 86
Cytochrome p450 se			AAQ49436	20	1.3	19	C 87
Reverse transcript			AAQ75578	20	1.3	19	C 88
Human oligonucleot			ABZ88266	20	1.3	19	C 89
Reverse transcript			AAQ75718	21	1.3	19	C 90
Reverse transcript			AAQ75715	21	1.3	19	C 91
Reverse transcript			AAQ75717	21	1.3	19	C 92
Human leukocyte ge			ABZ00175	50	1.3	50	C 93
Reverse transcript			AAQ75572	20	1.2	18	C 94
Reverse transcript			AAQ75748	21	1.2	18	C 95
Reverse transcript			AAQ75620	21	1.2	18	C 96
Reverse transcript			AAQ75732	21	1.2	18	C 97
Reverse transcript			AAQ75660	21	1.2	18	C 98
Reverse transcript			AAQ75684	21	1.2	18	C 99
Reverse transcript			AAQ75700	21	1.2	18	C 100
Reverse transcript			AAQ75659	21	1.2	18	C 101
Reverse transcript			AAQ75712	21	1.2	18	C 102
Reverse transcript			AAQ75704	21	1.2	18	C 103
Reverse transcript			AAQ75708	21	1.2	18	C 104
Reverse transcript			AAQ75662	21	1.2	18	C 105
Human CD81/TAPA-1			ADC35533	18	1.2	18	C 106

Query Match 1.4%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 668 AAGCTGTGTGTAAGACCTTC 688
 DB 1 AAGCTGTGTGTAAGACCTTC 21

RESULT 15

ACC78664/c

ID ACC78664 standard; DNA; 20 BP.

XX AC ACC78664;

XX DT 02-SRP-2003 (first entry)

XX DE Nucleotide sequence of a PCR primer CD81_R.

XX KW Cardiopathy; nucleic acid marker; therapy; human; PCR; primer; ss.

XX OS Homo sapiens.

XX PN WO2003040407-A2.

XX PD 15-MAY-2003.

XX PF 08-NOV-2002; 2002WO-EP012522.

XX PR 09-NOV-2001; 2001EP-00126800.

XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX PI Ruiz P, Grzeskowiak R, Drungowski M, Witt H, Osterziel KJ;
 XX PI Perrot A, Saleh A;

XX DR WPI; 2003-430678/40.

XX PT New diagnostic composition comprising at least one nucleic acid molecule
 XX PT that is capable of specifically hybridizing to the mRNA of the gene,
 XX PT useful for diagnosing cardiopathy, e.g. cardiomyopathy or dilated
 XX PT cardiomyopathy.

XX PS Example 1; Page 21; 82pp; English.

XX CC The invention relates to a diagnostic composition comprising at least one
 XX CC nucleic acid molecule listed in the specification that is capable of
 XX CC specifically hybridizing to the mRNA of at least one of the genes given
 XX CC in the specification. The diagnostic composition and nucleic acid
 XX CC molecules are useful for diagnosing cardiopathy or a disposition to
 XX CC cardiopathy, e.g. cardiomyopathy or dilated cardiomyopathy. The method
 XX CC involves contacting a target sample with the nucleic acid molecule cited
 XX CC above, and comparing the concentration of the individual mRNA(s) with the
 XX CC concentration of the corresponding mRNAs from at least one of the healthy
 XX CC donor. The nucleic acids are also useful for the isolation and
 XX CC development of a compound useful for therapy or prevention of a
 XX CC cardiopathy. Sequences ACC78653-700 represent primers used in real-time
 XX CC quantitative PCR for amplifying human genes, during the course of the
 XX CC invention

SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 931 GAACAGCTCCGTACTGAG 950

DB 20 GAACAGCTCCGTACTGAG 1

RESULT 16

ACC78664/c

ID ACC78664 standard; DNA; 20 BP.

XX AC ACC78664;

XX DT 02-SRP-2003 (first entry)

XX DE Nucleotide sequence of a PCR primer CD81_R.

XX KW Cardiopathy; nucleic acid marker; therapy; human; PCR; primer; ss.

XX OS Homo sapiens.

XX PN WO2003040407-A2.

XX PD 15-MAY-2003.

XX PF 08-NOV-2002; 2002WO-EP012522.

XX PR 09-NOV-2001; 2001EP-00126800.

XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX PI Ruiz P, Grzeskowiak R, Drungowski M, Witt H, Osterziel KJ;
 XX PI Perrot A, Saleh A;

XX DR WPI; 2003-430678/40.

XX PT New diagnostic composition comprising at least one nucleic acid molecule
 XX PT that is capable of specifically hybridizing to the mRNA of the gene,
 XX PT useful for diagnosing cardiopathy, e.g. cardiomyopathy or dilated
 XX PT cardiomyopathy.

XX PS Example 1; Page 21; 82pp; English.

XX CC The invention relates to a diagnostic composition comprising at least one
 XX CC nucleic acid molecule listed in the specification that is capable of
 XX CC specifically hybridizing to the mRNA of at least one of the genes given
 XX CC in the specification. The diagnostic composition and nucleic acid
 XX CC molecules are useful for diagnosing cardiopathy or a disposition to
 XX CC cardiopathy, e.g. cardiomyopathy or dilated cardiomyopathy. The method
 XX CC involves contacting a target sample with the nucleic acid molecule cited
 XX CC above, and comparing the concentration of the individual mRNA(s) with the
 XX CC concentration of the corresponding mRNAs from at least one of the healthy
 XX CC donor. The nucleic acids are also useful for the isolation and
 XX CC development of a compound useful for therapy or prevention of a
 XX CC cardiopathy. Sequences ACC78653-700 represent primers used in real-time
 XX CC quantitative PCR for amplifying human genes, during the course of the
 XX CC invention

SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 931 GAACAGCTCCGTACTGAG 950

DB 20 GAACAGCTCCGTACTGAG 1

ADC35543/c

ID ADC35543 standard; DNA; 20 BP.

XX AC ADC35543;

XX DT 18-DEC-2003 (first entry)

XX DE Human CD81/TAPA-1 antisense oligonucleotide #3.

XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 XX KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 XX KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 XX KW bacterial infection.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX modified_base 1..20

XX FT /tag= b

XX FT /mod_base= OTHER

XX FT /note= "Phosphorothioate backbone and all cytidines are 5

XX FT -methyl cytidines"

XX modified_base 1..5

XX FT /tag= a

XX FT /mod_base= OTHER

XX FT /note= "2'-methoxyethyl nucleotide"

XX modified_base 16..20

XX FT /tag= c

XX FT /mod_base= OTHER

XX FT /note= "2'-methoxyethyl nucleotide"

XX PN US2003113914-A1.

XX PD 19-JUN-2003.

XX PF 10-DEC-2001; 2001US-00006430.

XX PR 10-DEC-2001; 2001US-00006430.

XX PT (ISIS-) ISIS PHARM INC.

XX PI Graham MJ, Dobie K;

XX DR WPI; 2003-810907/76.

XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 XX PT inhibiting the expression of CD81, useful for treating infections and
 XX PT disease associated with expression of CD81 such as inflammation disorder.

XX PS Claim 3; SEQ ID NO 15; 55pp; English.

XX CC The invention relates to a compound (antisense oligonucleotide)
 XX CC hybridizing with the eighth nucleobase portion of an active site on a
 XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 XX CC and inhibiting the expression of CD81. Also included is a composition
 XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 XX CC in cells or tissues. The antisense oligonucleotide is also useful for
 XX CC treating infections preferably viral, bacterial and parasitic and
 XX CC diseases such as inflammatory disorders and autoimmune disorders. The
 XX CC disease or condition is characterised by chemical dependency (e.g.
 XX CC cocaine addiction). The present sequence is a CD81 antisense
 XX CC oligonucleotide of the invention.

SQ Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1221 GCTCTGCTGCTCAGCCAGG 1240

DB 20 GCTCTGCTGCTCAGCCAGG 1

Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 781 CATCAGCAACCTCTTCAAGG 800
Db 20 CATCAGCAACCTCTTCAAGG 1

RESULT 19
ADC35571/c
ID ADC35571 standard; DNA; 20 BP.
AC ADC35571;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #31.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
US2003113914-A1.
XX
PD 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 43; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridizing with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.

SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 841 GCTGTACCTCATCGGCATTG 860
Db 20 GCTGTACCTCATCGGCATTG 1

RESULT 20
ADC35574/c
ID ADC35574 standard; DNA; 20 BP.
XX
AC ADC35574;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #34.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
US2003113914-A1.
XX
PD 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 46; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridizing with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.

```
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
    Query Match      1.3%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 33;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 864 CCATCGTGCCTGCTGATC 883
Db 20 CCATCGTGCCTGCTGATC 1

RESULT 21
ADC35584/c
ID ADC35584 standard; DNA; 20 BP.
XX
AC ADC35584;
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #44.
XX
KW Antisense; ss; human; CD81; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= b
FT /*mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20 /*tag= c
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
PS Claim 3; SEQ ID NO 56; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for

CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
    Query Match      1.3%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 33;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 962 CTGGCCACAGGACCTCTGC 981
Db 20 CTGGCCACAGGACCTCTGC 1

RESULT 22
ADC35585/c
ID ADC35585 standard; DNA; 20 BP.
XX
AC ADC35585;
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #45.
XX
KW Antisense; ss; human; CD81; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= b
FT /*mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20 /*tag= c
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
PS Claim 3; SEQ ID NO 57; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
```

CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1015 GGGCCATCACC GGCTGTGTA 1034
 |||||
 Db 20 GGGCCATCACC GGCTGTGTA 1

RESULT 23
 ADC35591/c
 ID ADC35591 standard; DNA; 20 BP.
 XX
 AC ADC35591;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #51.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 modified_base 1..20
 /*tag= b
 /mod_base= OTHER
 /note= "Phosphorothioate backbone and all cytidines are 5
 modified_base 1..5
 /*tag= a
 /mod_base= OTHER
 /note= "2'-methoxyethyl nucleotide"
 modified_base 16..20
 /*tag= c
 /mod_base= OTHER
 /note= "2'-methoxyethyl nucleotide"

US2003113914-A1.
 19-JUN-2003.
 10-DEC-2001; 2001US-00006430.
 10-DEC-2001; 2001US-00006430.
 (ISIS-) ISIS PHARM INC.
 Graham MJ, Dobie K;
 WPI; 2003-810907/76.
 Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 inhibiting the expression of CD81, useful for treating infections and
 disease associated with expression of CD81 such as inflammation disorder.
 Claim 3; SEQ ID NO 63; 55pp; English.
 The invention relates to a compound (antisense oligonucleotide)

CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1184 GAGGGCAGGGGTCCTTCGC 1203
 |||||
 Db 20 GAGGGCAGGGGTCCTTCGC 1

RESULT 24
 ADC35595/c
 ID ADC35595 standard; DNA; 20 BP.
 XX
 AC ADC35595;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #55.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
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 /*tag= b
 /mod_base= OTHER
 /note= "Phosphorothioate backbone and all cytidines are 5
 modified_base 1..5
 /*tag= a
 /mod_base= OTHER
 /note= "2'-methoxyethyl nucleotide"
 modified_base 16..20
 /*tag= c
 /mod_base= OTHER
 /note= "2'-methoxyethyl nucleotide"

US2003113914-A1.
 19-JUN-2003.
 10-DEC-2001; 2001US-00006430.
 10-DEC-2001; 2001US-00006430.
 (ISIS-) ISIS PHARM INC.
 Graham MJ, Dobie K;
 WPI; 2003-810907/76.
 Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 inhibiting the expression of CD81, useful for treating infections and
 disease associated with expression of CD81 such as inflammation disorder.
 Claim 3; SEQ ID NO 63; 55pp; English.
 The invention relates to a compound (antisense oligonucleotide)

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PS Claim 3; SEQ ID NO 67; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1261 CCCAGAGACTCAGCTGGCC 1280
Db 20 CCCAGAGACTCAGCTGGCC 1

RESULT 25
ADC35599/c
ID ADC35599 standard; DNA; 20 BP.
XX
AC ADC35599;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #59.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= b
FT /*mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5 -methyl cytidines"
FT /*tag= a
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20 /*tag= c
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and

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PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 71; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 7 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1369 TCTGTGGGCACCTCTGTGCT 1388
Db 20 TCTGTGGGCACCTCTGTGCT 1

RESULT 26
ADC35616/c
ID ADC35616 standard; DNA; 20 BP.
XX
AC ADC35616;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #76.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= b
FT /*mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5 -methyl cytidines"
FT /*tag= a
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20 /*tag= c
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and

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DR WPI; 2003-810907/76.
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX Claim 3; SEQ ID NO 88; 55pp; English.
 XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX Sequence 20 BP; 9 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1096 GTTCTGAACCTTCCTGTTAC 1115
 DB 20 GTTCTGAACCTTCCTGTTAC 1
 RESULT 27
 ADC35545/C
 ID ADC35545 standard; DNA; 20 BP.
 AC ADC35545;
 XX 18-DEC-2003 (first entry)
 DT Human CD81/TAPA-1 antisense oligonucleotide #5.
 XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 PH modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX US2003113914-A1.
 PN 19-JUN-2003.
 PD 10-DEC-2001; 2001US-00006430.
 XX 10-DEC-2001; 2001US-00006430.
 XX (ISIS-) ISIS PHARM INC.

XX Graham MJ, Dobie K;
 PI WPI; 2003-810907/76.
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX Claim 3; SEQ ID NO 17; 55pp; English.
 XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX Sequence 20 BP; 8 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
 SQ Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 272 TACCTGCTCTCTGCTTCAA 291
 DB 20 TACCTGCTCTCTGCTTCAA 1
 RESULT 28
 ADC3548/C
 ID ADC3548 standard; DNA; 20 BP.
 AC ADC3548;
 XX 18-DEC-2003 (first entry)
 DT Human CD81/TAPA-1 antisense oligonucleotide #8.
 XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 PH modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX US2003113914-A1.
 PN 19-JUN-2003.
 PD 10-DEC-2001; 2001US-00006430.
 XX 10-DEC-2001; 2001US-00006430.
 XX (ISIS-) ISIS PHARM INC.

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PR 10-DEC-2001; 2001US-00006430.
XX (ISIS-) ISIS PHARM INC.
PA Graham MJ, Dobie K;
PI WPI; 2003-810907/76.
XX
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
PS Claim 3; SEQ ID NO 20; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 9 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 296 GTCTTCTGCTGCTGGAGG 315
DB 20 GTCTTCTGCTGCTGGAGG 1
RESULT 29
ADC3556/c
ID ADC3556 standard; DNA; 20 BP.
XX
AC ADC3556;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #16.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
PD 19-JUN-2003.

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XX 10-DEC-2001; 2001US-00006430.
PF
XX 10-DEC-2001; 2001US-00006430.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Graham MJ, Dobie K;
PI WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
PS Example 15; SEQ ID NO 28; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 536 ATCCGTGTTGCTGTGAGGT 555
DB 20 ATCCGTGTTGCTGTGAGGT 1
RESULT 30
ADC35568/c
ID ADC35568 standard; DNA; 20 BP.
XX
AC ADC35568;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #28.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX

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PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 40; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 790 CCTCTTCAGGAGGACTGCC 809
Db 20 CCTCTTCAGGAGGACTGCC 1

RESULT 31
ADC35551/c
ID ADC35551 standard; DNA; 20 BP.
XX
AC ADC35551;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #11.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT modified_base 16..20
FT /tag= c

PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 40; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 790 CCTCTTCAGGAGGACTGCC 809
Db 20 CCTCTTCAGGAGGACTGCC 1

RESULT 32
ADC35557/c
ID ADC35557 standard; DNA; 20 BP.
XX
AC ADC35557;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #17.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT modified_base 16..20
FT /tag= c

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FT      /note= "2'-methoxyethyl nucleotide"
FT      16..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl nucleotide"
FT      16..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl nucleotide"
PN      US2003113914-A1.
XX      19-JUN-2003.
XX      10-DEC-2001; 2001US-00006430.
XX      10-DEC-2001; 2001US-00006430.
XX      (ISIS-) ISIS PHARM INC.
XX      Graham MJ, Dobie K;
XX      WPI; 2003-810907/76.
XX      Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX      inhibiting the expression of CD81, useful for treating infections and
XX      disease associated with expression of CD81 such as inflammation disorder.
XX      Claim 3; SEQ ID NO 29; 55pp; English.
XX      The invention relates to a compound (antisense oligonucleotide)
XX      hybridizing with the eighth nucleobase portion of an active site on a
XX      nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX      and inhibiting the expression of CD81. Also included is a composition
XX      comprising the antisense oligonucleotide and a carrier or a diluent. The
XX      antisense oligonucleotide is useful for inhibiting the expression of CD81
XX      in cells or tissues. The antisense oligonucleotide is also useful for
XX      treating infections preferably viral, bacterial and parasitic and
XX      diseases such as inflammatory disorders and autoimmune disorders. The
XX      disease or condition is characterised by chemical dependency (e.g.
XX      cocaine addiction). The present sequence is a CD81 antisense
XX      oligonucleotide of the invention.
XX      Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
XX      Query Match      1.3%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 33;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      564 GCATCTGGGGCTTTGTCAAC 583
DB      |||||||
        20 GCATCTGGGGCTTTGTCAAC 1
RESULT 33
ADC35586/C
ID      ADC35586 standard; DNA; 20 BP.
XX      ADC35586;
XX      18-DEC-2003 (first entry)
XX      Human CD81/TAPA-1 antisense oligonucleotide #46.
DE      Antisense; ss; human; CD81; tetraspanin; viral infection;
XX      cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX      virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX      bacterial infection.
XX      Homo sapiens.
XX      Key      Location/Qualifiers
FH      modified_base 1..20
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone and all cytidines are 5
FT      -methyl cytidines"

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FT      modified_base 1..5
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl nucleotide"
FT      16..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl nucleotide"
PN      US2003113914-A1.
XX      19-JUN-2003.
XX      10-DEC-2001; 2001US-00006430.
XX      10-DEC-2001; 2001US-00006430.
XX      (ISIS-) ISIS PHARM INC.
XX      Graham MJ, Dobie K;
XX      WPI; 2003-810907/76.
XX      Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX      inhibiting the expression of CD81, useful for treating infections and
XX      disease associated with expression of CD81 such as inflammation disorder.
XX      Claim 3; SEQ ID NO 58; 55pp; English.
XX      The invention relates to a compound (antisense oligonucleotide)
XX      hybridizing with the eighth nucleobase portion of an active site on a
XX      nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX      and inhibiting the expression of CD81. Also included is a composition
XX      comprising the antisense oligonucleotide and a carrier or a diluent. The
XX      antisense oligonucleotide is useful for inhibiting the expression of CD81
XX      in cells or tissues. The antisense oligonucleotide is also useful for
XX      treating infections preferably viral, bacterial and parasitic and
XX      diseases such as inflammatory disorders and autoimmune disorders. The
XX      disease or condition is characterised by chemical dependency (e.g.
XX      cocaine addiction). The present sequence is a CD81 antisense
XX      oligonucleotide of the invention.
XX      Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
XX      Query Match      1.3%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 33;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1048 GTATTACTCTGCTACACGTA 1067
DB      |||||||
        20 GTATTACTCTGCTACACGTA 1
RESULT 34
ADC35597/C
ID      ADC35597 standard; DNA; 20 BP.
XX      ADC35597;
XX      18-DEC-2003 (first entry)
XX      Human CD81/TAPA-1 antisense oligonucleotide #57.
DE      Antisense; ss; human; CD81; tetraspanin; viral infection;
XX      cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX      virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX      bacterial infection.
XX      Homo sapiens.
XX      Key      Location/Qualifiers
FH      modified_base 1..20
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone and all cytidines are 5
FT      -methyl cytidines"

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FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX 19-JUN-2003.
XX 10-DEC-2001; 2001US-00006430.
XX 10-DEC-2001; 2001US-00006430.
XX (ISIS-) ISIS PHARM INC.
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX Example 15; SEQ ID NO 69; 55pp; English.
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX Sequence 20 BP; 6 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1327 ACAGCTCACCTGTTCCCTC 1346
Db |||||
20 ACAGCTCACCTGTTCCCTC 1
RESULT 35
ADC35544/c
ID ADC35544 standard; DNA; 20 BP.
AC ADC35544;
XX
DT 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #4.
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX Homo sapiens.
XX
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PH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX 19-JUN-2003.
XX 10-DEC-2001; 2001US-00006430.
XX 10-DEC-2001; 2001US-00006430.
XX (ISIS-) ISIS PHARM INC.
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX Claim 3; SEQ ID NO 16; 55pp; English.
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 TGGAGGGCTGCACCAAGTGC 265
Db |||||
20 TGGAGGGCTGCACCAAGTGC 1
RESULT 36
ADC35558/c
ID ADC35558 standard; DNA; 20 BP.
XX
AC ADC35558;
XX
DT 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #18.
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX
```

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XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone and all cytidines are 5
XX FT -methyl cytidines"
XX FT 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl nucleotide"
XX FT 15..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl nucleotide"
XX PN US2003113914-A1.
XX PD 19-JUN-2003.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX PI WPI; 2003-810907/76.
XX DR
XX XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 30; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridising with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX CC disease or condition is characterised by chemical dependency (e.g.
XX CC cocaine addiction). The present sequence is a CD81 antisense
XX CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 587 GACCAGATGCCAAGGATGT 606
Db 20 GACCAGATGCCAAGGATGT 1
|||||
RESULT 37
ADC35572/c
ID ADC35572 standard; DNA; 20 BP.
XX AC ADC35572;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 antisense oligonucleotide #32.
XX XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
```

```
KW cocaine addiction; autoimmune disorder; antinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone and all cytidines are 5
XX FT -methyl cytidines"
XX FT 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl nucleotide"
XX FT 15..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl nucleotide"
XX PN US2003113914-A1.
XX PD 19-JUN-2003.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX PI WPI; 2003-810907/76.
XX DR
XX XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 44; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridising with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX CC disease or condition is characterised by chemical dependency (e.g.
XX CC cocaine addiction). The present sequence is a CD81 antisense
XX CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 848 CTCATCGGCATGCTGCCAT 867
Db 20 CTCATCGGCATGCTGCCAT 1
|||||
RESULT 38
ADC35617/c
ID ADC35617 standard; DNA; 20 BP.
XX AC ADC35617;
XX DT 18-DEC-2003 (first entry)
```

DE Human CD81/TAPA-1 antisense oligonucleotide #77.
 XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 XX 19-JUN-2003.
 XX
 XX 10-DEC-2001; 2001US-00006430.
 XX
 XX 10-DEC-2001; 2001US-00006430.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Graham MJ, Dobie K;
 XX WPI; 2003-810907/76.
 DR
 XX
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX
 XX Claim 3; SEQ ID NO 89; 55pp; English.
 PS
 XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1110 TGTACCTTTTCAGGGCTGA 1129
 Db |||||
 20 TGTACCTTTTCAGGGCTGA 1
 RESULT 39
 ADC35577/c
 ID ADC35577 standard; DNA; 20 BP.
 XX
 AC ADC35577;

XX 18-DEC-2003 (first entry)
 DT Human CD81/TAPA-1 antisense oligonucleotide #37.
 XX
 DE Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 XX 19-JUN-2003.
 XX
 XX 10-DEC-2001; 2001US-00006430.
 PF
 XX
 XX 10-DEC-2001; 2001US-00006430.
 PR
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Graham MJ, Dobie K;
 PI WPI; 2003-810907/76.
 DR
 XX
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX
 XX Claim 3; SEQ ID NO 49; 55pp; English.
 PS
 XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 902 CTGACGATGCTGCTGCTG 921
 Db |||||
 20 CTGACGATGCTGCTGCTG 1
 RESULT 40
 ADC35590/c

```

ID ADC35590 standard; DNA; 20 BP.
AC ADC35590;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #50.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 15; SEQ ID NO 62; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1136 ATGTAGTGGCGGTATGAG 1155
Db |||||||||||||||||||
20 ATGTAGTGGCGGTATGAG 1
```

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RESULT 41
ADC35605/c
ID ADC35605 standard; DNA; 20 BP.
XX
AC ADC35605;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #65.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 15; SEQ ID NO 77; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 7 A; 2 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1440 CTGACTCCGTCATTAAATAA 1459
```

KW transcription; expression; reverse transcription; viral replication;
 KW RNase H cleavage; triple helix formation; ss.
 OS Synthetic.
 XX

Key Location/Qualifiers
 modified_base 1..18
 /*tag= a
 /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
 fluoro-beta-D-arabinoose"
 FT

XX WO9967378-A1.
 XX

XX 29-DEC-1999.
 XX

XX 17-JUN-1999; 99WO-CA000571.
 XX

XX 19-JUN-1998; 98CA-02241361.
 XX

XX (UYMC-) UNIV MCGILL.
 XX

XX Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
 XX

XX WPI; 2000-160584/14.
 XX

XX Therapeutic composition containing antisense oligonucleotides that
 XX include arabinose sugars, particularly for inhibiting viral replication.
 PT
 XX
 XX Example 2; Page 31; 91pp; English.

CC The invention relates to a new composition for selective, sequence-
 CC specific inhibition of gene transcription and expression in a host. The
 CC composition comprises oligonucleotides containing arabinose sugars that
 CC can hybridize to either a single-stranded (ss) RNA to induce RNase H
 CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
 CC helix, thereby inhibiting DNA replication and/or transcription. The
 CC oligoarabinonucleotides are used for antisense inhibition of gene
 CC expression or to prevent DNA replication, or reverse transcription of RNA
 CC by retroviruses. The compositions are therefore particularly used to
 CC inhibit retroviral replication. The oligoarabinonucleotides can also be
 CC used, in combination with RNase H, as reagents for sequence-specific
 CC cleavage or RNA mapping, and additionally for the study and control of
 CC gene expression in cells. The oligoarabinonucleotides have excellent
 CC affinity for RNA, increased resistance to nucleases and show little if
 CC any non-specific binding to cellular or serum proteins. They target ss
 CC RNA, but not complementary ss DNA, so may be useful for targeting
 CC retroviral genomic RNA to inhibit the early stages of viral replication.
 CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
 CC with significantly higher thermal stability than those produced by normal
 CC oligonucleotides. Sequences AAZ87165-287169 represent
 CC oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-
 CC arabinose used in an exemplification of the present invention
 XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 DB 18 AAAAAAAAAAAAAA 3

RESULT 274

AAZ87167

ID AAZ87167 standard; DNA; 18 BP.

XX AC AAZ87167;

XX DT 08-MAY-2000 (first entry)

XX DE Deoxyarabinonucleotide SEQ ID NO:8.

XX

KW 2'-deoxy-2'-fluoro-beta-D-arabinoose; antisense; inhibition;
 KW transcription; expression; reverse transcription; viral replication;
 KW RNase H cleavage; triple helix formation; ss.
 OS Synthetic.

XX

Key Location/Qualifiers
 modified_base 1..18
 /*tag= a
 /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
 fluoro-beta-D-arabinoose"
 FT

XX WO9967378-A1.
 XX

XX 29-DEC-1999.
 XX

XX 17-JUN-1999; 99WO-CA000571.
 XX

XX 19-JUN-1998; 98CA-02241361.
 XX

XX (UYMC-) UNIV MCGILL.
 XX

XX Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
 XX

XX WPI; 2000-160584/14.
 XX

XX Therapeutic composition containing antisense oligonucleotides that
 XX include arabinose sugars, particularly for inhibiting viral replication.
 PT
 XX
 XX Example 2; Page 31; 91pp; English.

CC The invention relates to a new composition for selective, sequence-
 CC specific inhibition of gene transcription and expression in a host. The
 CC composition comprises oligonucleotides containing arabinose sugars that
 CC can hybridize to either a single-stranded (ss) RNA to induce RNase H
 CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
 CC helix, thereby inhibiting DNA replication and/or transcription. The
 CC oligoarabinonucleotides are used for antisense inhibition of gene
 CC expression or to prevent DNA replication, or reverse transcription of RNA
 CC by retroviruses. The compositions are therefore particularly used to
 CC inhibit retroviral replication. The oligoarabinonucleotides can also be
 CC used, in combination with RNase H, as reagents for sequence-specific
 CC cleavage or RNA mapping, and additionally for the study and control of
 CC gene expression in cells. The oligoarabinonucleotides have excellent
 CC affinity for RNA, increased resistance to nucleases and show little if
 CC any non-specific binding to cellular or serum proteins. They target ss
 CC RNA, but not complementary ss DNA, so may be useful for targeting
 CC retroviral genomic RNA to inhibit the early stages of viral replication.
 CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
 CC with significantly higher thermal stability than those produced by normal
 CC oligonucleotides. Sequences AAZ87165-287169 represent
 CC oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-
 CC arabinose used in an exemplification of the present invention
 XX

SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 DB 1 AAAAAAAAAAAAAA 16

RESULT 275

AAZ03565/c

ID AAZ03565 standard; DNA; 18 BP.

XX AC AAZ03565;

XX DT 19-JUN-2001 (first entry)

```
XX Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
DE Rat; secreted factor; clone P00188_D12; cardiant; antiinflammatory;
KW antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;
KW antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;
KW antibacterial; osteopathic; cerebroprotective; vasotropic; antiulcer;
KW neurotropic; neuroprotective; congestive heart failure; myocarditis;
KW hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
KW kidney disease; acute renal failure; renal glucosuria; renal infarction;
KW polycystic kidney disease; hereditary nephritis; inflammatory disease;
KW tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
KW stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
KW ulcerative colitis; Alzheimer's disease; gene therapy; ss.
XX Rattus norvegicus.
XX WO200123564-A1.
XX 05-APR-2001.
XX 27-SEP-2000; 2000WO-US026544.
XX 27-SEP-1999; 99US-0156280P.
XX (SCIO-) SCIOS INC.
XX Stanton LW, Kapoun AM;
XX WPI; 2001-266159/27.
XX Novel secreted factor encoded by clone P00188D12 which is differentially
PT expressed in certain disease states, useful in diagnosing and treating
PT cardiac, renal or inflammatory diseases.
XX Example 1; Page 42; 71pp; English.
XX The patent discloses novel secreted factor protein encoded by clone
CC P00188_D12. The secreted factor is differentially expressed in certain
CC disease states. Secreted protein, its antibodies, antagonists or
CC compositions comprising them are useful in the diagnosis and treatment of
CC cardiac diseases such as congestive heart failure, myocarditis,
CC hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,
CC cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal
CC failure, renal glucosuria, renal infarction, nephrogenic diabetes
CC insipidus, polycystic kidney disease, hereditary nephritis and
CC inflammatory diseases such as asthma, autoimmune diabetes, tumour
CC angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,
CC asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,
CC Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted
CC protein DNA is useful in antisense-mediated gene inhibition and in gene
CC therapy. An array comprising one or more oligonucleotides complementary
CC to reference RNA or DNA encoding the secreted factor is useful for
CC detecting cardiac, kidney and inflammatory disease. The present DNA
CC sequence is an oligonucleotide which is used in the preparation of a
CC normalised cDNA library containing secreted factor DNAs. The normalised
CC cDNA libraries are used in the identification of differentially expressed
CC rat secreted factor P00188_D12 gene
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAAAAA 3
RESULT 276
AADI7014
ID AAD17014 standard; DNA; 18 BP.
```

```
XX AAD17014;
AC 29-NOV-2001 (first entry)
XX Oligonucleotide A18-2PEG linker.
DE Scaffold protein; antibody mimic; fibronectin type III domain;
KW randomised loop; randomised beta-sheet; diagnostic purpose;
KW protein designing; ss.
XX Unidentified.
OS Key Location/Qualifiers
FT 18 misc_feature
FT /*tag= a
FT /note= "Linked to (PEG)2CCPuromycin"
XX WO200164942-A1.
XX 07-SEP-2001.
XX 28-FEB-2001; 2001WO-US006414.
XX 29-FEB-2000; 2000US-00515260.
XX (PHYL-) PHYLLOS INC.
XX Lipovsek D, Wagner RW, Kuimelis RG;
XX WPI; 2001-557782/62.
XX Fibronectin scaffold protein array for obtaining a protein/compound which
PT binds to a compound/protein, comprises a fibronectin type III domain
PT having a randomized loop, a randomized beta-sheet or their combination.
XX Disclosure; Page 25; 67pp; English.
XX The present invention relates to an array of proteins (antibody mimics)
CC comprising a fibronectin type III domain having a randomised loop, a
CC randomised beta-sheet, or their combination, and has the capacity to bind
CC to a compound that is not bound by a corresponding naturally- occurring
CC fibronectin, immobilised onto a solid support. The antibody mimics is
CC useful for detecting a compound preferably a protein, in a biological
CC sample. It is also useful to detect one or more different analytes
CC simultaneously in a sample. Hence is useful for diagnostic purposes. It
CC is also useful for the purpose of designing proteins capable of binding
CC to virtually any compound of interest. The present sequence is an
CC oligonucleotide A18-2PEG linker used in an exemplification of the
CC invention
XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16
RESULT 277
AAF75598/c
ID AAF75598 standard; DNA; 18 BP.
XX AAF75598;
XX AAF75598;
XX 10-MAY-2001 (first entry)
XX Binary encoded sequence tag method anchored primer #3.
DE Binary encoded sequence tag; BEST; nucleic acid analysis;
KW Binary encoded sequence tag; BEST; nucleic acid analysis;
```

```
KW gene expression; adaptor; PCR primer; ss.
OS Synthetic.
XX WO200112855-A2.
XX 22-FEB-2001.
XX 11-AUG-2000; 2000WO-US022164.
XX 13-AUG-1999; 99US-0148870P.
PR 06-APR-2000; 2000US-00544713.
XX (UYVA ) UNIV YALE.
XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX WPI; 2001-202878/20.
XX Producing binary sequence tags, useful for analyzing nucleic acid
PT sequence tags, gene expression or gene-expression patterns, involves
PT generating nucleic acid fragments, which are mixed with offset adaptors
PT and adaptor-indexers.
XX Disclosure; Page 101; 101pp; English.
XX The present invention describes a method of producing binary sequence
CC tags from nucleic acid fragments in a sample, involving incubating the
CC sample with cleaving reagents, mixing offset adaptors with the sample,
CC incubating with more cleaving reagents and mixing the sample with adaptor
CC -indexers where the adaptors are coupled to binary sequence tags. The
CC method is useful in sequence analysis, including analysis and comparison
CC of gene expression, nucleic acid samples and genomes
XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
SQ Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1
RESULT 278
AA75597/C
ID AAF75597 standard; DNA; 18 BP.
XX AAF75597;
XX 10-MAY-2001 (first entry)
XX Binary encoded sequence tag method anchored primer #2.
XX Binary encoded sequence tag; BEST; nucleic acid analysis;
KW gene expression; adaptor; PCR primer; ss.
OS Synthetic.
XX WO200112855-A2.
XX 22-FEB-2001.
XX 11-AUG-2000; 2000WO-US022164.
XX 13-AUG-1999; 99US-0148870P.
PR 06-APR-2000; 2000US-00544713.
XX (UYVA ) UNIV YALE.
XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX WPI; 2001-202878/20.
XX Producing binary sequence tags, useful for analyzing nucleic acid
PT sequence tags, gene expression or gene-expression patterns, involves
PT generating nucleic acid fragments, which are mixed with offset adaptors
PT and adaptor-indexers.
XX Disclosure; Page 101; 101pp; English.
XX The present invention describes a method of producing binary sequence
CC tags from nucleic acid fragments in a sample, involving incubating the
CC sample with cleaving reagents, mixing offset adaptors with the sample,
CC incubating with more cleaving reagents and mixing the sample with adaptor
CC -indexers where the adaptors are coupled to binary sequence tags. The
CC method is useful in sequence analysis, including analysis and comparison
CC of gene expression, nucleic acid samples and genomes
XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
SQ Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1
RESULT 278
AA75597/C
ID AAF75597 standard; DNA; 18 BP.
XX AAF75597;
XX 10-MAY-2001 (first entry)
XX Binary encoded sequence tag method anchored primer #2.
XX Binary encoded sequence tag; BEST; nucleic acid analysis;
KW gene expression; adaptor; PCR primer; ss.
OS Synthetic.
XX WO200112855-A2.
XX 22-FEB-2001.
XX 11-AUG-2000; 2000WO-US022164.
XX 13-AUG-1999; 99US-0148870P.
PR 06-APR-2000; 2000US-00544713.
XX (UYVA ) UNIV YALE.
XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX WPI; 2001-202878/20.
XX Producing binary sequence tags, useful for analyzing nucleic acid
PT sequence tags, gene expression or gene-expression patterns, involves
PT generating nucleic acid fragments, which are mixed with offset adaptors
PT and adaptor-indexers.
XX Disclosure; Page 100; 101pp; English.
XX The present invention describes a method of producing binary sequence
CC tags from nucleic acid fragments in a sample, involving incubating the
CC sample with cleaving reagents, mixing offset adaptors with the sample,
CC incubating with more cleaving reagents and mixing the sample with adaptor
CC -indexers where the adaptors are coupled to binary sequence tags. The
CC method is useful in sequence analysis, including analysis and comparison
CC of gene expression, nucleic acid samples and genomes
XX Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
SQ Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1
RESULT 279
AAD20091
ID AAD20091 standard; mRNA; 18 BP.
XX AAD20091;
XX 03-JAN-2002 (first entry)
XX mRNA fragment used in 3' end PCR/IVT method of the invention.
XX RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.
XX Unidentified.
XX US6271002-B1.
XX 07-AUG-2001.
XX 04-OCT-1999; 99US-00411074.
XX 04-OCT-1999; 99US-00411074.
XX (ROSE-) ROSETTA INPHARMATICS INC.
XX Linsley PS, Schelter JM;
XX WPI; 2001-624273/72.
XX Amplifying and detecting RNA derived from a population of cells by
PT employing a primer that contains an RNA polymerase promoter in a
PT polymerase chain reaction.
XX Example 3; Fig 1; 29pp; English.
XX The invention relates to methods and kits for amplification of mRNA using
CC a primer in PCR that contains an RNA polymerase (RNAP) promoter. The
CC invention provides methods for amplification and detection of RNA derived
CC from a population of cells, preferably eukaryotic cells and most
CC to sequence and transcript representation and additionally enable
CC amplification of extremely small amounts of mRNA. The method and kit are
CC useful for amplifying and detecting RNA derived from a population of
CC cells, especially eukaryotic cells like mammals. The RNAs generated are
CC useful for profiling gene expression in different populations of cells.
CC The present sequence is a mRNA fragment used in 3' end PCR/IVT (in vitro
```

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CC transcription) method of the invention
XX
SQ Sequence 18 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 2 AAAAAAAAAAAAAA 17

RESULT 280
AAF99708/c
ID AAF99708 standard; DNA; 18 BP.
AC AAF99708;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #824.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
XX
PR 27-SEP-1999; 99US-0156135P.
XX
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 282
AAF82472/c
ID AAF82472 standard; DNA; 18 BP.

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XX AC AAF82472;
XX DT 29-JUN-2001 (first entry)
XX DE Phagemid vector pCR2.1 polylinker oligonucleotide #6.
XX KW Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiant;
XX KW nephrotropic; antiinflammatory; gene therapy; cardiac disease;
XX KW renal disease; inflammatory disease; polylinker; ss.
XX OS Synthetic.
XX PN W0200123419-A2.
XX PD 05-APR-2001.
XX PF 27-SEP-2000; 2000WO-US026582.
XX PR 27-SEP-1999; 99US-0156277P.
XX PA (SCIO-) SCIOS INC.
XX PI Stanton LM, Kapoun AM;
XX DR WPI; 2001-328177/34.
XX PT Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
XX PT treating and/or preventing various cardiac, renal and inflammatory
XX PT diseases.
XX PS Example 1; Page 41; 69pp; English.
XX CC The present sequence corresponds to polylinker DNA of the phagemid vector
XX CC pCR2.1. It was used in the construction of a normalised rat cDNA library,
XX CC which was used in an example demonstrating differential expression of a
XX CC rat gene referred to as clone P00210D09. The invention relates to a
XX CC polypeptide comprising a sequence of at least 80% identity to residues 22
XX CC -122 of the present sequence, or a sequence encoded by a nucleic acid
XX CC hybridising under stringent conditions to the complement of the coding
XX CC region comprising 1031 nucleotides, and having at least one biological
XX CC activity of the polypeptide encoded by clone P00210D09. The polypeptides
XX CC and polynucleotides of the invention are useful for the treatment of
XX CC cardiac, renal and inflammatory diseases. The polynucleotides are useful
XX CC in antisense mediated gene inhibition and in gene therapy. The
XX CC polypeptides are useful in assays for identifying lead compounds that may
XX CC be used as therapeutic agents in the treatment of cardiac, kidney or
XX CC inflammatory diseases
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAAAAAA 3

RESULT 283
ID ABK51158 standard; DNA; 18 BP.
AC ABK51158;
XX 30-JUL-2002 (first entry)
XX Human cytomegalovirus (HCMV) RT-PCR primer TXN.
XX Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV;
XX cellular kinase; RICK; RIP; Nck-interacting kinase; MKK3; SRPK-2;
XX reverse transcriptase PCR; RT-PCR; primer; ss.

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XX OS Human cytomegalovirus.
XX FH Key Location/Qualifiers
XX FT misc_difference 17 /*tag= a
XX FT /label= n
XX FT /note= "n= dATP, dCTP or dGTP"
XX PN EPI201765-A2.
XX PD 02-MAY-2002.
XX PF 15-OCT-2001; 2001EP-00124604.
XX PR 16-OCT-2000; 2000US-0240750P.
XX PA (AXXI-) AXIIMA PHARM AG.
XX PI Schubart D, Habenberger P, Stein-Gerlach M, Bavec D;
XX DR WPI; 2002-373930/41.
XX PT Identifying agents for treatment or prevention of cytomegalovirus
XX PT infection, comprises contacting test compound with cellular kinase and
XX PT detecting change in cellular kinase activity.
XX PS Example 1; Page 13; 49pp; English.
XX CC The present invention relates to a new method for identifying compounds
XX CC for treating and/or preventing cytomegalovirus (CMV) infection and/or
XX CC related diseases. The method of the invention comprises contacting a test
XX CC compound with at least one of the cellular kinases RICK, RIP, Nck-
XX CC interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase
XX CC activity. The method of the invention can be used to treat and/or prevent
XX CC CMV infections and related diseases. Oligonucleotides that can detect the
XX CC specified kinases can also be used for diagnosis of infection. The
XX CC present nucleic acid sequence represents human CMV reverse transcriptase
XX CC (RT)-PCR primer TXN that was used in the methods of the invention for
XX CC preparation of radioactively labelled cDNA probes
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
DB 16 AAAAAAAAAAAAAAAAAA 1

RESULT 284
ID AAS94743 standard; DNA; 18 BP.
XX AAS94743;
XX 12-MAR-2002 (first entry)
XX Rat secreted factor DNA oligonucleotide probe #6.
XX Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;
XX inflammatory disease; congestive heart failure; myocarditis; asthma; ss;
XX dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;
XX myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;
XX atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;
XX renal infarction; hereditary nephritis; polycystic kidney disease;
XX chronic renal failure; renal vein thrombosis; medullary sponge kidney;
XX rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer;
XX graft versus host reaction; Crohn's disease; ulcerative colitis; probe;
XX Alzheimer's disease; gene therapy.

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OS Synthetic.
 PN WO200174901-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009555.
 XX
 PR 31-MAR-2000; 2000US-0193548P.
 XX
 PR 14-MAR-2001; 2001US-00809545.
 XX
 PR (SCIO-) SCIOS INC.
 PA Stanton LW, White RT;
 XX WPI; 2002-010779/01.
 DR
 XX
 XX Novel secreted factor polypeptide useful for treating cardiac diseases
 PT such as arteriosclerosis, myocardial infarction, inflammatory diseases
 PT such as asthma, stroke, and rheumatoid arthritis and renal diseases.
 XX
 PS Example 1; Page 51; 189pp; English.
 XX
 CC The invention relates to rat secreted factor polypeptides and the
 CC polynucleotides encoding them. The sequences are useful for treating
 CC cardiac, renal or inflammatory diseases. These include cardiac diseases
 CC such as congestive heart failure, myocarditis, dilated congestive
 CC cardiomyopathy, angina pectoris, myocardial infarction, cardiac
 CC arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and
 CC cardiac tumours, renal diseases such as glomerulonephritis, nephrotic
 CC syndrome, renal infarction, hereditary nephritis, polycystic kidney
 CC disease, chronic renal failure, renal vein thrombosis and medullary
 CC sponge kidney and inflammatory diseases such as asthma, rheumatoid
 CC arthritis, osteoarthritis, stroke, psoriasis, stenosis, graft versus
 CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's
 CC disease. Sequences AAG94693-AAS94745 represent cDNA clones, which encode
 CC the secreted factor polypeptides of the invention, and oligonucleotide
 CC probes and PCR primers
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 Db 18 AAAAAAAAAAAAAA 3
 XX
 RESULT 285
 ABS78455/c
 ID ABS78455 standard; DNA; 18 BP.
 XX
 AC ABS78455;
 XX
 DT 13-DEC-2002 (first entry)
 DE
 DE Angiogenesis inhibitory oligonucleotide #939.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophiliac joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX

PD 11-JUL-2002.
 XX
 PF 14-DEC-2001; 2001WO-US048458.
 XX
 PR 14-DEC-2000; 2000US-0255534P.
 XX
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Bratzler RL;
 XX
 DR WPI; 2002-566690/60.
 XX
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 PT
 XX Claim 2; Page 36; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 Db 18 AAAAAAAAAAAAAA 3
 XX
 RESULT 286
 ABS78429/c
 ID ABS78429 standard; DNA; 18 BP.
 XX
 AC ABS78429;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Angiogenesis inhibitory oligonucleotide #913.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophiliac joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 14-DEC-2001; 2001WO-US048458.
 XX
 PR 14-DEC-2000; 2000US-0255534P.
 XX
 PA (COLE-) COLEY PHARM GROUP INC.

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XX PT Bratzler RL;
XX PI
XX DR WPI; 2002-566690/60.
XX PT Inhibiting angiogenesis in a subject, involves administering at least one
XX PT antiangiogenic nucleic acid molecule to the subject.
XX PS Claim 2; Page 35; 276pp; English.
XX CC The invention relates to inhibiting angiogenesis in a subject, comprising
XX CC administering at least one antiangiogenic nucleic acid molecule. Also
XX CC included is a kit comprising a first container housing the antiangiogenic
XX CC nucleic acids, and instructions for administering them to a subject
XX CC having a condition characterised by unwanted angiogenesis. The method is
XX CC useful for inhibiting angiogenesis associated with solid tumour growth,
XX CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
XX CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
XX CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
XX CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
XX CC neovascularisation, telangiectasia, haemophilic joints, angiodermoma,
XX CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
XX CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
XX CC acid of the invention
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 287
ABL39401/C
ID ABL39401 standard; DNA; 18 BP.
AC ABL39401;
XX
XX 16-APR-2002 (first entry)
XX
XX Immunostimulatory nucleic acid SEQ ID NO: 837.
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX angiogenesis; metastasis; cytostatic; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..18
XX /*tag= a
XX /mod_base= OTHER
XX /note= "phosphorothioate backbone"
XX
XX W0200197843-A2.
XX
XX 27-DEC-2001.
XX
XX 22-JUN-2001; 2001WO-US020154.
XX
XX 22-JUN-2000; 2000US-0213346P.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Weiner G, Hartmann G;
XX
XX WPI; 2002-154611/20.
XX
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
XX PT administering immunostimulatory nucleic acids that induce expression of

```

```

PT cell surface antigens and antibodies to a subject having or at risk of
XX developing cancer.
XX PS Disclosure; Page 308; 312pp; English.
XX
XX The present invention relates to methods for treating or preventing
XX cancer, involving administering to a subject having or at risk of
XX developing cancer immunostimulatory nucleic acids that induce expression
XX of cell surface antigens and antibodies. The methods are useful for
XX treating or preventing cancer such as basal cell carcinoma, bladder
XX cancer, bone cancer, brain and central nervous system (CNS) cancer,
XX breast cancer, cervical cancer, colon and rectum cancer, connective
XX tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
XX Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
XX cancer, stomach cancer, testicular cancer, and uterine cancer. The
XX present sequence is an immunostimulatory oligonucleotide described in the
XX exemplification of the invention
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 288
AAD41497/C
ID AAD41497 standard; DNA; 18 BP.
XX
XX AAD41497;
XX
XX 30-OCT-2002 (first entry)
XX
XX Oligonucleotide used for amplifying sea hare cytoplasm L DNA.
XX
XX Apoptosis; ion channel modulator; hyperproliferative disease; tumour;
XX therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;
XX Alzheimer's disease; Parkinson's disease; arteriosclerosis;
XX heart disease; stroke; vascular disease; nootropic; neuroprotective;
XX cerebroprotective; cardiant; cytotoxic protein; cytoplasm L; ss.
XX Unidentified.
XX
XX W0200231144-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-EP011837.
XX
XX 13-OCT-2000; 2000EP-00122466.
XX
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Butzke D, Machuy N, Rudel T, Meyer TF;
XX
XX WPI; 2002-537205/57.
XX
XX Novel polypeptide having cytotoxic activity obtainable from Aplysia,
XX useful for destroying tumors, for identifying novel targets for the
XX development of anti-tumor agents, and as specific ion channel modulators.
XX Example 5; Page 37; 87pp; English.
XX
XX The present invention relates to novel polypeptides having cytotoxic
XX activity obtainable from sea hare Aplysia. Sequences of the invention are
XX useful for the manufacture of cytotoxic agents against apoptosis-
XX resistant cells, where the agents are useful for diagnosis, prevention,
XX

```

CC treatment of disorders associated with dysfunctions of GAP-SH3 binding
 CC protein, factors for generating or detoxifying reactive oxygen species
 CC (ROS) and factors for blocking and/or by-passing of caspases. They are
 CC useful for tumour therapy. Cytotoxic proteins of the invention are useful
 CC for destroying tumours and/or selectively killing cells in tissues, for
 CC identifying novel targets for the development of pharmaceutical agents,
 CC preferably anti-tumour agents and as specific ion channel modulators,
 CC e.g., blockers or openers for therapy, diagnostic or research. They are
 CC useful for the diagnosis and therapy of hyperproliferative diseases,
 CC preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma.
 CC They are also useful for development of drugs for the treatment of
 CC degenerative diseases such as Alzheimer's disease, Parkinson's disease,
 CC arteriosclerosis, heart diseases, stroke and vascular diseases. The
 CC present sequence is an oligonucleotide which is used for amplifying sea
 CC hare cytoplasm L DNA. This sequence is used in the exemplification of the
 CC invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 DB 18 AAAAAAAAAAAAAA 3
 RESULT 289
 ABS53437/C
 ID ABS53437 standard; DNA; 18 BP.
 AC ABS53437;
 DT 29-NOV-2002 (first entry)
 XX Poly d(T) primer.
 XX Terminal continuation; TC; ss; second strand cDNA synthesis; primer;
 KW poly d(T).
 XX Synthetic.
 OS WO200265093-A2.
 PN 22-AUG-2002.
 XX 14-FEB-2002; 2002WO-US005713.
 XX 14-FEB-2001; 2001US-02686645P.
 PR 18-FEB-2001; 2001US-02686645P.
 PR 18-JUL-2001; 2001US-0306216P.
 PR 07-NOV-2001; 2001US-0344557P.
 PR 07-NOV-2001; 2001US-0348242P.
 PR 09-NOV-2001; 2001US-0350176P.
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA (REME-) RES FOUND MENTAL HYGIENE INC.
 XX Ginsberg SD, Che S;
 XX WPI; 2002-567050/60.
 DR Increasing efficiency of second strand cDNA synthesis using terminal
 PT continuation model before performing further RNA amplification by RNA
 PT transcription.
 XX Example 7; Page 80; 128pp; English.
 XX This invention relates to a novel method for increasing the efficiency of
 CC second strand cDNA synthesis through a mechanism of terminal
 CC continuation. In the method an RNA molecule is obtained and a first
 CC primer is added that comprises a region that hybridises to a

CC complementary region of the molecule before a second primer is added
 CC comprising at least one riboguanine at the 3' end of the primer. A first
 CC complementary nucleic acid molecule is synthesised, the RNA molecule and
 CC second primer are removed and a second complementary nucleic acid
 CC molecule is synthesised to form a second hybrid with an extension product
 CC of the third primer bound to the first complementary molecule. The method
 CC of the invention is useful for increasing the efficiency of second strand
 CC cDNA synthesis and may be used for linear amplification of genetic
 CC signals from histologically stained tissue. The present sequence
 CC represents a poly d(T) PCR primer used in the method of the invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 DB 18 AAAAAAAAAAAAAA 3
 RESULT 290
 ABA93239/C
 ID ABA93239 standard; DNA; 18 BP.
 XX ABA93239;
 AC ABA93239;
 XX 18-APR-2002 (first entry)
 DT Adaptor oligonucleotide SEQ ID NO:2.
 DE Detection; comparative detection; adaptor; ss.
 XX Synthetic.
 OS JP2001333800-A.
 PN 04-DEC-2001.
 XX 30-MAY-2000; 2000JP-00160324.
 XX 30-MAY-2000; 2000JP-00160324.
 PR (UNIT-) UNITECH CO LTD.
 XX WPI; 2002-135950/18.
 XX Comparative detection of the amounts of RNA and DNA.
 PT Disclosure; Page 9; 9pp; Japanese.
 XX The present invention describes a method for the comparative detection of
 CC the amount of an RNA. The method comprises: (a) cDNAs obtained by
 CC transcribing respectively from at least two tissue RNAs are respectively
 CC fragmented by using a same restriction enzyme; (b) each different adaptor
 CC and a common adaptor are added to each of the cDNA fragments derived from
 CC the same or different tissues by the step (a); (c) the resultant adaptor-
 CC added cDNAs are mixed together; (d) an adaptor primer having the common
 CC sequence to said different adaptor and a gene-specific adaptor are used
 CC to amplify said adaptor-added cDNAs containing no region derived from
 CC polyadenylic acid of the mRNA before the addition of the adaptor among
 CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
 CC cDNA amounts are measured between the tissues; (f) the RNA is detected
 CC from the measured result; (g) each different adaptor and a common adaptor
 CC are added to each of the genomic DNA fragments derived from a same or
 CC different individuals; (h) the resultant adaptor-added genomic DNAs are
 CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using
 CC an adaptor primer having the common sequence to the different adaptor and
 CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts
 CC of the genomic DNAs are measured between the individuals. The method is
 CC used for the detection of the amounts of RNA and DNA. The present
 CC sequence represents an oligonucleotide which is used in the

CC exemplification of the present invention

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

SQ Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 291
AAD52799/c

ID AAD52799 standard; DNA; 18 BP.

XX AC AAD52799;

DT 14-MAY-2003 (first entry)

XX Primer used to prepare radioactively labelled cDNA probes from RNA.

XX Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;
KW cellular protein phosphatase; cellular signal transduction; prophylaxis;
KW prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;
KW CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;
KW TSE; BSE; Gerstmann-Strausler-Scheinker syndrome; GSS; Alpers syndrome;
KW fatal familial insomnia; FFI; kuru; neurodegenerative disease; neurotropic;
KW Alzheimer's disease; primer; ss.

XX OS Homo sapiens.

XX PN WO200293164-A2.

XX PD 21-NOV-2002.

XX PF 16-MAY-2002; 2002WO-EP005420.

XX PR 16-MAY-2001; 2001EP-00111858.

PR 29-MAY-2001; 2001US-0293528P.

PR 13-JUL-2001; 2001EP-00117113.

PR 18-JUL-2001; 2001US-0305898P.

XX PA (AXXI-) AXXIWA PHARM AG.

XX PI Stein-Gerlach M, Salassidis K, Bacher G, Mueller S;

XX WPI; 2003-120714/11.

XX New pyridylpyrimidine derivatives useful in the treatment or prevention of infectious disease e.g. Kuru syndrome and Creutzfeld-Jacob disease (CJD).

XX Example; Page 38; 96pp; English.

XX The invention relates to novel pyridylpyrimidine derivatives and methods of detecting prion infections and/or prion disease in an individual or in cells, cell cultures and/or cell lysates. The method involves adding at least one monoclonal or polyclonal antibody, oligonucleotide or pyridylpyrimidine derivative to the sample or in cells, cell cultures and/or cell lysates and detecting the activity of at least one human cellular protein kinases (e.g., FGF-R1 (also known as fig, Flt-1, Flt-2, b-FGFR), Tkt (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also known as c-abl), ctk1, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also known as CDK1), PRK), human cellular protein phosphatases such as PTP-SL (also known as MCP83) and PTP-zeta, the cellular signal transduction molecules HSP80 and GPR-1. The invention is useful for regulating the production of prions in cells and in the manufacture of pharmaceutical composition for prophylaxis and/or treatment of infectious disease (e.g. Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy (BSE), variant CJD, Gerstmann-Strausler-Scheinker syndrome (GSS), fatal

CC familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD, vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans or ruminants. The present DNA sequence is a primer used to prepare radioactively labelled cDNA probes from RNA. This sequence is used in the exemplification of the invention

XX Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

SQ Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 292
AAD56466

ID AAD56466 standard; RNA; 18 BP.

XX AC AAD56466;

XX 07-AUG-2003 (first entry)

DT Target RNA #1 used in the exemplification of the invention.

XX DE Target RNA #1 used in the exemplification of the invention.

XX KW Acyclic linker; gene expression; gene therapy; ss.

XX OS Unidentified.

XX PN WO2003037909-A1.

XX PD 08-MAY-2003.

XX PF 29-OCT-2002; 2002WO-CA001628.

XX PR 29-OCT-2001; 2001US-0330719P.

XX (UYMC-) UNIV MCGILL.

XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

XX WPI; 2003-421516/39.

XX Novel acyclic linker-containing oligonucleotide useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.

XX Example 2; Fig 5; 104pp; English.

XX The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is a target RNA, used in the exemplification of the invention

XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

```
RESULT 293
AAD56440/c
ID AAD56440 standard; DNA; 18 BP.
XX
XX AAD56440;
AC
DT 07-AUG-2003 (first entry)
XX
DE Antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX
XX Unidentified.
XX
XX WO2003037909-A1.
PN
XX
XX 08-MAY-2003.
PD
XX
XX 29-OCT-2002; 2002WO-CA001628.
PF
XX
XX 29-OCT-2001; 2001US-0330719P.
PR
XX
XX (UYMC-) UNIV MCGILL.
PA
XX
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
PI
XX
XX WPI; 2003-421516/39.
DR
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 9; 104pp; English.
PS
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3
RESULT 294
AAD56446/c
ID AAD56446 standard; DNA; 18 BP.
XX
XX AAD56446;
AC
DT 07-AUG-2003 (first entry)
XX
DE 2' F-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
```

```
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
PH modified_base 1..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX
XX WO2003037909-A1.
PN
XX
XX 08-MAY-2003.
PD
XX
XX 29-OCT-2002; 2002WO-CA001628.
PF
XX
XX 29-OCT-2001; 2001US-0330719P.
PR
XX
XX (UYMC-) UNIV MCGILL.
PA
XX
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
PI
XX
XX WPI; 2003-421516/39.
DR
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 7; 104pp; English.
PS
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3
RESULT 295
ACH03247/c
ID ACH03247 standard; DNA; 18 BP.
XX
XX ACH03247;
AC
XX
XX 25-SEP-2003 (first entry)
DT
XX
XX Immunostimulatory nucleic acid #882.
DE
XX
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
XX Synthetic.
OS
XX
XX US2003050268-A1.
PN
XX
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PD 13-MAR-2003.
XX
XX 29-MAR-2002; 2002US-00112653.
XX
XX 29-MAR-2001; 2001US-0279642P.
XX
XX (KRIE/) KRIEG A. M.
XX (BERG/) BERG D. J.
XX
XX Krieg AM, Berg DJ;
XX
XX WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
XX allergic contact dermatitis, latex dermatitis or inflammatory bowel
XX disease by administering an immunostimulatory nucleic acid.
XX
XX Disclosure; Page 33; 229pp; English.
XX
XX The invention describes a method of treating non-allergic inflammatory
XX disease comprising administering to a subject having or at risk of
XX developing a non-allergic inflammatory disease an immunostimulatory
XX nucleic acid for prevention or treatment of the disease. The method is
XX useful for treating non-allergic inflammatory diseases, such as
XX psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
XX inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
XX This sequence represents an immunostimulatory nucleic acid
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 296
AAD57871/C
ID AAD57871 standard; DNA; 18 BP.
XX
XX AAD57871;
XX
XX 20-NOV-2003 (first entry)
XX
XX Antisense oligo #1 used in the exemplification of the invention.
XX
XX Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
XX hepatitis B; gene therapy; virucide; anti-HIV; antisense; ss.
XX
XX Unidentified.
XX
XX WO2003064441-A2.
XX
XX 07-AUG-2003.
XX
XX 31-JAN-2003; 2003WO-CA000129.
XX
XX 01-FEB-2002; 2002US-0352873P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Parniak MA;
XX
XX WPI; 2003-689523/65.
XX
XX New oligonucleotide, useful for preventing or treating a disease related
XX to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
XX Example 2; Page 35; 73pp; English.
XX

```

The present invention relates to a new oligonucleoside which comprises alternating first and second segments. The first segment comprises at least one sugar modified nucleoside. The second segment comprises at least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of each of the first and second segments, so that it comprises at least 4 alternating segments. The oligonucleoside is useful for preparing a composition for inducing RNase H-mediated cleavage of a target RNA in a system, preventing or decreasing translation, transcription or replication of a target RNA in a system, detecting the presence of a target RNA in a system, validating a gene target corresponding to a target RNA in a system or preventing or treating a disease related to a target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS) or hepatitis B. The invention is useful in gene therapy. The present sequence is an antisense oligonucleotide used in the exemplification of the invention

Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 297
AAD57878/C
ID AAD57878 standard; DNA; 18 BP.
XX
XX AAD57878;
XX
XX 20-NOV-2003 (first entry)
XX
XX Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
XX
XX Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS; hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX misc_RNA 1. .3
XX /tag= a
XX /label= RNA
XX /note= "2'-O-methyl-D-uridine"
XX 7. .9
XX misc_RNA
XX /tag= b
XX /label= RNA
XX /note= "2'-O-methyl-D-uridine"
XX 13. .15
XX /tag= c
XX /label= RNA
XX /note= "2'-O-methyl-D-uridine"
XX
XX WO2003064441-A2.
XX
XX 07-AUG-2003.
XX
XX 31-JAN-2003; 2003WO-CA000129.
XX
XX 01-FEB-2002; 2002US-0352873P.
XX
XX (UYMC-) UNIV MCGILL;
XX
XX Damha MJ, Parniak MA;
XX
XX WPI; 2003-689523/65.
XX
XX New oligonucleotide, useful for preventing or treating a disease related to a target RNA in a system, e.g., AIDS or hepatitis B.

```

XX Example 2; Page 35; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 298
AAD57879/c
ID AAD57879 standard; DNA; 18 BP.
XX
AC AAD57879;
XX
DT 20-NOV-2003 (first entry)
XX
DE Antisense DNA-RNA hybrid #3 used in the exemplification of the invention.
XX
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_RNA 1.6
FT /*tag= a
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 13..18
FT /*tag= b
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
XX
PN WO2003064441-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-CA000129.
XX
PR 01-FEB-2002; 2002US-0352873P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA;
XX
DR WPI; 2003-689523/65.
XX
PT New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX

```

```

PS Example 2; Page 35; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 299
AAD57877/c
ID AAD57877 standard; DNA; 18 BP.
XX
AC AAD57877;
XX
DT 20-NOV-2003 (first entry)
XX
DE Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.
XX
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_RNA 1
FT /*tag= a
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 3
FT /*tag= b
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 5
FT /*tag= c
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 7
FT /*tag= d
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 9
FT /*tag= e
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 11
FT /*tag= f
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 13
FT /*tag= g
FT /label= RNA

```



```
FT misc_RNA /note= "2'-O-methyl-D-uridine"  
FT 15  
FT /*tag= h  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT 17  
FT misc_RNA  
FT /*tag= i  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT 18  
XX  
XX WO2003064441-A2.  
XX  
XX  
XX PD 07-AUG-2003.  
XX PF 31-JAN-2003; 2003WO-CA000129.  
XX PR 01-FEB-2002; 2002US-0352873P.  
XX PA (UYMC-) UNIV MCGILL.  
XX PI Damha MJ, Parniak MA;  
XX WI; 2003-689523/65.  
XX  
XX PT New oligonucleotide, useful for preventing or treating a disease related  
XX to a target RNA in a system, e.g., AIDS or hepatitis B.  
XX  
XX PS Example 4; Page 38; 73pp; English.  
XX  
XX CC The present invention relates to a new oligonucleoside which comprises  
XX alternating first and second segments. The first segment comprises at  
XX least one sugar modified nucleoside. The second segment comprises at  
XX least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of  
XX each of the first and second segments, so that it comprises at least 4  
XX alternating segments. The oligonucleotide is useful for preparing a  
XX composition for inducing RNase H-mediated cleavage of a target RNA in a  
XX system, preventing or decreasing translation, transcription or  
XX replication of a target RNA in a system, detecting the presence of a  
XX target RNA in a system, validating a gene target corresponding to a  
XX target RNA in a system or preventing or treating a disease related to a  
XX target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)  
XX or hepatitis B. The invention is useful in gene therapy. The present  
XX sequence is an antisense DNA-RNA hybrid used in the exemplification of  
XX the invention  
XX  
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;  
  
Query Match 1.1%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1481 AAAAAAAAAAAAAA 1496  
DB 18 AAAAAAAAAAAAAA 3  
  
RESULT 300  
AAD57890  
ID AAD57890 standard; RNA; 18 BP.  
AC AAD57890;  
DT 20-NOV-2003 (first entry)  
XX  
XX DE Target RNA #1 used in RNase H assay.  
XX  
XX KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;  
XX hepatitis B; gene therapy; virucide; anti-HIV; ss.  
XX  
XX OS Unidentified.  
XX  
XX PN WO2003064441-A2.  
XX  
XX  
PD 07-AUG-2003.  
PF 31-JAN-2003; 2003WO-CA000129.  
PR 01-FEB-2002; 2002US-0352873P.  
PA (UYMC-) UNIV MCGILL.  
PI Damha MJ, Parniak MA;  
WI; 2003-689523/65.  
PT New oligonucleotide, useful for preventing or treating a disease related  
to a target RNA in a system, e.g., AIDS or hepatitis B.  
PS Example 2; Page 35; 73pp; English.  
CC The present invention relates to a new oligonucleoside which comprises  
alternating first and second segments. The first segment comprises at  
least one sugar modified nucleoside. The second segment comprises at  
least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of  
each of the first and second segments, so that it comprises at least 4  
alternating segments. The oligonucleotide is useful for preparing a  
composition for inducing RNase H-mediated cleavage of a target RNA in a  
system, preventing or decreasing translation, transcription or  
replication of a target RNA in a system, detecting the presence of a  
target RNA in a system, validating a gene target corresponding to a  
target RNA in a system or preventing or treating a disease related to a  
target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)  
or hepatitis B. The invention is useful in gene therapy. The present  
sequence is an antisense DNA-RNA hybrid used in the exemplification of  
the invention  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;  
  
Query Match 1.1%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1481 AAAAAAAAAAAAAA 1496  
DB 18 AAAAAAAAAAAAAA 3  
  
RESULT 300  
AAD57890  
ID AAD57890 standard; RNA; 18 BP.  
AC AAD57890;  
DT 20-NOV-2003 (first entry)  
XX  
XX DE Target RNA #1 used in RNase H assay.  
XX  
XX KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;  
XX hepatitis B; gene therapy; virucide; anti-HIV; ss.  
XX  
XX OS Unidentified.  
XX  
XX PN WO2003064441-A2.  
XX  
XX  
PD 07-AUG-2003.  
PF 31-JAN-2003; 2003WO-CA000129.  
PR 01-FEB-2002; 2002US-0352873P.  
PA (UYMC-) UNIV MCGILL.  
PI Damha MJ, Parniak MA;  
WI; 2003-689523/65.  
PT New oligonucleotide, useful for preventing or treating a disease related  
to a target RNA in a system, e.g., AIDS or hepatitis B.  
PS Example 4; Page 38; 73pp; English.  
XX  
XX CC The present invention relates to a new oligonucleoside which comprises  
XX alternating first and second segments. The first segment comprises at  
XX least one sugar modified nucleoside. The second segment comprises at  
XX least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of  
XX each of the first and second segments, so that it comprises at least 4  
XX alternating segments. The oligonucleotide is useful for preparing a  
XX composition for inducing RNase H-mediated cleavage of a target RNA in a  
XX system, preventing or decreasing translation, transcription or  
XX replication of a target RNA in a system, detecting the presence of a  
XX target RNA in a system, validating a gene target corresponding to a  
XX target RNA in a system or preventing or treating a disease related to a  
XX target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)  
XX or hepatitis B. The invention is useful in gene therapy. The present  
XX sequence is a target RNA used in RNase H assay. This sequence is used in  
XX the exemplification of the invention  
XX  
XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 1.1%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1481 AAAAAAAAAAAAAA 1496  
DB 1 AAAAAAAAAAAAAA 16  
  
RESULT 301  
ADB37210/c  
ID ADB37210 standard; DNA; 18 BP.  
AC ADB37210;  
DT 04-DEC-2003 (first entry)  
XX  
XX DE Immunostimulatory nucleic acid #824.  
XX  
XX KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
XX hypo-responsive subject; immunostimulatory.  
XX  
XX OS Synthetic.  
XX  
XX PN US2003087848-A1.  
XX  
XX PD 08-MAY-2003.  
XX  
XX PF 02-FEB-2001; 2001US-00776479.  
XX  
XX PR 03-FEB-2000; 2000US-0179991P.  
XX  
XX PA (BRAT/) BRATZLER R L.  
XX (PETE/) PETERSEN D M.  
XX (FOUR/) FOURON Y.  
XX  
XX PI Bratzler RL, Petersen DM, Fouron Y;  
XX
```

DR WPI; 2003-657977/62.
 XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 PS Disclosure; Page 17; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1481 AAAAAAAAAAAAAA 1496
 18 AAAAAAAAAAAAAA 3
 XX
 RESULT 302
 ADB37236/C
 ID ADB37236 standard; DNA; 18 BP.
 XX
 AC ADB37236;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #850.
 XX
 KW de; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX
 OS Synthetic.
 XX
 US2003087848-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 02-FEB-2001; 2001US-0076479.
 XX
 PR 03-FEB-2000; 2000US-0179991P.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 XX
 XX WPI; 2003-657977/62.
 XX
 XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 PS Disclosure; Page 18; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 18 AAAAAAAAAAAAAA 3
 DB
 RESULT 303
 ADE77617
 ID ADE77617 standard; DNA; 18 BP.
 XX
 AC ADE77617;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
 XX
 KW probe; as; negative control; CFTR; human leukocyte antigen; HLA;
 KW genetic testing; carrier screening; genotyping; profiling; polymorphic;
 KW multiplexed elongation assay; enzymatic recognition;
 KW cystic fibrosis conductance transmembrane regulator.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003034029-A2.
 XX
 PD 24-APR-2003.
 XX
 PF 15-OCT-2002; 2002WO-US033012.
 XX
 PR 15-OCT-2001; 2001US-0329427P.
 PR 15-OCT-2001; 2001US-0329428P.
 PR 15-OCT-2001; 2001US-0329619P.
 PR 15-OCT-2001; 2001US-0329620P.
 PR 14-MAR-2002; 2002US-0364416P.
 XX
 PA (BIOA-) BIOARRAY SOLUTIONS LTD.
 XX
 PI Li AX, Hashmi G, Seul M;
 XX
 XX WPI; 2003-393553/37.
 XX
 XX Concurrent interrogation of a number of polymorphic sites, useful for
 PT genetic testing, carrier screening, genetic profiling, and identity
 PT testing, comprises conducting a multiplexed elongation assay using
 PT probes.
 XX
 PS Example 9; Page 46; 143pp; English.
 XX
 CC This invention relates to a novel method for the concurrent interrogation
 CC of a number of polymorphic sites in the presence of, and without
 CC interference from, non-designated polymorphic sites. Specifically, it
 CC comprises conducting a multiplexed elongation assay by applying one or
 CC more temperature cycles to achieve linear amplification of the target or
 CC a combination of annealing and elongation steps under temperature-
 CC controlled conditions. Furthermore, this detection method uses probe
 CC extension or elongation and relies on enzymatic recognition, a superior
 CC technique that no longer depends on differential hybridisation. The
 CC present invention describes probes and methods useful for identifying or
 CC detecting polymorphisms at one or more designated sites, such that they
 CC can identify mutations within the cystic fibrosis conductance
 CC transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)
 CC genes. In addition, concurrent interrogation of a multiplicity of
 CC polymorphic sites is useful for genetic testing, carrier screening,
 CC genotyping or genetic profiling, and identity testing. This
 CC oligonucleotide is the negative control probe used for the elongation
 CC mediated multiplexed analysis of HLA-DR, in an exemplification of the
 CC invention.
 XX
 XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
 |||||
 Db 1 AAAAAAAAAAAAAA 16

RESULT 304
 AAD44129
 ID AAD44129 standard; DNA; 18 BP.
 AC AAD44129;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE PCR primer #4 designed to bind human MMP PPR region.
 XX
 KW Sequential consensus region-directed amplification; gene expression;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase; MMP;
 KW propeptide region; PPR; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6277571-B1.
 XX
 PD 21-AUG-2001.
 XX
 PF 30-SEP-1998; 98US-00163485.
 XX
 PR 03-OCT-1997; 97US-00943162.
 PR 03-OCT-1997; 97US-0108152P.
 XX
 PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
 XX
 PI Fillmore H, Broadus W, Gillies G;
 XX
 DR WPI; 2002-412824/44.
 XX
 PT Sequential consensus region-directed amplification for sorting mixture of
 PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
 PT 2 samples, useful for disease diagnosis and gene analysis.
 XX
 XX Example; Col 12; 19pp; English.
 PS
 SS The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
 CC for disease diagnosis and gene analysis. The present sequence is a PCR
 CC primer designed to bind to human matrix metalloproteinase (MMP)
 CC propeptide region (PPR). This primer is used to illustrate the method of
 CC the invention
 XX
 SQ Sequence 18 BP; 6 A; 2 C; 3 G; 3 T; 0 U; 4 Other;

Query Match 1.1%; Score 15.8; DB 1; Length 18;
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 599 AAGGATGTGAAGCAGTTC 616
 |||||
 Db 1 AARGAYGTNAACAGTTC 18

RESULT 305
 AAV19118/c
 ID AAV19118 standard; DNA; 17 BP.
 AC AAV19118;
 XX
 DT 28-AUG-1998 (first entry)
 XX
 XX

Anchored oligo(T) primer.
 Secreted apoptosis-related protein; SARP; msARP1; mouse; prostate cancer;
 breast cancer; diagnosis; gene therapy; PCR; primer; ss.
 Synthetic.
 WO9813493-A2.
 02-APR-1998.
 24-SEP-1997; 97WO-US017154.
 24-SEP-1996; 96US-0026603P.
 11-OCT-1996; 96US-0028363P.
 (LXRB-) LXR BIOTECHNOLOGY INC.
 Umansky S, Melkonian H;
 WPI; 1998-230704/20.
 New secreted apoptosis-related proteins - useful for modulating
 apoptosis, particularly for treatment of prostatic or breast cancer, also
 for diagnosis and monitoring of disease.
 Example 1; Page 30; 101pp; English.
 This oligo(T) synthetic oligonucleotide was used for first strand cDNA
 synthesis from total RNA isolated from either logarithmically growing or
 quiescent 10T1/2 mouse fibroblast cells. It was also used with an
 arbitrary d(N10) primer in PCR. The PCR products were used in a
 differential display to identify the msARP1 gene (see AAV19112) that
 codes for novel murine secreted apoptosis-related protein msARP1 (see
 AAV37814). The invention relates to SARP polynucleotides (see also
 AAV19113-15) and polypeptides (see also AAV37815-17), antibodies specific
 for SARP, and use of such polynucleotides and antibodies in diagnostic
 and therapeutic methods, and methods for treating diseases related to the
 regulation of SARP expression in tissue and body fluid samples, including
 cancers
 Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 1.0%; Score 15.6; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.7e+02;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1479 CTAAAAAAAAAAAAA 1495
 : |||||
 Db 17 SNAAAAAAAAAAAAAA 1

RESULT 306
 AAZ89372/c
 ID AAZ89372 standard; DNA; 17 BP.
 XX
 AC AAZ89372;
 XX
 DT 15-JUN-2000 (first entry)
 XX
 DE RNA detecting primer #2.
 KW Amplification; detection; gene expression; primer; ss.
 XX
 OS Unidentified.
 XX
 PN DE19840731-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 07-SEP-1998; 98DE-01040731.
 XX
 PR 07-SEP-1998; 98DE-01040731.

XX (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 XX WPI; 2000-257789/23.
 DR
 XX
 XX Analysis of RNA samples, useful for detection of differential gene
 PT expression uses two differently labeled primers.
 PT
 XX Disclosure; Page 10; 10pp; German.
 PS
 XX This invention describes a novel method for analysis of an RNA sample
 CC which comprises amplifying cDNA with first and second differentially labeled
 CC primers and analysis of the amplified labeled cDNA. The method is useful
 CC for analyzing differential gene expression, for identifying and/or
 CC characterizing pharmacological activities or for identifying target
 CC genes. The use of different primer combinations allow more cDNAs to be
 CC amplified. The method also provides a more detailed analysis than prior
 CC art methods. This sequence represents a primer used to illustrate the
 CC method of the invention
 CC
 XX Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;
 SQ

Query Match 1.0%; Score 15.6; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.7e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX

QY 1480 TAAAAAAAAAAAAA 1495
 Db 16 KAAAAAAAAAAAAA 1

RESULT 307
 AAT76338/c
 ID AAT76338 standard; DNA; 17 BP.
 XX
 AC AAT76338;
 XX
 XX 15-SEP-1997 (first entry)
 DT
 XX Human fibronectin antisense oligonucleotide HUMFNA/HSFIB1A55.
 DE
 XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
 KW chronic obstructive pulmonary disease; bronchitis; ss.
 KW
 XX Synthetic.
 OS
 XX WO9640162-A1.
 PN
 XX 19-DEC-1996.
 PD
 XX 06-JUN-1996; 96WO-US009306.
 PF
 XX 07-JUN-1995; 95US-00474497.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW, Metzger WJ;
 PI
 XX WPI; 1997-051871/05.
 DR
 XX Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligo:nucleotide to airway epithelium of
 PT subject.
 XX
 XX Claim 5; Page 36; 71pp; English.
 PS
 XX A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide
 CC HUMFNA/HSFIB1A55 specific for the human fibronectin. The method can be
 CC used to treat airway diseases such as cystic fibrosis, asthma, chronic
 CC obstructive pulmonary disease, bronchitis and other airway diseases
 CC

CC Characterised by an inflammatory response. By eliminating adenosine from
 CC the antisense ON, its liberation upon antisense degradation is prevented,
 CC thereby preventing adenosine- induced bronchoconstriction in patients
 CC with hyper-reactive airways
 CC
 XX Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;
 SQ

Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX

QY 89 CCCCCGCGCCCGCGCC 105
 Db 17 CCCCCGCGCCCGCGCC 1

RESULT 308
 AAX54140/c
 ID AAX54140 standard; DNA; 17 BP.
 XX
 AC AAX54140;
 XX
 XX 05-JUL-1999 (first entry)
 DT
 XX Human fibronectin antisense oligonucleotide fragment.
 DE
 XX
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 KW
 XX Synthetic.
 OS
 XX WO9913886-A1.
 PN
 XX 25-MAR-1999.
 PD
 XX 17-SEP-1998; 98WO-US019419.
 PF
 XX 17-SEP-1997; 97US-0059160P.
 PR 09-JUN-1998; 98US-00093972.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 PI
 XX WPI; 1999-229400/19.
 DR
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction.
 PT
 XX Disclosure; Page 55; 120pp; English.
 PS
 XX The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene initiation
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
 CC end and the juxta-section between coding and non-coding regions and all
 CC segments of RNAs encoding proteins associated with one or more diseases,
 CC conditions or mixtures. The antisense oligonucleotides may be derived
 CC from sequences AAX55272-74. These multiple target oligonucleotides
 CC (specifically AAX55180-271) can be used for the antisense treatment of
 CC diseases and conditions. Typical diseases and conditions are those
 CC associated with impaired respiration and inflammation, including lung
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 CC acute asthma, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 CC

CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer
 XX
 SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 89 CCCCCGCGCCCGCGCC 105
 DB 17 CCCCCGCGCCCGCGCC 1
 RESULT 309
 AAA33584/c
 ID AAA33584 standard; DNA; 17 BP.
 XX
 AC AAA33584;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Low adenosine antisease oligonucleotide SEQ ID NO:1273.
 XX
 KW Human; adenosine receptor; low adenosine antisease oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US017712.
 XX
 PR 03-AUG-1998; 98US-0095212P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 WPI; 2000-205971/18.
 XX
 XX New antisease oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Claim 18; Page 424; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisease
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including

CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 89 CCCCCGCGCCCGCGCC 105
 DB 17 CCCCCGCGCCCGCGCC 1
 RESULT 310
 AAF19706/c
 ID AAF19706 standard; DNA; 17 BP.
 XX
 AC AAF19706;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human fibronectin polynucleotide fragment #1273.
 XX
 KW Low adenosine antisease oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2000062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 WPI; 2000-679535/66.
 XX
 XX Low adenosine (A) content antisease oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 PS Claim 14; Page 220; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisease
 CC oligonucleotides and compositions (1) comprising them. In the antisease
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.

CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 CCCCCCGCGCCGCGCC 105
Db 17 CCCCCCGCGCCGCGCC 1

RESULT 311
AA24533/C
ID AAA25453 standard; DNA; 17 BP.
XX
AC AAA25453;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1951.
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX

PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodi(thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAA 1496
Db 17 TACAAAAAATAAAAAA 1

RESULT 312
ABK18911
ID ABK18911 standard; RNA; 17 BP.
XX
AC ABK18911;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG DNAzyme target sequence Seq ID No 1558.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulvovaginal; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing; ss;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW
XX
OS Homo sapiens.
XX
PN WO20018124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX
DR WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
XX

PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX Claim 4; Page 105; 149pp; English.
PS The invention relates to a nucleic acid molecule (I) which down regulates
XX expression of an ERG-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
XX related PCR primers of the invention
SQ Sequence 17 BP; 1 A; 7 C; 9 G; 0 T; 0 U; 0 Other;
Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 25 CGGCGCGCGCGCGCGCG 41
DB 1 CGGCGCGCGCGCGCGCG 17
RESULT 313
ID ABZ95400/c
XX ABZ95400 standard; DNA; 17 BP.
XX AC ABZ95400;
XX 17-OCT-2003 (first entry)
DT Human fibronectin antisense fragment no.1264.
DE Human
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; lung; adenosine sensitivity;
KW lung inflammation; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
OS Homo sapiens.
XX
XX W0200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (SPIG-) EPIGENESIS PHARM INC.
XX Nvce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX

DR WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
PS Disclosure; SEQ ID NO 10642; 872pp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;
Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 89 CCCCCCGCGCGCGCGCGCG 105
DB 17 CCCCCCGCGCGCGCGCGCG 1
RESULT 314
ID ADB04273/c
XX ADB04273 standard; DNA; 17 BP.
XX AC ADB04273;
XX 20-NOV-2003 (first entry)
DT Human MD27 scanning oligonucleotide SEQ ID 5259.
DE Human
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
PT

PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX Example 8; SEQ ID NO 5259; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1. MDZ4 is encoded at chromosome 6p21.3-22.2.
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 17 TCAAAAAAAAAAAAAAAAAA 1
RESULT 315
ADB04274/C
ID ADB04274 standard; DNA; 17 BP.
XX
AC ADB04274;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5260.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3, MDZ4, MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5260; 103pp; English.
PS
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is

CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;
Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1495
DB 17 CTCAAAAAATAAAAAAAAAA 1
RESULT 316
ADB03682
ID ADB03682 standard; DNA; 17 BP.
XX
AC ADB03682;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 4668.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3, MDZ4, MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 4668; 103pp; English.
PS
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic

CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 946 CTGAGGCCCGCAGCTC 962
 Db 1 CTGAGGCCCGCAGCTC 17

RESULT 317

ABZ61368
 ID ABZ61368 standard; RNA; 17 BP.

XX AC ABZ61368;

XX DT 21-MAR-2003 (first entry)

XX DE Human H-Ras DNase target #159.

XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US016940.

XX PR 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX DR WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX PS Claim 58; Page 114; 185pp; English.

XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention

SQ Sequence 17 BP; 0 A; 6 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 25 CGCGCGCGACGGCGCG 41
 Db 1 CGCGCGCGCGCGCG 17

RESULT 318

AAQ30446/C

XX ID AAQ30446 standard; DNA; 18 BP.

XX AC AAQ30446;

XX DT 25-MAR-2003 (revised)

XX DT 07-DEC-1992 (first entry)

XX DE Oligomer TNFR941 for forming triplex with HUMNFR target duplex.

XX KW Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;

XX KW HPV; malignancy; hepatitis; inflammation; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT modified_base 5

XX FT /tag= a

XX FT /mod_base= m5c

XX FT modified_base 18

XX FT /tag= b

XX FT /mod_base= OTHER

XX FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

XX PN WO9209705-A1.

XX PD 11-JUN-1992.

XX PF 25-NOV-1991; 91WO-US008811.

XX PR 23-NOV-1990; 90US-00617907.

XX PR 18-JAN-1991; 91US-00643382.

XX PR 08-APR-1991; 91US-00683420.

XX PR 17-APR-1991; 91US-00686544.

XX PR 17-APR-1991; 91US-00686546.

XX PR 17-APR-1991; 91US-00686547.

XX PR 27-SEP-1991; 91US-00766733.

XX PA (GILE-) GILEAD SCI INC.

XX PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;

XX DR WPI; 1992-217083/26.

XX PT New oligomers contg. modified bases - which form a triplex with G-C
 PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
 PT herpes malignancy and inflammation.

XX PS Claim 12; Page 72; 77pp; English.

XX CC The synthetic oligomer is capable of forming a triplex at physiological
 CC pH with a purine rich target sequence by coupling into the major groove
 CC of the duplex. The specific target sequence of this oligomer is the human
 CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
 CC a purine rich sequence concd. on one strand of the duplex. The oligomer,
 CC and others like it are useful in diagnosis and therapy of diseases
 CC characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
 CC hepatitis B, herpes, malignant tumours and inflammation. The triple
 CC helices form under mild conditions thus assays may be carried out without
 CC subjecting the test specimen to harsh conditions. See also AAQ25452-25501
 CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PD field.)

SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 2e+02; Mismatches 0; Indels 1; Gaps 0;
 Matches 16; Conservative 0;
 QY 1480 TAAAAAAGAAAAA 1496
 DB 18 TAAAAAAGAAAAA 2

RESULT 319
 AAV54174/C
 ID AAV54174 standard; cDNA; 18 BP.

XX AC AAV54174;
 XX DT 21-DEC-1998 (first entry)
 XX DE Nucleotide sequence PCR primer 11.
 XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX KW immunohistological staining.

XX OS Synthetic.
 XX PN WO9839437-A1.
 XX PD 11-SEP-1998.
 XX PF 05-MAR-1998; 98WO-JP000905.
 XX PR 05-MAR-1997; 97JP-00050302.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Sakaki Y;
 XX WPI; 1998-495844/42.
 XX PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 PT treating diseases associated with apoptosis.
 XX PS Example 1; Page 47; 70pp; Japanese.
 XX CC This is the nucleotide sequence of a PCR primer used in the method of the
 CC invention, involving the use of novel apoptosis-related DNAs and
 CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 CC immunohistological staining, as apoptosis inhibitors. It can also be used
 CC for treatment of apoptosis-related diseases
 XX SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAAGAAAAA 1496
 DB 18 TAAAAAAGAAAAA 2

RESULT 321
 AAV54166/C
 ID AAV54166 standard; cDNA; 18 BP.
 XX AC AAV54166;
 XX DT 21-DEC-1998 (first entry)
 XX DE Nucleotide sequence PCR primer 3.
 XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX KW immunohistological staining.

XX OS Synthetic.
 XX PN WO9839437-A1.
 XX PD 11-SEP-1998.
 XX PF 05-MAR-1998; 98WO-JP000905.
 XX PR 05-MAR-1997; 97JP-00050302.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Sakaki Y;
 XX WPI; 1998-495844/42.
 XX PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 PT treating diseases associated with apoptosis.
 XX PS Example 1; Page 48; 70pp; Japanese.
 XX CC This is the nucleotide sequence of a PCR primer used in the method of the
 CC invention, involving the use of novel apoptosis-related DNAs and
 CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 CC immunohistological staining, as apoptosis inhibitors. It can also be used
 CC for treatment of apoptosis-related diseases

XX SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAAGAAAAA 1494
 DB 18 GCTAAAAAAGAAAAA 2

RESULT 320
 AAV54165/C
 ID AAV54165 standard; cDNA; 18 BP.

XX AC AAV54165;
 XX DT 21-DEC-1998 (first entry)
 XX DE Nucleotide sequence PCR primer 2.
 XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX KW immunohistological staining.

CC This is the nucleotide sequence of a PCR primer used in the method of the
 CC invention, involving the use of novel apoptosis-related DNAs and
 CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 CC immunohistological staining, as apoptosis inhibitors. It can also be used
 CC for treatment of apoptosis-related diseases

SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 1480 TAAAAAATAAAAAAAAAA 1496
 Db 18 TGAATAAAAAAAAAAAAAA 2

RESULT 322
 AAV54172/C

ID AAV54172 standard; cDNA; 18 BP.

XX AC AAV54172;

XX DT 21-DEC-1998 (first entry)

XX DE Nucleotide sequence PCR primer 9.

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX immunohistological staining.

XX OS Synthetic.

XX PN WO9839437-A1.

XX PD 11-SEP-1998.

XX PF 05-MAR-1998; 98WO-JP000905.

XX PR 05-MAR-1997; 97JP-00050302.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Sakaki Y;

XX WPI; 1998-495844/42.

XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 XX treating diseases associated with apoptosis.
 XX Example 1; Page 50; 70pp; Japanese.

CC This is the nucleotide sequence of a PCR primer used in the method of the
 CC invention, involving the use of novel apoptosis-related DNAs and
 CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 CC immunohistological staining, as apoptosis inhibitors. It can also be used
 CC for treatment of apoptosis-related diseases

SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 1479 CTAATAAAAAAAAAAAAAA 1495
 Db 18 CGAATAAAAAAAAAAAAAA 2

RESULT 323
 AAV54171/C

ID AAV54171 standard; cDNA; 18 BP.

XX AC AAV54171;

XX DT 21-DEC-1998 (first entry)

XX DE Nucleotide sequence PCR primer 8.

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX immunohistological staining.

XX OS Synthetic.

XX PN WO9839437-A1.

XX PD 11-SEP-1998.

XX PF 05-MAR-1998; 98WO-JP000905.

XX PR 05-MAR-1997; 97JP-00050302.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Sakaki Y;

XX WPI; 1998-495844/42.

XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 XX treating diseases associated with apoptosis.
 XX Example 1; Page 49; 70pp; Japanese.

CC This is the nucleotide sequence of a PCR primer used in the method of the
 CC invention, involving the use of novel apoptosis-related DNAs and
 CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 CC immunohistological staining, as apoptosis inhibitors. It can also be used
 CC for treatment of apoptosis-related diseases

SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 2e+02; Mismatches 0; Gaps 0;

Matches 16; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 1479 CTAATAAAAAAAAAAAAAA 1495
 Db 18 CGAATAAAAAAAAAAAAAA 2

RESULT 324

AAZ90648/C

ID AAZ90648 standard; DNA; 18 BP.

XX AC AAZ90648;

XX DT 13-JUN-2000 (first entry)

XX DE Human adipose tissue gene amplifying primer #9.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 XX OS Homo sapiens.

XX PN JP2000037190-A.

XX PD 08-FEB-2000.

XX PF 23-JUL-1998; 98JP-00225228.

XX PR 23-JUL-1998; 98JP-00225228.

XX PA (NIBS) JAPAN TOBACCO INC.

XX WPI; 2000-306578/27.
XX A physiologically active protein specifically derived from mammal tissue.
XX Example 2; Page 18; 50pp; Japanese.
XX The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAZ90631-633) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 18 TGAATAAAAAAAAAAAAAA 2
RESULT 325
AAZ90642/c
ID AAZ90642 standard; DNA; 18 BP.
AC AAZ90642;
XX
XX 13-JUN-2000 (first entry)
DE Human adipose tissue gene amplifying primer #3.
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX Homo sapiens.
XX JP2000037190-A.
XX 08-FEB-2000.
XX 23-JUL-1998; 98JP-00225228.
XX 23-JUL-1998; 98JP-00225228.
XX (NIBS) JAPAN TOBACCO INC.
XX WPI; 2000-306578/27.
XX A physiologically active protein specifically derived from mammal tissue.
XX Example 2; Page 18; 50pp; Japanese.
XX The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAZ90631-633) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
SQ Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1495
DB 18 TGAATAAAAAAAAAAAAAA 2

Db 18 CGAAAAAATAAAAAAAAAA 2
RESULT 326
AAZ90641/c
ID AAZ90641 standard; DNA; 18 BP.
XX
XX AAZ90641;
XX 13-JUN-2000 (first entry)
DE Human adipose tissue gene amplifying primer #2.
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX Homo sapiens.
XX JP2000037190-A.
XX 08-FEB-2000.
XX 23-JUL-1998; 98JP-00225228.
XX 23-JUL-1998; 98JP-00225228.
XX (NIBS) JAPAN TOBACCO INC.
XX WPI; 2000-306578/27.
XX A physiologically active protein specifically derived from mammal tissue.
XX Example 2; Page 18; 50pp; Japanese.
XX The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAZ90631-633) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;
SQ Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1495
DB 18 CGAAAAAATAAAAAAAAAA 2
RESULT 327
AAZ90650/c
ID AAZ90650 standard; DNA; 18 BP.
XX
XX AAZ90650;
XX 13-JUN-2000 (first entry)
DE Human adipose tissue gene amplifying primer #11.
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX Homo sapiens.
XX JP2000037190-A.
XX 08-FEB-2000.
XX 23-JUL-1998; 98JP-00225228.

```
XX PR 23-JUL-1998; 98JP-00225228.
XX PA (NISB ) JAPAN TOBACCO INC.
XX XX
XX DR WPI; 2000-306578/27.
XX XX
XX PT A physiologically active protein specifically derived from mammal tissue.
XX PS Example 2; Page 18; 50pp; Japanese.
XX CC The invention relates to identification of genes and proteins of adipose
XX CC tissue relating to obesity, particularly complications of visceral
XX CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
XX CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
XX CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
XX CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
XX CC represent PCR primers amplifying the human adipose tissue genes
XX SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15.4; DB 1; Length 18;
XX Best Local Similarity 94.1%; Pred. No. 2e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1478 GCTAATAAAAAAAAAAAAAA 1494
DB 18 GCATAAAAAAAAAAAAAA 2

RESULT 328
AAZ90647/C
ID AAZ90647 standard; DNA; 18 BP.
XX AC AAZ90647;
XX DT 13-JUN-2000 (first entry)
XX DE Human adipose tissue gene amplifying primer #8.
XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX OS Homo sapiens.
XX XX JP2000037190-A.
XX PD 08-FEB-2000.
XX PF 23-JUL-1998; 98JP-00225228.
XX PR 23-JUL-1998; 98JP-00225228.
XX PA (NISB ) JAPAN TOBACCO INC.
XX DR WPI; 2000-306578/27.
XX PT A physiologically active protein specifically derived from mammal tissue.
XX PS Example 2; Page 18; 50pp; Japanese.
XX CC The invention relates to identification of genes and proteins of adipose
XX CC tissue relating to obesity, particularly complications of visceral
XX CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
XX CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
XX CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
XX CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
XX CC represent PCR primers amplifying the human adipose tissue genes
XX SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15.4; DB 1; Length 18;
XX Best Local Similarity 94.1%; Pred. No. 2e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1480 TAAAAAATAAAAAAAAAAAAAA 1496
DB 18 TCATAAAAAAAAAAAAAA 2

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAAAAAAAAAA 1496
DB 18 TCATAAAAAAAAAAAAAA 2

RESULT 329
AAF85699
ID AAF85699 standard; DNA; 18 BP.
XX AC AAF85699;
XX DT 13-JUL-2001 (first entry)
XX DE Multiple repeated heat process PCR related oligonucleotide #3.
XX KW Multiple repeated heat circulation; polymerase chain reaction; PCR;
XX KW target DNA production; DNA synthesis; ds.
XX OS Unidentified.
XX PN CN1278558-A.
XX PD 03-JAN-2001.
XX PF 22-JUN-1999; 99CN-00114949.
XX PR 22-JUN-1999; 99CN-00114949.
XX PA (XIAQ/) XIA Q.
XX PI Xia Q;
XX DR WPI; 2001-245741/26.
XX PT Asynchronous chain-extending polymerase chain reaction for producing lots
XX PT of target DNA fragments, comprises a multiple repeated heat circulation
XX PS Disclosure; Page 3; 4pp; Chinese.
XX CC The present invention relates to a kind of two chains asynchronously-
XX CC elongated DNA amplification technology in vitro, which is characterized
XX CC by that firstly, a pair of specific primers is synthesized according to
XX CC the target DNA sequence to be amplified, then a repetitive sequence
XX CC complementary oligo-repetitive sequence of 3' target DNA chain whose tail
XX CC end is modified and elongation vitality is lost, then the oligo-
XX CC repetitive sequence, chain primer, heat-resisting DNA polymerase, dNTP
XX CC substrate, template DNA, magnesium ion, polymerase chain reaction (PCR)
XX CC buffer solution and ultra-pure water are mixed uniformly and made into a
XX CC reaction system. The reaction system then undergoes the processes of high
XX CC -temp., low-temp., medium-low temp., medium-temp, and repeated heat
XX CC circulation treatment in the heat-circulating instrument to obtain
XX CC million copies of specific target DNA fragments. The invention adopts a
XX CC multiple repeated heat circulation process, so that it can produce lots
XX CC of target DNA fragments. The present sequence was used in the
XX CC exemplification of the invention
XX SQ Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15.4; DB 1; Length 18;
XX Best Local Similarity 94.1%; Pred. No. 2e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 25 CGGCGCGCGACGCGCGCG 41
DB 1 CGGCGCGCGCGCGCGCG 17

RESULT 330
ADA27361
ID ADA27361 standard; DNA; 18 BP.
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XX AC ADA27361;
XX AC
XX PD
XX PD
XX DT 20-NOV-2003 (first entry)
XX DE
XX DE Human microsatellite repeat M2_3_8.
XX KW ds; HLA-related research; HLA class II-associated disease;
XX KW transplantation matching; recombination hot spot identification;
XX KW linkage disequilibrium study; human; microsatellite.
XX OS Homo sapiens.
XX XX
XX XX US2003108940-A1.
XX XX
XX XX 12-JUN-2003.
XX XX
XX XX 06-DEC-2002; 2002US-00314405.
XX XX
XX XX 15-NOV-2000; 2000US-00713616.
XX XX
XX XX (INOK/) INOKO H.
XX XX
XX XX Inoko H, Tamiya G, Matsuzaka Y;
XX XX WPI; 2003-616782/58.
XX XX
XX XX New oligonucleotide primer capable of specifically hybridizing to a DNA
XX XX having the sequence of the flanking regions of a microsatellite (e.g.
XX XX M249), useful for HLA-related research, e.g. transplantation matching.
XX XX
XX XX Example 2; Page 5; 20pp; English.
XX XX
XX XX The invention relates to an oligonucleotide primer capable of
XX XX specifically hybridizing to a DNA having the sequence of the flanking
XX XX regions of a microsatellite selected from M2-4-9, M2-2-9, M2-2-12, M2-3-
XX XX 11, M2-2-20, M2-2-21, M2-2-22, M2-2-23, M2-2-24, M2-4-25, M2-4-26, M2-2-
XX XX 29, M2-2-32, M2-4-32, M2-4-33, M2-4-37, M2-3-22, M2-2-36, M2-5-11, M2-2-
XX XX 46, and M2-2-48. The primer is useful for determining the number of
XX XX repeat units of the microsatellite cited above. The primer is useful in
XX XX HLA-related research, such as genetic mapping of HLA class II-associated
XX XX diseases, transplantation matching, population genetics, and
XX XX identification of recombination hot spots as well as linkage
XX XX disequilibrium studies. The present sequence represents the human
XX XX microsatellite repeat M2_3_8.
XX XX
XX XX Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;
XX XX
XX XX Query Match 1.0%; Score 15.4; DB 1; Length 18;
XX XX Best Local Similarity 94.1%; Pred. No. 2e+02;
XX XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
QY 25 CGCGCGCGACGCGGCG 41
XX |||||
Db 2 CGCGCGCGCGCGGCG 18
XX |||||

RESULT 331
AD26385
ID AD26385 standard; DNA; 18 BP.
XX
XX AC AD26385;
XX XX
XX DT 18-DEC-2003 (first entry)
XX XX
XX DE NOV protein-related reverse PCR primer SEQ ID 210.
XX XX
XX KW NOV; cytostatic; metabolic disorder; immune; neurodegenerative;
XX KW circulatory; haemopoietic; wasting; cancer; gene therapy; vaccine;
XX KW transgenic; human; ss; PCR; primer.
XX OS Homo sapiens.
XX XX

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PN WO2003004687-A2.
XX
XX 16-JAN-2003.
XX
XX 03-JUL-2002; 2002WO-US021361.
XX
XX 05-JUL-2001; 2001US-0303046P.
XX PR
XX 09-JUL-2001; 2001US-0303828P.
XX PR
XX 11-JUL-2001; 2001US-0304016P.
XX PR
XX 11-JUL-2001; 2001US-0304502P.
XX PR
XX 13-JUL-2001; 2001US-0305262P.
XX PR
XX 16-JUL-2001; 2001US-0305673P.
XX PR
XX 17-JUL-2001; 2001US-0306085P.
XX PR
XX 24-JUL-2001; 2001US-0307536P.
XX PR
XX 27-JUL-2001; 2001US-0308228P.
XX PR
XX 30-JUL-2001; 2001US-0308677P.
XX PR
XX 01-AUG-2001; 2001US-0309255P.
XX PR
XX 17-AUG-2001; 2001US-0313328P.
XX PR
XX 12-SEP-2001; 2001US-0318711P.
XX PR
XX 19-SEP-2001; 2001US-0323380P.
XX PR
XX 21-SEP-2001; 2001US-0323969P.
XX PR
XX 04-JAN-2002; 2002US-0345022P.
XX PR
XX 28-FEB-2002; 2002US-0361172P.
XX PR
XX 01-MAR-2002; 2002US-0360814P.
XX PR
XX 01-MAR-2002; 2002US-0360830P.
XX PR
XX 01-MAR-2002; 2002US-0361133P.
XX PR
XX 01-MAR-2002; 2002US-0361147P.
XX PR
XX 05-MAR-2002; 2002US-0361677P.
XX PR
XX 02-APR-2002; 2002US-0363637P.
XX PR
XX 12-APR-2002; 2002US-0372326P.
XX PR
XX 16-APR-2002; 2002US-0372990P.
XX PR
XX 19-APR-2002; 2002US-0373881P.
XX PR
XX 19-APR-2002; 2002US-0373921P.
XX PR
XX 02-JUL-2002; 2002US-00188186.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Anderson DW, Berghs C, Boldog FL, Burgess CE, Casman SJ;
XX Catterton E, Edinger S, Eisen AJ, Ellerman K, Gerlach V, Gorman L;
XX Guo X, Jeffers M, Kekuda R, Li L, Malyankar UM, Miller CE;
XX Padigaru M, Patturajan M, Pena CE, Rastelli L, Shenoy S;
XX Shimkets RA, Spaderna SK, Spytek KA, Stone DJ, Taupier RJ;
XX Vernet CAM, Voss EZ, Zhong M;
XX WPI; 2003-221607/21.
XX
XX New isolated NOVX polypeptide, useful for determining the presence of, or
XX predisposition to a disease associated with altered levels of expression
XX of the polypeptide, and for treating or preventing cancer.
XX
XX Example C; SEQ ID NO 210; 478pp; English.
XX
XX The invention relates to a novel isolated NOV polypeptide. The
XX polypeptide of the invention demonstrates cytostatic activity and may be
XX used for determining the presence of, or predisposition to a disease
XX associated with altered levels of expression of the polypeptide,
XX including metabolic disorders, immune disorders, neurodegenerative
XX disorders, circulatory diseases, haemopoietic disorders, wasting diseases
XX and cancer. The polypeptide may also be utilised during gene therapy
XX procedures, vaccine development and transgenic animal production. The
XX current sequence is that of the PCR primer of the invention which was
XX used to analyse human NOV DNA.
XX
XX Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15.4; DB 1; Length 18;
XX Best Local Similarity 94.1%; Pred. No. 2e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 714 CCAGCACACTGACTGCT 730
XX |||||
Db 2 CCAGGACACTGACTGCT 18
XX |||||

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RESULT 332
AAAF82119/C
ID   AAF82119 standard; DNA; 16 BP.
XX
AC   AAF82119;
XX
DT   27-JUN-2001 (first entry)
XX
DE   Human TSA7005 gene isolation related PCR primer SEQ ID NO:4.
XX
KW   Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
KW   diagnosis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JF2001025389-A.
XX
PD   30-JAN-2001.
XX
PF   15-JUL-1999; 99JP-00201279.
XX
PR   15-JUL-1999; 99JP-00201279.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 2001-303742/32.
XX
PT   TSA7005 gene, encoding a polypeptide useful for the diagnosis and
PT   treatment of diseases associated with its expression.
XX
PS   Example 1; Page 24; 25pp; Japanese.
XX
CC   The present sequence represents a PCR primer which is used in an example
CC   from the present invention for the isolation of human TSA7005 gene. The
CC   human TSA7005 protein shares 32% homology with human and mouse Reg
CC   proteins, and 34% homology with the rat Reg protein. TSA7005 has
CC   pancreatic beta cell growth activity and hypoglycaemic activity. The
CC   TSA7005 protein can be used for the diagnosis and treatment of diseases
CC   associated with the gene and its expression product
XX
SQ   Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
Query Match 1.0%; Score 15.2; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1480 TAAAAAATAAAAAA 1495
Db 16 TAAAAAATAAAAAA 1
RESULT 333
AAAX18388/C
ID   AAAX18388 standard; DNA; 17 BP.
XX
AC   AAAX18388;
XX
DT   11-MAY-1999 (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 29.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997; 97JP-00208312.
XX
PR   18-JUL-1997; 97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Example 1; Page 12; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;
Query Match 1.0%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1480 TAAAAAATAAAAAA 1495
Db 16 BAAAAAATAAAAAA 1
RESULT 334
AAS141174/C
ID   AAS141174 standard; DNA; 17 BP.
XX
AC   AAS141174;
XX
DT   18-DEC-2001 (first entry)
XX
DE   Modified Poly-T Primer #1 used in construction of probe sets.
XX
KW   WRAP-Probe; gene expression array; global amplification; RNA array; ss;
KW   tissue microarray; drug discovery assay; reporter binding site; forensic;
KW   diagnostic; genomic analysis; universal linker; poly-T primer.
XX
OS   Synthetic.
XX
PN   WO200166802-A1.
XX
PD   13-SEP-2001.
XX
PF   09-MAR-2001; 2001WO-US007508.
XX
PR   09-MAR-2000; 2000US-0187982P.
XX
PA   (GENE-) GENETAG TECHNOLOGY INC.
XX
PI   Shafer DA;
XX
PT   WPI; 2001-596845/67.
XX
PT   Novel probe sets with common universal linkers at one or both ends (WRAP
PT   probes) for gene expression arrays to provide global amplification of
PT   probe set and to provide common equivalent signaling regardless of
PT   length.
XX
PS   Disclosure; Page 88; 97pp; English.
XX
CC   The invention relates to a probe set for gene expression arrays to

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CC provide common equivalent signalling per probe and global amplification
CC of the set. The probe set has a pool of modified cDNA probes, each probe
CC having a central target specific segment copied from a portion of a
CC single mRNA transcript and a universal linker (a WRAP-Probe) located on
CC one or both terminal ends. The universal linker has reporter binding
CC sites to join common reporters to the probes and primer binding sites to
CC copy and amplify the probe. The probes and reporters are useful in
CC diagnostic or drug discovery assays for a wide range of biomedical
CC samples, including detection of nucleic acids and gene expression
CC profiles in human diagnostics, forensics and genomic analysis. The
CC methods are useful for amplifying and identifying any unknown DNA
CC fragment and also for improving sensitivity with tissue microarrays or
CC RNA arrays. The methods improve the quantification of gene expression and
CC allow highly improved detection of rare transcripts or very small
CC samples. This sequence represents a poly-T primer used in the
CC construction of probe sets
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match      1.0%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
Db 16 BAAAAAAAAAAAAA 1

RESULT 335
AAQ79185
ID AAQ79185 standard; DNA; 15 BP.
XX
AC AAQ79185;
XX
DT 25-MAR-2003 (revised)
DT 21-JUN-1995 (first entry)
XX
DE Nuclease resistant oligonucleotide.
XX
KW Nuclease resistant oligonucleotide; inhibition of gene expression;
KW 9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 13 /*tag= a
FT /*mod_base= OTHER
FT /*note= "9-methyl-acyclo-adenosine"
XX
PN W09422864-A1.
XX
PD 13-OCT-1994.
XX
PF 21-MAR-1994; 94WO-US002995.
XX
PR 30-MAR-1993; 93US-00040326.
XX
PA (STER ) STERLING WINTHROP INC.
XX
PI Cook PD, Delecki DJ, Guinasso C;
XX
DR WPI; 1994-333078/41.
XX
PT New acyclic nucleoside analogues - used to prepare nuclease resistant
PT oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS Example 11; Page 20; 37pp; English.
XX
AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acyclic
CC nucleoside analogues which inhibit nuclease degradation. The nuclease
CC resistant oligonucleotides can themselves be used to inhibit gene
CC expression as antisense agents, in nucleic acid sequencing and diagnostic
CC
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```
CC assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 336
AAQ79184
ID AAQ79184 standard; DNA; 15 BP.
XX
AC AAQ79184;
XX
DT 25-MAR-2003 (revised)
DT 21-JUN-1995 (first entry)
XX
DE Nuclease resistant oligonucleotide.
XX
KW Nuclease resistant oligonucleotide; inhibition of gene expression;
KW 9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 14 /*tag= a
FT /*mod_base= OTHER
FT /*note= "9-methyl-acyclo-adenosine"
XX
PN W09422864-A1.
XX
PD 13-OCT-1994.
XX
PF 21-MAR-1994; 94WO-US002995.
XX
PR 30-MAR-1993; 93US-00040326.
XX
PA (STER ) STERLING WINTHROP INC.
XX
PI Cook PD, Delecki DJ, Guinasso C;
XX
DR WPI; 1994-333078/41.
XX
PT New acyclic nucleoside analogues - used to prepare nuclease resistant
PT oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS Example 10; Page 20; 37pp; English.
XX
AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acyclic
CC nucleoside analogues which inhibit nuclease degradation. The nuclease
CC resistant oligonucleotides can themselves be used to inhibit gene
CC expression as antisense agents, in nucleic acid sequencing and diagnostic
CC assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 337
AAT52136/c
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ID	AAT52136	standard; RNA; 15 BP.
XX		
AC	AAT52136;	
XX		
DT	25-MAR-2003	(revised)
XX		
DT	25-MAR-1997	(first entry)
XX		
DE	Human ICAM hammerhead ribozyme target sequence (nt. position 2910).	
XX		
KW	Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;	
XX	gene expression; downregulation; interleukin-5; IL-5; ICAM-1;	
KW	intercellular adhesion molecule; rel A; tumour necrosis factor;	
XX	TNP-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;	
KW	translocation; chronic myelogenous leukaemia; CML; cancer;	
XX	Philadelphia chromosome; inflammation; autoimmune disease;	
KW	atherosclerosis; myocardial infarction; stroke; restenosis;	
XX	transplant rejection; rheumatoid arthritis; psoriasis;	
KW	myocardial ischaemia; Kawasaki disease; septic shock; HIV;	
XX	human immunodeficiency virus; acquired immune deficiency syndrome; AIDS	
XX	ss.	
OS	Homo sapiens.	
XX		
PN	WO9523225-A2.	
XX		
XX	31-AUG-1995.	
PD		
XX	23-FEB-1995;	95WO-IB000156.
XX		
PR	23-FEB-1994;	94US-00201109.
XX		
PR	04-MAR-1994;	94US-00218934.
XX		
PR	04-APR-1994;	94US-00222795.
XX		
PR	07-APR-1994;	94US-00224483.
XX		
PR	15-APR-1994;	94US-00227958.
XX		
PR	15-APR-1994;	94US-00228041.
XX		
PR	18-MAY-1994;	94US-00245736.
XX		
PR	08-JUL-1994;	94US-00271280.
XX		
PR	15-AUG-1994;	94US-00291932.
XX		
PR	16-AUG-1994;	94US-00291433.
XX		
PR	17-AUG-1994;	94US-00292620.
XX		
PR	19-AUG-1994;	94US-00293520.
XX		
PR	02-SEP-1994;	94US-00300000.
XX		
PR	08-SEP-1994;	94US-00303039.
XX		
PR	23-SEP-1994;	94US-00311486.
XX		
PR	23-SEP-1994;	94US-00311749.
XX		
PR	28-SEP-1994;	94US-00314397.
XX		
PR	03-OCT-1994;	94US-00316771.
XX		
PR	07-OCT-1994;	94US-00319492.
XX		
PR	11-OCT-1994;	94US-00321993.
XX		
PR	04-NOV-1994;	94US-00334847.
XX		
PR	10-NOV-1994;	94US-00337608.
XX		
PR	28-NOV-1994;	94US-00345516.
XX		
PR	16-DEC-1994;	94US-00357577.
XX		
PR	23-DEC-1994;	94US-00363233.
XX		
PR	30-JAN-1995;	95US-00380734.
XX		
PA	(RIBO-) RIBOZYME PHARM INC.	
XX		
PI	Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;	
XX	Grimm S, Karpaisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;	
PI	Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;	
XX	Tracz D, Usman N, Wincott FE, Woolf T;	
XX		
DR	WPI; 1995-351090/45.	
XX		
XX	Ribozymes having modified bases and methods for producing them - for use	
FT	in inhibiting disease related genes.	
XX		
PS	Claim 2; Page 175; 407pp; English.	
XX		
CC	The present sequence represents a preferred target sequence for an	
CC	enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the	
CC	nucleotide base position indicated in the DE line. Regions of the mRNA	

CC		that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid arthritis, asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to correct PI field.)
XX		
XX		
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;	
	Query Match 1.0%; Score 15; DB 1; Length 15;	
	Best Local Similarity 100.0%; Pred. NO. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;	
	Matches 15; Conservative 0;	
Oy	1481 AAAAAAAAAAAAAA 1495 	
Dd	15 AAAAAAAAAAAAAA 1	
RESULT 338		
AAT52138/c		
ID	AAT52138 standard; RNA; 15 BP.	
XX		
AC	AAT52138;	
XX		
XX	25-MAR-2003 (revised)	
DT	25-MAR-1997 (first entry)	
XX		
DE	Human ICAM hammerhead ribozyme target sequence (nt. position 2911).	
XX		
KW	Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;	
KW	gene expression; downregulation; interleukin-5; IL-5; ICAM-1;	
KW	intercellular adhesion molecule; rel A; tumour necrosis factor;	
KW	TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;	
KW	translocation; chronic myelogenous leukaemia; CMV; cancer;	
KW	Philadelphia chromosome; inflammation; autoimmune disease;	
KW	atherosclerosis; myocardial infarction; stroke; restenosis;	
KW	transplant rejection; rheumatoid arthritis; psoriasis;	
KW	myocardial ischaemia; Kawasaki disease; septic shock; HIV;	
KW	human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;	
ss.		
OS	Homo sapiens.	
XX		
PN	WO9523225-A2.	
XX		
PD	31-AUG-1995.	
XX		
PF	23-FEB-1995; 95WO-IB000156.	
XX		
PR	23-FEB-1994; 94US-00201109.	
FR	29-MAR-1994; 94US-00218934.	
PR	04-APR-1994; 94US-00222795.	
PR	07-APR-1994; 94US-00224483.	
PR	15-APR-1994; 94US-00227958.	
PR	15-APR-1994; 94US-00228041.	
PR	18-MAY-1994; 94US-00245736.	
PR	06-JUL-1994; 94US-00271280.	
PR	15-AUG-1994; 94US-00291932.	
PR	16-AUG-1994; 94US-00291433.	
PR	17-AUG-1994; 94US-00292620.	
PR	19-AUG-1994; 94US-00293520.	
PR	02-SEP-1994; 94US-00300000.	
PR	08-SEP-1994; 94US-00303039.	
PR	23-SEP-1994; 94US-00311486.	
PR	23-SEP-1994; 94US-00311749.	
PR	28-SEP-1994; 94US-00314397.	
PR	03-OCT-1994; 94US-00316771.	
PR	07-OCT-1994; 94US-00319492.	
PR	11-OCT-1994; 94US-00321993.	
PR	04-NOV-1994; 94US-00334847.	

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PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PR (RIBO-) RIBOZYME PHARM INC.
PA
XX Stinchcomb DT, Chowrira B, Dizenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpaisky A, Bisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Favco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
DR
XX
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
PT
XX
XX Claim 2; Page 175; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 339
AAV01604
ID AAV01604 standard; DNA; 15 BP.
XX
XX AAV01604;
XX
DT 25-MAR-2003 (revised)
DT 31-MAR-1998 (first entry)
XX
DE Oligonucleotide containing phosphoramidate linkages.
XX phosphoramidate linkage; solid phase synthesis; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..15
XX /tag= a
XX /note= "these residues have N3'-->P5' phosphoramidate
XX linkages"
XX
XX WO9731009-A1.
XX
XX 28-AUG-1997.
XX
XX 14-JUN-1996; 96WO-US010418.
XX
XX 21-FEB-1996; 96US-00603566.
XX
XX
XX

```

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PA (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Hirschbein BL, Fearon KL, Gryaznov SM, Mccurdy SN, Nelson JS;
PI Schultz RG;
XX
XX WPI; 1997-435080/40.
DR
XX
XX Synthesis of N3' to P5' phosphoramidate oligonucleotide - by reacting
PT immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
PT phosphoramidite then oxidation, useful as research, diagnostic and
PT therapeutic agents.
XX
XX Disclosure; Page 28; 60pp; English.
XX
XX A new method is provided for the synthesis of oligonucleotides having N3'
XX -->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
XX protected amino nucleoside to a solid support; (b) deprotecting the 3'-
XX amino; (c) reacting with a 3'-protected aminonucleoside-5'-
XX phosphoramidite monomer to form an internucleoside N3'-->P5'
XX phosphoramidite link; (d) oxidising this link to phosphoramidate; and
XX optionally repeating steps (b)-(d) until the required oligonucleotide is
XX completed. This method provides better yields with lower reagent
XX consumption than known processes, and can be operated on a large scale.
XX The obtained oligos, containing phosphoramidate linkages, have favourable
XX binding properties, nuclease resistance and solubility, and are useful as
XX research, diagnostic and therapeutic agents. The present sequence is an
XX example of an oligonucleotide in which N3'-->P5' phosphoramidate linkages
XX have been introduced by the new method. (Updated on 25-MAR-2003 to
XX correct PR field.)
XX
XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 1 AAAAAAAAAAAAAA 15
RESULT 340
AAV01603/c
ID AAV01603 standard; DNA; 15 BP.
XX
XX AAV01603;
XX
DT 25-MAR-2003 (revised)
DT 31-MAR-1998 (first entry)
XX
DE Oligonucleotide containing phosphoramidate linkages.
XX phosphoramidate linkage; solid phase synthesis; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..15
XX /tag= a
XX /note= "these residues have N3'-->P5' phosphoramidate
XX linkages"
XX
XX WO9731009-A1.
XX
XX 28-AUG-1997.
XX
XX 14-JUN-1996; 96WO-US010418.
XX
XX 21-FEB-1996; 96US-00603566.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Hirschbein BL, Fearon KL, Gryaznov SM, Mccurdy SN, Nelson JS;
PI

```


CC bound to a polyacrylamide gel via a linking group. The invention relates
 CC to selective separation of electrically charged target molecules in an
 CC analytical mixture. It comprises capillary affinity gel electrophoresis
 CC using a capillary tube which is at least partly filled with a polymer
 CC gel. Receptors for target molecules are covalently bound to the polymer.
 CC An electric field of at least 50 volts/cm is applied. The capillary tube
 CC is charged with the analytical mixture. In a first separation stage, the
 CC target molecules in the mixture are bound to the receptors and the
 CC remaining components are eluted, optionally whilst splitting open. In a
 CC second stage, the elution conditions are changed, optionally in stages,
 CC so that the affinity of the target molecules for the receptor is
 CC eliminated and the target molecules are eluted and detected, optionally
 CC whilst splitting open. The process is useful for selective separation
 CC and/or determination of charged organic compounds, such as
 CC oligonucleotides, peptides or carbohydrates. It may be used, e.g. for
 CC isolation of specific proteins and DNA molecules, purification of
 CC antibodies, analysis of antisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity than
 CC prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods
 CC
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 DB 15 AAAAAAAAAAAAAA 1

RESULT 343
 AAT86605/c
 ID AAT86605 standard; DNA; 15 BP.
 XX
 AC AAT86605;
 XX
 DT 04-JUN-1998 (first entry)
 XX
 DE Oligonucleotide separated by capillary affinity gel electrophoresis.
 XX
 KW Capillary affinity gel electrophoresis; separation; polymer-gel;
 KW polyacrylamide; ss.
 XX
 OS Synthetic.
 XX
 PN W09745721-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 23-MAY-1997; 97MO-EP002647.
 XX
 PR 24-MAY-1996; 96CH-00001320.
 XX
 PA (NOVS) NOVARTIS AG.
 XX
 PI Muscate A, Paulus A, Natt F;
 XX
 DR WPI; 1998-041763/04.

PT Separation of electrically charged target molecules - by capillary
 PT affinity gel electrophoresis using polymer-gel to which receptors for
 PT target molecules are bound.
 PS
 PS Example D3; Page 25; 41pp; English.
 XX
 CC A mixture of oligonucleotides (AAT86604-7) were separated by a new
 CC process using capillary affinity gel electrophoresis. The invention
 CC relates to selective separation of electrically charged target molecules
 CC in an analytical mixture. It comprises capillary affinity gel

CC electrophoresis using a capillary tube which is at least partly filled
 CC with a polymer gel. Receptors for target molecules are covalently bound
 CC to the polymer. An electric field of at least 50 volts/cm is applied. The
 CC capillary tube is charged with the analytical mixture. In a first
 CC separation stage, the target molecules in the mixture are bound to the
 CC receptors and the remaining components are eluted, optionally whilst
 CC splitting open. In a second stage, the elution conditions are changed,
 CC optionally in stages, so that the affinity of the target molecules for
 CC the receptor is eliminated and the target molecules are eluted and
 CC detected, optionally whilst splitting open. The process is useful for
 CC selective separation and/or determination of charged organic compounds,
 CC such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
 CC for isolation of specific proteins and DNA molecules, purification of
 CC antibodies, analysis of antisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity than
 CC prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods
 CC
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 DB 15 AAAAAAAAAAAAAA 1

RESULT 344
 AAX31736
 ID AAX31736 standard; DNA; 15 BP.
 XX
 AC AAX31736;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Transcript tag sequence increased in pancreatic and colorectal cancer.
 XX
 KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09853319-A2.
 XX
 PD 26-NOV-1998.
 XX
 PF 20-MAY-1998; 98WO-US010277.
 XX
 PR 21-MAY-1997; 97US-0047352P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW;
 XX
 DR WPI; 1999-070161/06.

PT Use of isolated gene transcripts - useful for developing products for the
 PT diagnosis, prognosis and treatment of cancers, particularly colon and
 PT pancreatic cancer.

PS Disclosure; Page 73; 120pp; English.

XX AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or
 CC in both. The tag sequences can be used to identify genes by matching the
 CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a
 CC sample suspected of being neoplastic. The method comprises comparing the

CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer
 CC
 SQ Sequence 15 BP; 10 A; 2 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1475 CATGCTAAAAAAA 1489
 DB 1 CATGCTAAAAAAA 15
 RESULT 345
 AAX31131
 ID AAX31131 standard; DNA; 15 BP.
 XX AC AAX31131;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Tag sequence of a transcript increased in colorectal cancer.
 XX
 KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9853319-A2.
 XX
 PD 26-NOV-1998.
 XX
 PF 20-MAY-1998; 98WO-US010277.
 XX
 PR 21-MAY-1997; 97US-0047352P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW;
 XX
 DR WPI; 1999-070161/06.
 XX
 XX Use of isolated gene transcripts - useful for developing products for the
 PT diagnosis, prognosis and treatment of cancers, particularly colon and
 PT pancreatic cancer.
 XX
 PS Claim 2; Page 32; 120pp; English.
 XX
 CC AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or
 CC in both. The tag sequences can be used to identify genes by matching the
 CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a
 CC sample suspected of being neoplastic. The method comprises comparing the
 CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer
 CC
 SQ Sequence 15 BP; 10 A; 2 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1475 CATGCTAAAAAAA 1489
 DB 1 CATGCTAAAAAAA 15
 RESULT 346
 AAX31539
 ID AAX31539 standard; DNA; 15 BP.
 XX AC AAX31539;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Tag sequence of a transcript increased in pancreatic cancer.
 XX
 KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9853319-A2.
 XX
 PD 26-NOV-1998.
 XX
 PF 20-MAY-1998; 98WO-US010277.
 XX
 PR 21-MAY-1997; 97US-0047352P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW;
 XX
 DR WPI; 1999-070161/06.
 XX
 XX Use of isolated gene transcripts - useful for developing products for the
 PT diagnosis, prognosis and treatment of cancers, particularly colon and
 PT pancreatic cancer.
 XX
 PS Claim 13; Page 59; 120pp; English.
 XX
 CC AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or
 CC in both. The tag sequences can be used to identify genes by matching the
 CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a
 CC sample suspected of being neoplastic. The method comprises comparing the
 CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer
 CC
 SQ Sequence 15 BP; 2 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1390 CATGCACCTGCTCTT 1404
 DB 1 CATGCACCTGCTCTT 15
 RESULT 347
 AAX00787/C
 ID AAX00787 standard; DNA; 15 BP.
 XX AC AAX00787;
 XX
 DT 13-APR-1999 (first entry)
 XX

```
DE N3-P5 phosphoramidate oligonucleotide #3.
XX
KW Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..15
FT /*tag= a
FT /note= "contains internucleotide N3-P5 phosphoramidate
FT internucleotide linkages"
XX
XX US5859233-A.
XX
XX 12-JAN-1999.
XX
XX 20-DEC-1996; 96US-00771789.
XX
XX 21-FEB-1996; 96US-00603566.
XX 14-JUN-1996; 96US-00663918.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Gryaznov SM, Nelson JS, McCurdy SN, Hirschbein BL, Schultz RG;
XX Fearon KL;
XX WPI; 1999-120007/10.
XX
XX 20-DEC-1996; 96US-00771789.
XX
XX 21-FEB-1996; 96US-00603566.
XX 14-JUN-1996; 96US-00663918.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Gryaznov SM, Nelson JS, McCurdy SN, Hirschbein BL, Schultz RG;
XX Fearon KL;
XX WPI; 1999-120007/10.
XX
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
XX the synthesis of oligo-nucleotide(s).
XX
XX Example 10; Col 33; 34pp; English.
XX
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a 5'-
XX phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidised to form a stable
XX protected phosphoramidate linkage
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Example 10; Col 33; 34pp; English.
XX
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a 5'-
XX phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidised to form a stable
XX protected phosphoramidate linkage
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX DB 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 348
XX AAX00788
XX ID AAX00788 standard; DNA; 15 BP.
XX
XX AC AAX00788;
XX
XX 13-APR-1999 (first entry)
XX
XX DE N3-P5 phosphoramidate oligonucleotide #4.
XX
XX Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_difference 1..15
XX /*tag= a
XX /note= "contains internucleotide N3-P5 phosphoramidate
XX internucleotide linkages"
XX
XX FT
XX FT
XX FT
```

```
PN US5859233-A.
XX
XX 12-JAN-1999.
XX
XX 20-DEC-1996; 96US-00771789.
XX
XX 21-FEB-1996; 96US-00603566.
XX 14-JUN-1996; 96US-00663918.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Gryaznov SM, Nelson JS, McCurdy SN, Hirschbein BL, Schultz RG;
XX Fearon KL;
XX WPI; 1999-120007/10.
XX
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
XX the synthesis of oligo-nucleotide(s).
XX
XX Example 10; Col 33; 34pp; English.
XX
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a 5'-
XX phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidised to form a stable
XX protected phosphoramidate linkage
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX DB 1 AAAAAAAAAAAAAA 15
XX
XX RESULT 349
XX AAZ61854/c
XX ID AAZ61854 standard; RNA; 15 BP.
XX
XX AC AAZ61854;
XX
XX 28-MAR-2000 (first entry)
XX
XX DE HCV 3' non core region substrate for Hammerhead ribozyme HCV.3-118.
XX
XX KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
XX cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
XX autoimmune disease; ss.
XX
XX OS Hepatitis C virus.
XX
XX PN WO955847-A2.
XX
XX 04-NOV-1999.
XX
XX 26-APR-1999; 99WO-US009027.
XX
XX 27-APR-1998; 98US-0083217P.
XX 18-SEP-1998; 98US-0100842P.
XX 25-FEB-1999; 99US-00257608.
XX 23-MAR-1999; 99US-00274553.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Mcswiggen JA, Roberts E, Favco PA, Macejak D;
XX WPI; 2000-062023/05.
XX
XX
```

XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX Claim 1; Page 49; 123pp; English.
XX The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The
CC HCV sequence was screened for optimal ribozyme target sites using a
CC computer folding algorithm and regions of the mRNA which did not form
CC secondary folding structures and contained potential ribozyme cleavage
CC sites were identified. Ribozymes were synthesised to target these sites
CC and their activities optimised by either varying the length of the
CC binding arms or by modification to prevent degradation by nucleases. The
CC ribozymes of the invention inhibit gene expression and/or viral
CC replication, and are used to treat diseases associated with Hepatitis C
CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC carcinoma. The ribozymes may be used in combination with interferon to
CC treat HCV infection, other infectious diseases, autoimmune diseases, and
CC cancer
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
RESULT 350
AAZ64910/c
ID AAZ64910 standard; RNA; 15 BP.
AC AAZ64910;
XX 28-MAR-2000 (first entry)
DT
XX Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.
DE
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX Hepatitis C virus.
OS
XX WO9955847-A2.
PN
XX 04-NOV-1999.
PD
XX 26-APR-1999; 99WO-US009027.
PF
XX 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
PI
XX WPI; 2000-062023/05.
DR
XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX Claim 1; Page 102; 123pp; English.
XX The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves

CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
RESULT 351
AAA46502/c
ID AAA46502 standard; cDNA; 15 BP.
XX
AC AAA46502;
XX 04-SEP-2000 (first entry)
DT
XX PCR primer used to amplify DNA encoding an endo-beta-mannanase.
DE
XX Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
KW PCR primer; ss.
KW
XX Coffea arabica.
OS
XX WO200028046-A1.
PN
XX 18-MAY-2000.
PD
XX 28-OCT-1999; 99WO-EP008314.
PF
XX 11-NOV-1998; 98EP-00203742.
PR
XX (NEST) SOC PROD NESTLE SA.
PA
XX Marraccini P, Rogers J;
PI
XX WPI; 2000-399535/34.
DR
XX New DNA encoding endo-beta-mannanase from coffee, used e.g. in
PT pharmaceutical, cosmetic or food compositions to hydrolyze polymannans.
PT
XX Disclosure; Page 32; 41pp; French.
PS
XX PCR primers AAA46501-02 were used to amplify DNA encoding an endo-beta-
CC mannanase enzyme, which is involved in the hydrolysis of polysaccharides
CC that consist of molecules of mannan, either simple or branched, linked
CC together by beta(1-4) bonds. The mannanase polynucleotide sequence is
CC used for in vivo modification of the coffee endo-beta-mannanase gene. It
CC is also used to produce transgenic plant cells (especially coffee cells)
CC which have modified properties of mannan polysaccharide, and thus altered
CC flavour or structure. The enzyme is used for modification, degradation or
CC synthesis of mannan polysaccharides in vitro, particularly to treat
CC coffee beans to increase the percentage of dry matter extraction, and
CC thus reduce the quantity of sediment
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

```
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 352
AAA75048/c
ID AAA75048 standard; DNA; 15 BP.
XX
AC AAA75048;
XX
DT 15-JAN-2001 (first entry)
XX
DE Primer used to reverse transcribe human RNA.
XX
KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW wound healing; infection; burn; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease;
KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200052178-A1.
XX
PD 08-SEP-2000.
XX
PF 14-FEB-2000; 2000WO-US003542.
XX
PR 01-MAR-1999; 99US-00258892.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
WPI; 2000-579285/54.
XX
PT New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
XX
PS Disclosure; Page 44; 152pp; English.
XX
CC The present primer was used to reverse transcribe human RNA, from which a
CC cDNA sequence encoding a protein with heparanase catalytic activity was
CC amplified. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC particularly in treating tumour, inflammation or autoimmunity.
CC Particularly, the polynucleotide is useful in modulating the
CC bioavailability of heparin-binding growth factors, cellular responses to
CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
CC susceptibility to certain viral and some bacterial and protozoa
CC infections, or disintegration of neurodegenerative plaques. The
CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC radiation burns), and in the treatment of angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC bacterial or protozoa infections
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 353
AAA07792/c
ID AAA07792 standard; DNA; 15 BP.
XX
AC AAA07792;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-e.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07792 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
```



```

AC AAA07790;
XX
XX DT 23-JUN-2000 (first entry)
XX DE
XX DE Nucleic acid sequence of ODN-c.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; ss.
XX
XX OS Synthetic.
XX
XX PN WO200011013-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 20-AUG-1999; 99WO-US019029.
XX
XX PR 22-AUG-1998; 98US-0097712P.
XX
XX PA (UYNE-) UNIV NEBRASKA.
XX
XX PI Gold B;
XX
XX DR WPI; 2000-246530/21.
XX
XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics.
XX
XX PS Disclosure; Page 20; 42pp; English.
XX
XX CC The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation, antisense
XX CC technology, diagnostic applications to detect target sequences in
XX CC biological samples such as those containing pathogenic bacteria, fungi
XX CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX CC interleukins associated with pathological conditions such as inflammatory
XX CC conditions, cardiovascular disorders, immune reactions, cancer, viral
XX CC infections and bacterial infections (see AAA07786 for details of other
XX CC uses for which the oligomers are suitable for). Oligomers comprising the
XX CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX CC target nucleic acid sequences, are physiologically stable, non-toxic and
XX CC able to penetrate into cells while maintaining stringent base pair
XX CC fidelity for target DNA sequences. The oligomers demonstrate significant
XX CC single- or double-stranded target nucleic acid binding activity to form
XX CC duplexes, triplexes or other forms of stable association. Sequences
XX CC AAA07788-803 represent oligonucleotides forming a third strand along with
XX CC the duplex sequences
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 357
AAA07789/c
ID AAA07789 standard; DNA; 15 BP.
XX
XX AC AAA07789;
XX
XX DT 23-JUN-2000 (first entry)
XX
XX DE
XX DE Nucleic acid sequence of ODN-b.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; ss.
XX
XX OS Synthetic.
XX
XX PN WO200011013-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 20-AUG-1999; 99WO-US019029.
XX
XX PR 22-AUG-1998; 98US-0097712P.
XX
XX PA (UYNE-) UNIV NEBRASKA.
XX
XX PI Gold B;
XX
XX DR WPI; 2000-246530/21.
XX
XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics.
XX
XX PS Disclosure; Page 20; 42pp; English.
XX
XX CC The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation, antisense
XX CC technology, diagnostic applications to detect target sequences in
XX CC biological samples such as those containing pathogenic bacteria, fungi
XX CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX CC interleukins associated with pathological conditions such as inflammatory
XX CC conditions, cardiovascular disorders, immune reactions, cancer, viral
XX CC infections and bacterial infections (see AAA07786 for details of other
XX CC uses for which the oligomers are suitable for). Oligomers comprising the
XX CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX CC target nucleic acid sequences, are physiologically stable, non-toxic and
XX CC able to penetrate into cells while maintaining stringent base pair
XX CC fidelity for target DNA sequences. The oligomers demonstrate significant
XX CC single- or double-stranded target nucleic acid binding activity to form
XX CC duplexes, triplexes or other forms of stable association. Sequences
XX CC AAA07788-803 represent oligonucleotides forming a third strand along with
XX CC the duplex sequences
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 358
AAA07795/c
ID AAA07795 standard; DNA; 15 BP.
XX
XX AC AAA07795;
XX
XX DT 23-JUN-2000 (first entry)
XX
XX DE

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```

DE XX Nucleic acid sequence of ODN-h.
KW XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW XX viral infection; inflammatory response; cellular proliferation;
KW XX psoriasis; duplex; ss.
OS XX Synthetic.
XX XX
XX XX WO200011013-A1.
XX XX
XX XX 02-MAR-2000.
XX XX
XX XX 20-AUG-1999; 99WO-US019029.
XX XX
XX XX 22-AUG-1998; 98US-0097712P.
XX XX
XX XX (UYNE-) UNIV NEBRASKA.
XX XX
XX XX Gold B;
XX XX
XX XX WPI; 2000-246530/21.
XX XX
XX XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX XX oligomers used to inhibit expression of nucleic acids and in gene
XX XX regulation, antisense technology and diagnostics.
XX XX
XX XX Disclosure; Page 20; 42pp; English.
XX XX
XX XX The invention provides modified nucleomonomers of specified formula and
XX XX their pharmaceutically acceptable salts. The nucleomonomers are used as
XX XX monomers in oligomers, which are used in pharmaceutical compositions to
XX XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX XX infected cells. They are used in oligomers for gene regulation, antisense
XX XX technology, diagnostic applications to detect target sequences in
XX XX biological samples such as those containing pathogenic bacteria, fungi
XX XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX XX molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX XX interleukins associated with pathological conditions such as inflammatory
XX XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX XX infections and bacterial infections (see AAA07786 for details of other
XX XX uses for which the oligomers are suitable for). Oligomers comprising the
XX XX nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX XX able to penetrate into cells while maintaining stringent base pair
XX XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX XX single- or double-stranded target nucleic acid binding activity to form
XX XX duplexes, triplexes or other forms of stable association. Sequences
XX XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX XX the duplex sequences
XX XX
XX XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 359
AAA07797/c
ID AAA07797 standard; DNA; 15 BP.
XX AC.
XX AAA07797;
XX
XX 23-JUN-2000 (first entry)
XX
XX Nucleic acid sequence of ODN-j.
KW XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW XX viral infection; inflammatory response; cellular proliferation;

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```

KW XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW XX viral infection; inflammatory response; cellular proliferation;
KW XX psoriasis; duplex; ss.
OS XX Synthetic.
XX XX
XX XX WO200011013-A1.
XX XX
XX XX 02-MAR-2000.
XX XX
XX XX 20-AUG-1999; 99WO-US019029.
XX XX
XX XX 22-AUG-1998; 98US-0097712P.
XX XX
XX XX (UYNE-) UNIV NEBRASKA.
XX XX
XX XX Gold B;
XX XX
XX XX WPI; 2000-246530/21.
XX XX
XX XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX XX oligomers used to inhibit expression of nucleic acids and in gene
XX XX regulation, antisense technology and diagnostics.
XX XX
XX XX Disclosure; Page 20; 42pp; English.
XX XX
XX XX The invention provides modified nucleomonomers of specified formula and
XX XX their pharmaceutically acceptable salts. The nucleomonomers are used as
XX XX monomers in oligomers, which are used in pharmaceutical compositions to
XX XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX XX infected cells. They are used in oligomers for gene regulation, antisense
XX XX technology, diagnostic applications to detect target sequences in
XX XX biological samples such as those containing pathogenic bacteria, fungi
XX XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX XX molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX XX interleukins associated with pathological conditions such as inflammatory
XX XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX XX infections and bacterial infections (see AAA07786 for details of other
XX XX uses for which the oligomers are suitable for). Oligomers comprising the
XX XX nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX XX able to penetrate into cells while maintaining stringent base pair
XX XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX XX single- or double-stranded target nucleic acid binding activity to form
XX XX duplexes, triplexes or other forms of stable association. Sequences
XX XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX XX the duplex sequences
XX XX
XX XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 360
AAA07799/c
ID AAA07799 standard; DNA; 15 BP.
XX AC.
XX AAA07799;
XX
XX 23-JUN-2000 (first entry)
XX
XX Nucleic acid sequence of ODN-l.
KW XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW XX viral infection; inflammatory response; cellular proliferation;

```

```

KW psoriasis; duplex; ss.
XX
XX Synthetic.
XX WO200011013-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 20-AUG-1999; 99WO-US019029.
XX
XX PR 22-AUG-1998; 98US-0097712P.
XX
XX PA (UYNE-) UNIV NEBRASKA.
XX
XX PI Gold B;
XX
XX DR WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics.
XX
XX PS Disclosure; Page 20; 42pp; English.
XX
XX CC The invention provides modified nucleomonomers of specified formula and
XX their pharmaceutically acceptable salts. The nucleomonomers are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX infected cells. They are used in oligomers for gene regulation, antisense
XX technology, diagnostic applications to detect target sequences in
XX biological samples such as those containing pathogenic bacteria, fungi
XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX interleukins associated with pathological conditions such as inflammatory
XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX infections and bacterial infections (see AAA07786 for details of other
XX uses for which the oligomers are suitable for). Oligomers comprising the
XX nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX able to penetrate into cells while maintaining stringent base pair
XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX |||||
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 361
XX AAA07802/C
XX ID AAA07802 standard; DNA; 15 BP.
XX
XX AC AAA07802;
XX
XX DT 23-JUN-2000 (first entry)
XX
XX DE Nucleic acid sequence of ODN-0.
XX
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; ss.
XX
XX OS Synthetic.
XX
XX PN WO200011013-A1.
XX
XX XX 02-MAR-2000.
XX
XX XX 20-AUG-1999; 99WO-US019029.
XX
XX XX 22-AUG-1998; 98US-0097712P.
XX
XX XX (UYNE-) UNIV NEBRASKA.
XX
XX XX Gold B;
XX
XX XX WPI; 2000-246530/21.
XX
XX XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics.
XX
XX XX Disclosure; Page 20; 42pp; English.
XX
XX CC The invention provides modified nucleomonomers of specified formula and
XX their pharmaceutically acceptable salts. The nucleomonomers are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX infected cells. They are used in oligomers for gene regulation, antisense
XX technology, diagnostic applications to detect target sequences in
XX biological samples such as those containing pathogenic bacteria, fungi
XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX interleukins associated with pathological conditions such as inflammatory
XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX infections and bacterial infections (see AAA07786 for details of other
XX uses for which the oligomers are suitable for). Oligomers comprising the
XX nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX able to penetrate into cells while maintaining stringent base pair
XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX |||||
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 362
XX AAA07825/C
XX ID AAA07825 standard; DNA; 15 BP.
XX
XX AC AAA07825;
XX
XX DT 23-JUN-2000 (first entry)
XX
XX DE Nucleic acid sequence of a strand of triplex oligomer 14.
XX
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; triplex; ss.
XX
XX OS Synthetic.
XX

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PN WO200011013-A1.
 XX
 PD 02-MAR-2000.
 XX
 XX 20-AUG-1999; 99WO-US019029.
 XX PF
 XX 22-AUG-1998; 98US-0097712P.
 XX PR
 XX (UYNE-) UNIV NEBRASKA.
 XX PA
 XX Gold B;
 XX PI
 XX WPI; 2000-246530/21.
 XX DR
 XX Modified nucleomoners, used in physiologically stable, non-toxic
 XX PT oligomers used to inhibit expression of nucleic acids and in gene
 XX PT regulation, antisense technology and diagnostics.
 XX PT
 XX PS Disclosure; Page 30; 42pp; English.
 XX PS
 XX CC The invention provides modified nucleomoners of specified formula and
 CC CC their pharmaceutically acceptable salts. The nucleomoners are used as
 CC CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC CC infected cells. They are used in oligomers for gene regulation, antisense
 CC CC technology, diagnostic applications to detect target sequences in
 CC CC biological samples such as those containing pathogenic bacteria, fungi
 CC CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC CC interleukins associated with pathological conditions such as inflammatory
 CC CC infections and bacterial infections (see AAA07786 for details of other
 CC CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
 CC CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC CC able to penetrate into cells while maintaining stringent base pair
 CC CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC CC single- or double-stranded target nucleic acid binding activity to form
 CC CC duplexes, triplexes or other forms of stable association. Sequences
 CC CC AAA07820-834 represent sequences forming triplex oligomers
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 363
 AAA07831/c
 ID AAA07831 standard; DNA; 15 BP.
 XX AC AAA07831;
 XX DT 23-JUN-2000 (first entry)
 XX DE Nucleic acid sequence of a strand of triplex oligomer 16.
 XX DE Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 XX KW viral infection; inflammatory response; cellular proliferation;
 XX KW psoriasis; duplex; triplex; ss.
 XX OS Synthetic.
 XX XX WO200011013-A1.
 XX PN 02-MAR-2000.
 XX PD

XX 20-AUG-1999; 99WO-US019029.
 XX PF
 XX 22-AUG-1998; 98US-0097712P.
 XX PR
 XX (UYNE-) UNIV NEBRASKA.
 XX PA
 XX Gold B;
 XX PI
 XX WPI; 2000-246530/21.
 XX DR
 XX Modified nucleomoners, used in physiologically stable, non-toxic
 XX PT oligomers used to inhibit expression of nucleic acids and in gene
 XX PT regulation, antisense technology and diagnostics.
 XX PT
 XX PS Disclosure; Page 30; 42pp; English.
 XX PS
 XX CC The invention provides modified nucleomoners of specified formula and
 CC CC their pharmaceutically acceptable salts. The nucleomoners are used as
 CC CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC CC infected cells. They are used in oligomers for gene regulation, antisense
 CC CC technology, diagnostic applications to detect target sequences in
 CC CC biological samples such as those containing pathogenic bacteria, fungi
 CC CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC CC interleukins associated with pathological conditions such as inflammatory
 CC CC infections and bacterial infections (see AAA07786 for details of other
 CC CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
 CC CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC CC able to penetrate into cells while maintaining stringent base pair
 CC CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC CC single- or double-stranded target nucleic acid binding activity to form
 CC CC duplexes, triplexes or other forms of stable association. Sequences
 CC CC AAA07820-834 represent sequences forming triplex oligomers
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 364
 AAA07803/c
 ID AAA07803 standard; DNA; 15 BP.
 XX AC AAA07803;
 XX DT 23-JUN-2000 (first entry)
 XX DE Nucleic acid sequence of ODN-p.
 XX DE Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 XX KW viral infection; inflammatory response; cellular proliferation;
 XX KW psoriasis; duplex; ss.
 XX OS Synthetic.
 XX XX WO200011013-A1.
 XX PN 02-MAR-2000.
 XX PD 20-AUG-1999; 99WO-US019029.
 XX PF
 XX XX

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PR 22-AUG-1998; 98US-0097712P.
XX (UYNE-) UNIV NEBRASKA.
PA Gold B;
XX WPI; 2000-246530/21.
XX Modified nucleomoners, used in physiologically stable, non-toxic
DR oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics.
XX Disclosure; Page 20; 42pp; English.
XX The invention provides modified nucleomoners of specified formula and
XX their pharmaceutically acceptable salts. The nucleomoners are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX infected cells. They are used in oligomers for gene regulation, antisense
XX technology, diagnostic applications to detect target sequences in
XX biological samples such as those containing pathogenic bacteria, fungi
XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX interleukins associated with pathological conditions such as inflammatory
XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX infections and bacterial infections (see AAA07786 for details of other
XX uses for which the oligomers are suitable for). Oligomers comprising the
XX nucleomoners exhibit increased duplex DNA stability when hybridizing to
XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX able to penetrate into cells while maintaining stringent base pair
XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1481 AAAAAAAAAAAAAA 1495
XX |||||
XX 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 365
XX AAA07834/C
XX ID AAA07834 standard; DNA; 15 BP.
XX AC AAA07834;
XX XX 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of a strand of triplex oligomer 17.
XX KW Nucleomonmer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; triplex; ss.
XX OS Synthetic.
XX XX WO200011013-A1.
XX PN 02-MAR-2000.
XX PD 20-AUG-1999; 99WO-US019029.
XX PF 20-AUG-1999; 99WO-US019029.
XX PR 22-AUG-1998; 98US-0097712P.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;

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PA (UYNE-) UNIV NEBRASKA.
XX Gold B;
XX WPI; 2000-246530/21.
XX Modified nucleomoners, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
PS Disclosure; Page 30; 42pp; English.
XX The invention provides modified nucleomoners of specified formula and
XX their pharmaceutically acceptable salts. The nucleomoners are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX infected cells. They are used in oligomers for gene regulation, antisense
XX technology, diagnostic applications to detect target sequences in
XX biological samples such as those containing pathogenic bacteria, fungi
XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX interleukins associated with pathological conditions such as inflammatory
XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX infections and bacterial infections (see AAA07786 for details of other
XX uses for which the oligomers are suitable for). Oligomers comprising the
XX nucleomoners exhibit increased duplex DNA stability when hybridizing to
XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX able to penetrate into cells while maintaining stringent base pair
XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07820-834 represent sequences forming triplex oligomers
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1481 AAAAAAAAAAAAAA 1495
XX |||||
XX 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 366
XX AAA07796/C
XX ID AAA07796 standard; DNA; 15 BP.
XX AC AAA07796;
XX XX 23-JUN-2000 (first entry)
XX DT Nucleic acid sequence of ODN-i.
XX DE Nucleomonmer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; ss.
XX OS Synthetic.
XX XX WO200011013-A1.
XX PN 02-MAR-2000.
XX PD 20-AUG-1999; 99WO-US019029.
XX PF 20-AUG-1999; 98US-0097712P.
XX PR 22-AUG-1998; 98US-0097712P.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;

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XX WPI; 2000-246530/21.
XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics.
XX
XX Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
XX their pharmaceutically acceptable salts. The nucleomonomers are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX infected cells. They are used in oligomers for gene regulation, antisense
XX technology, diagnostic applications to detect target sequences in
XX biological samples such as those containing pathogenic bacteria, fungi
XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX interleukins associated with pathological conditions such as inflammatory
XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX infections and bacterial infections (see AAA07786 for details of other
XX uses for which the oligomers are suitable for). Oligomers comprising the
XX nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX able to penetrate into cells while maintaining stringent base pair
XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 367
AAA07800/C
ID AAA07800 standard; DNA; 15 BP.
XX
XX AAA07800;
XX
XX 23-JUN-2000 (first entry)
XX
XX Nucleic acid sequence of ODN-m.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; ss.
XX
XX Synthetic.
XX
XX WO200011013-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US019029.
XX
XX 22-AUG-1998; 98US-0097712P.
XX
XX (UYNE-) UNIV NEBRASKA.
XX
XX Gold B;
XX
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic

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PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
PS Disclosure; Page 20; 42pp; English.
XX
XX
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 369
AAA07798/c
ID AAA07798 standard; DNA; 15 BP.
XX
XX
AC AAA07798;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-k.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
XX Synthetic.
XX
XX WO200011013-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US019029.
XX
XX 22-AUG-1998; 98US-0097712P.
XX
XX (UYNE-) UNIV NEBRASKA.
XX
XX Gold B;
XX
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.

XX Disclosure; Page 20; 42pp; English.

XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 370
AAA07788/c
ID AAA07788 standard; DNA; 15 BP.
XX
XX
AC AAA07788;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-a.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
XX Synthetic.
XX
XX WO200011013-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US019029.
XX
XX 22-AUG-1998; 98US-0097712P.
XX
XX (UYNE-) UNIV NEBRASKA.
XX
XX Gold B;
XX
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
XX Disclosure; Page 20; 42pp; English.

XX The invention provides modified nucleomoners of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomoners are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07788-803 represent oligonucleotides forming a third strand along with
 CC the duplex sequences

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1

RESULT 371
 AAA07791/c
 ID AAA07791 standard; DNA; 15 BP.

XX AC AAA07791;
 XX DT 23-JUN-2000 (first entry)
 XX DE Nucleic acid sequence of ODN-d.
 XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 XX KW viral infection; inflammatory response; cellular proliferation;
 XX KW psoriasis; duplex; ss.
 XX OS Synthetic.
 XX PN WO200011013-A1.
 XX PD 02-MAR-2000.
 XX PF 20-AUG-1999; 99WO-US019029.
 XX PR 22-AUG-1998; 98US-0097712P.
 XX PA (UYNE-) UNIV NEBRASKA.
 XX PI Gold B;
 XX DR WPI; 2000-246530/21.
 XX PT Modified nucleomoners, used in physiologically stable, non-toxic
 XX PT oligomers used to inhibit expression of nucleic acids and in gene
 XX PT regulation, antisense technology and diagnostics.
 XX PS Disclosure; Page 20; 42pp; English.
 XX CC The invention provides modified nucleomoners of specified formula and

CC their pharmaceutically acceptable salts. The nucleomoners are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07788-803 represent oligonucleotides forming a third strand along with
 CC the duplex sequences

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1

RESULT 372
 AAA07801/c
 ID AAA07801 standard; DNA; 15 BP.

XX AC AAA07801;
 XX DT 23-JUN-2000 (first entry)
 XX DE Nucleic acid sequence of ODN-n.
 XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 XX KW viral infection; inflammatory response; cellular proliferation;
 XX KW psoriasis; duplex; ss.
 XX OS Synthetic.
 XX PN WO200011013-A1.
 XX PD 02-MAR-2000.
 XX PF 20-AUG-1999; 99WO-US019029.
 XX PR 22-AUG-1998; 98US-0097712P.
 XX PA (UYNE-) UNIV NEBRASKA.
 XX PI Gold B;
 XX DR WPI; 2000-246530/21.
 XX PT Modified nucleomoners, used in physiologically stable, non-toxic
 XX PT oligomers used to inhibit expression of nucleic acids and in gene
 XX PT regulation, antisense technology and diagnostics.
 XX PS Disclosure; Page 20; 42pp; English.
 XX CC The invention provides modified nucleomoners of specified formula and
 XX CC their pharmaceutically acceptable salts. The nucleomoners are used as
 XX CC monomers in oligomers, which are used in pharmaceutical compositions to

CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences

XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 373
AAA62350/C
ID AAA62350 standard; DNA; 15 BP.
XX
AC AAA62350;
XX
DT 06-NOV-2000 (first entry)
XX
DE Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX
KW Conformationally-locked oligonucleotide; antisense inhibitor;
XX bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS Synthetic.

Key Location/Qualifiers
FT modified_base 7 /*tag= a
FT /mod_base= OTHER
FT /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT modified_base 9
FT /*tag= b
FT /mod_base= OTHER
FT /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"

XX US6083482-A.

PN

XX 04-JUL-2000.

XX 11-MAY-1999; 99US-00309742.

XX 11-MAY-1999; 99US-00309742.

XX (ICNC) ICN PHARM INC.

XX Wang G;

XX WPI; 2000-451496/39.

XX New conformationally restricted 3',5'-bridged nucleosides and
XX oligonucleotides useful as antisense therapeutics or as gene-specific

PT diagnostics.

XX Example 20; Col 16; 10pp; English.

CC The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-
CC C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC the sequence were incorporated by phosphoramidite chemistry using a DNA
CC synthesizer. Bicyclic sugar nucleosides are conformationally restricted
CC 3',5'-bridged nucleosides which can be used as building blocks for
CC oligonucleotides. Oligonucleotides can be produced that have certain,
CC desired, geometrical shapes and entropy advantages. They may have
CC superior hybridisation to DNA and RNA, and excellent biological
CC stability. The conformationally-modified oligonucleotides may be useful
CC as antisense inhibitors of gene expression or as gene probes, and may
CC therefore be used in antisense therapeutics or gene-specific diagnostics

XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 374
AAA62347/C
ID AAA62347 standard; DNA; 15 BP.
XX
AC AAA62347;
XX
DT 06-NOV-2000 (first entry)
XX
DE Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX
KW Conformationally-locked oligonucleotide; antisense inhibitor;
XX bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS Synthetic.

Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT modified_base 3
FT /*tag= b
FT /mod_base= OTHER
FT modified_base 5
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT modified_base 9
FT /*tag= d
FT /mod_base= OTHER
FT modified_base 11
FT /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT modified_base 13
FT /*tag= e
FT /mod_base= OTHER
FT modified_base 15
FT /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT modified_base 15
FT /*tag= f
FT /mod_base= OTHER
FT modified_base 15
FT /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT modified_base 15
FT /*tag= g
FT /mod_base= OTHER
FT modified_base 15
FT /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"

PN US6083482-A.

```

XX 04-JUL-2000.
XX
XX PF 11-MAY-1999; 99US-00309742.
XX
XX PR 11-MAY-1999; 99US-00309742.
XX
XX PA (ICNC ) ICN PHARM INC.
XX
XX PI Wang G;
XX
XX DR WPI; 2000-451496/39.
XX
XX PT New conformationally restricted 3',5'-bridged nucleosides and
XX oligonucleotides useful as antisense therapeutics or as gene-specific
XX diagnostics.
XX
XX PS Example 20; Col 15; 10pp; English.
XX
XX CC The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
XX C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
XX the sequence were incorporated by phosphoramidite chemistry using a DNA
XX synthesizer. Bicyclic sugar nucleosides are conformationally restricted
XX 3',5'-bridged nucleosides which can be used as building blocks for
XX oligonucleotides. Oligonucleotides can be produced that have certain,
XX desired, geometrical shapes and entropy advantages. They may have
XX superior hybridisation to DNA and RNA, and excellent biological
XX stability. The conformationally-modified oligonucleotides may be useful
XX as antisense inhibitors of gene expression or as gene probes, and may
XX therefore be used in antisense therapeutics or gene-specific diagnostics
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
XX
RESULT 375
AAH62348/c
ID AAA62348 standard; DNA; 15 BP.
XX
XX AC AAA62348;
XX
XX DT 06-NOV-2000 (first entry)
XX
XX DE Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX
XX KW Conformationally-locked oligonucleotide; antisense inhibitor;
XX bicyclic sugar nucleoside analogue; gene probe; ds.
XX
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX modified_base 7 /*tag= a
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
XX modified_base 9
XX /*tag= b
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
XX
XX PN US6083482-A.
XX
XX PD 04-JUL-2000.
XX
XX PF 11-MAY-1999; 99US-00309742.
XX
XX

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PR 11-MAY-1999; 99US-00309742.
XX
XX PA (ICNC ) ICN PHARM INC.
XX
XX PI Wang G;
XX
XX DR WPI; 2000-451496/39.
XX
XX PT New conformationally restricted 3',5'-bridged nucleosides and
XX oligonucleotides useful as antisense therapeutics or as gene-specific
XX diagnostics.
XX
XX PS Example 20; Col 15; 10pp; English.
XX
XX CC The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
XX C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
XX the sequence were incorporated by phosphoramidite chemistry using a DNA
XX synthesizer. Bicyclic sugar nucleosides are conformationally restricted
XX 3',5'-bridged nucleosides which can be used as building blocks for
XX oligonucleotides. Oligonucleotides can be produced that have certain,
XX desired, geometrical shapes and entropy advantages. They may have
XX superior hybridisation to DNA and RNA, and excellent biological
XX stability. The conformationally-modified oligonucleotides may be useful
XX as antisense inhibitors of gene expression or as gene probes, and may
XX therefore be used in antisense therapeutics or gene-specific diagnostics
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
XX
RESULT 376
AAH20308/c
ID AAH20308 standard; DNA; 15 BP.
XX
XX AC AAH20308;
XX
XX DT 31-JUL-2001 (first entry)
XX
XX DE Oligo dt15 EDTA labelled probe.
XX
XX KW Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently attached
XX at C-5"
XX modified_base 5
XX /*tag= b
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently attached
XX at C-5"
XX modified_base 8
XX /*tag= c
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently attached
XX at C-5"
XX
XX PN US2001002314-A1.
XX
XX PD 31-MAY-2001.
XX
XX PF 04-AUG-1998; 98US-00128732.
XX

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XX 30-OCT-1987; 87US-00115922.
PR 16-NOV-1990; 90US-00614205.
PR 12-NOV-1993; 93US-00152250.
XX (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
XX Dervan PB, Moser HE;
XX WPI; 2001-342909/36.
XX New hybridization probe for specific triplex formation with large double
PT helices, useful e.g. for site-specific diagnostic cleavage, contains
PT attached functional residue.
XX Example 1; Fig 3B; 20pp; English.
XX This invention relates to hybridisation probes which target a specific
CC sequence within a large double-helical nucleic acid. The probe is
CC complementary to the target sequence and contains at least one nucleotide
CC with an attached molecule that is able to cleave double-helical DNA e.g.
CC EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes
CC where the attached molecule is a label or compound that alters gene
CC expression, are used for specific detection and/or cleavage of double-
CC helical DNA, e.g. for diagnosis, for treatment of disease (particularly
CC caused by viruses, genetic defects or oncogenes), for chromosomal
CC analysis, and for the isolation and mapping of genes. The present
CC sequence represents probe of the invention used in an example
CC illustrating how the probe binds to and cleaves double stranded DNA
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 377
AAF30882/c
ID AAF30882 standard; DNA; 15 BP.
XX AAF30882;
XX 09-JUL-2001 (first entry)
XX Oligonucleotide portion of ODN-MGB-LF conjugate.
XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX hybridisation; detection; fluorescence; probe; ss.
XX Synthetic.
XX WO200131063-A1.
XX 03-MAY-2001.
XX 26-OCT-2000; 2000WO-US029786.
XX 26-OCT-1999; 99US-00428236.
XX (EPOC-) EPOCH BIOSCIENCES INC.
XX Dempcy RO, Afonina IA, Vermeulen NMJ;
XX WPI; 2001-328656/34.
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX mismatch discrimination.

XX Disclosure; Page 58; 105pp; English.
XX The present sequence is that of the oligonucleotide (ODN) component of an
CC ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
CC invention. MGBs bind in a non-intercalating manner to the minor groove of
CC non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
CC but in an intercalating manner, or lies in the minor groove, or is
CC oriented in some other way to the DNA molecule by MGB, such that it
CC becomes fluorescent (or its fluorescent properties change detectably).
CC The conjugates are used as hybridisation probes and amplification primers
CC for fluorescent detection of specifically hybridising sequences, for
CC analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
CC mismatch discrimination, target or signal amplification, array-based
CC assays and sequencing, including detection of double-stranded DNA by
CC triplex formation. Many different targets can be detected a single
CC reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
CC hybridisation-triggered fluorescence. Upon hybridisation to the
CC complementary target sequence there was an increase in fluorescence
CC yield, measured as the ratio of the fluorescence emitted by the hybrid
CC between the ODN-MGB-LF conjugate and its target sequence to the
CC fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
CC of 8.3
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 378
AAH20511/c
ID AAH20511 standard; DNA; 15 BP.
XX AAH20511;
XX 31-JUL-2001 (first entry)
XX Oligonucleotide b) for solid phase synthesis of oligonucleotides.
XX Cross-linked vinyl acetate copolymer carrier material; AIDS treatment;
XX phosphorothioate; solid phase synthesis; modified oligonucleotide;
XX clinical diagnostic; cancer treatment; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..14
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate deoxynucleotides"
XX
PN DE10051726-A1.
XX 10-MAY-2001.
XX 18-OCT-2000; 2000DE-01051726.
XX 30-OCT-1999; 99DE-01052376.
XX (MERE ) MERCK PATENT GMBH.
XX Seliger H, Sobkowski M, Hinz M;
XX WPI; 2001-336414/36.
XX Intermediate for oligonucleotide synthesis comprises partially hydrolysed
PT cross-linked vinyl acetate copolymer loaded with nucleotide derivative.

```

XX Example 2; Page 5; 8pp; German.

XX This invention describes a novel chemical product comprising a partially

CC hydrolysed cross-linked vinyl acetate copolymer carrier material loaded

CC with nucleotide derivative(s). The product is an intermediate for the

CC large (gram) scale solid phase synthesis of modified oligonucleotides

CC useful e.g. as clinical diagnostics and therapeutics, e.g. for the

CC treatment of AIDS and cancers. The presence of the partially hydrolysed

CC copolymer facilitates the synthesis of larger amounts of oligonucleotides

CC compared with the use of Merckogel (RTM; macroporous polyvinyl acetate)

CC described in Nucleic Acid Res. Sympos. Ser. 31, p. 153, 1994.

CC Oligonucleotides are obtained in very good quality and high yields. Also,

CC the nucleosides do not display the reduced activity seen in some prior

CC art procedures, less carrier material, reagents and solvent are required.

CC Further, the carrier material is biodegradable and thus does not present

CC disposal problems. It also swells uniformly in a range of solvents, which

CC obviates expansion or contraction during use or solvent exchange.

CC AAH20510-AAH20513 represent oligonucleotides containing modified

CC deoxynucleotides which are used to illustrate the method of the invention

XX

XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

XX

Query Match 1.0%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

DB 15 AAAAAAAAAAAAAA 1

RESULT 379

AAFI6603

ID AAF16603 standard; DNA; 15 BP.

XX

AC AAF16603;

XX

XX 13-MAR-2001 (first entry)

XX

DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 90.

XX

XX Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;

KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;

KW DNA-RNA hybrid; ss.

XX

OS Homo sapiens.

XX

XX WO200071164-A1.

XX

XX 30-NOV-2000.

XX

XX 24-MAY-2000; 2000WO-AU000498.

XX

XX 24-MAY-1999; 99AU-00000510.

XX

XX (TACH/) TACHAS G.

XX

XX Tachas G;

XX

XX WPI; 2001-025093/03.

XX

XX Treating gastric acid disturbance by administering an oligonucleotide

PT which modulates the activity of a polypeptide involved in gastric acid

PT production or secretion.

XX

XX Example 3; Page 148; 164pp; English.

XX

XX The present invention provides oligonucleotides, and methods for their

CC use, which are useful in modulating the action of proteins involved in

CC gastric acid production. The target protein is preferably the histamine

CC H2 receptor or one of the proteins which form part of the gastric proton

CC pump. The sequences and methods of the invention are useful in the

CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,

CC duodenal ulcers and other gastric acid disturbances, most of which are

CC caused by Helicobacter pylori

XX

XX Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

XX

Query Match 1.0%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1494

DB 1 TAAAAAAAAAAAAA 15

RESULT 380

AAH49243/c

ID AAH49243 standard; DNA; 15 BP.

XX

AC AAH49243;

XX

XX 26-NOV-2001 (first entry)

XX

XX PNA-forming oligonucleotide #7.

XX

XX Polyamide-oligonucleotide derivative; anticancer; antiproliferative;

KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;

KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;

KW peptide nucleic acid; ss.

XX

XX Synthetic.

OS

XX

XX Key Location/Qualifiers

FT modified_base 9

FT /*tag= a

FT /mod_base= OTHER

FT /note= "t-but"

FT modified_base 15

FT /*tag= b

FT /mod_base= OTHER

FT /note= "t-hex"

XX

XX EPI113021-A2.

XX

XX 04-JUL-2001.

XX

XX 08-MAR-1995; 2001EP-00104012.

XX

XX 14-MAR-1994; 94DE-04408528.

PR 08-MAR-1995; 95EP-00103332.

XX

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX

XX Uhlmann E, Breipohl G;

XX

XX WPI; 2001-591267/67.

XX

XX New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents

PT for treating e.g. cancer, also as diagnostic probes and primers.

XX

XX Example 26; Page 40; 54pp; German.

XX

XX This invention describes novel polyamide-oligonucleotide derivatives (I)

CC and their physiologically acceptable salts of formula F(DNA)-Li) Q(PNA-

CC Li) F(DNA-Li) S(PNA) t) XP' where q, r, s, t = 0 or 1, with the sum of

CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid

CC (such as DNA or RNA or their known derivatives); Li = covalent linkage

CC between DNA and PNA, i.e. a bond or a residue containing at least one

CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure

CC containing at least one nucleobase different from thymine; and F, F' =

CC end groups and/or are connected through a covalent bond. The products of

CC the invention have anticancer, antiproliferative, antiviral, hepatotropic

CC and vasotropic activity and can be used for the inhibition of gene

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 383
AAL49453
ID AAL49453 standard; DNA; 15 BP.
XX
AC AAL49453;
XX
DT 14-NOV-2002 (first entry)
XX Mutation detection method tag peptide coding sequence SEQ ID NO: 1.
DE Mutation detection; primer; mutant; tag; tumour suppressor gene;
XX protein production; cancer; ds.
KW Synthetic.
XX
XX Key Location/Qualifiers
FH 1. .15
FT /*tag= a
FT /product= "tag peptide"
FT /partial
FT /note= "no start or stop"
XX
XX WO200266675-A2.
XX
XX 29-AUG-2002.
XX
XX 15-FEB-2002; 2002WO-EP001651.
XX
XX 16-FEB-2001; 2001DE-01007317.
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Kahmann S, Mueller O;
XX WPI; 2002-674959/72.
XX P-PSDB; AAO19054.
XX
XX Detecting mutations in nucleic acid, useful for diagnosis and
XX characterization of tumors, by amplification, in vitro transcription and
XX translation, then protein detection.
XX
XX Claim 11; Fig 5; 62pp; German.
XX
XX The present invention relates to a method of detecting mutations in a
XX nucleic acid by amplifying the nucleic acid to produce a double-stranded
XX amplicon, in vitro transcription and translation of this amplicon, and
XX detection of the translated protein. The primers used for amplification
XX are designed to produce an amplicon that is translatable and allows
XX differentiation between translation products of wild-type and mutated
XX nucleic acids. The method is used to detect mutations in tumour
XX suppressor genes, for (early) diagnosis, monitoring and characterisation
XX of tumours (especially of bladder and intestines) and in the germ line
XX (using nucleic acids from embryos or blood cells). A new multi-tag vector
XX is used to detect or verify the reading frame of a nucleic acid cloned in
XX it, and to determine the suitability of detectable peptides for analysis
XX and/or purification of a recombinant protein, expressed from a sequence
XX cloned in the vector. The present sequence encodes a tag peptide and was
XX used in the invention
XX
XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 1 AAAAAAAAAAAAAA 15
RESULT 384
AAL49455
ID AAL49455 standard; DNA; 15 BP.
XX
AC AAL49455;
XX
DT 14-NOV-2002 (first entry)
XX Mutation detection method tag peptide coding sequence SEQ ID NO: 3.
DE Mutation detection; primer; mutant; tag; tumour suppressor gene;
XX protein production; cancer; ds.
KW Synthetic.
XX
XX Key Location/Qualifiers
FH 1. .15
FT /*tag= a
FT /product= "tag peptide"
FT /partial
FT /note= "no start or stop"
XX
XX WO200266675-A2.
XX
XX 29-AUG-2002.
XX
XX 15-FEB-2002; 2002WO-EP001651.
XX
XX 16-FEB-2001; 2001DE-01007317.
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Kahmann S, Mueller O;
XX WPI; 2002-674959/72.
XX P-PSDB; AAO19056.
XX
XX Detecting mutations in nucleic acid, useful for diagnosis and
XX characterization of tumors, by amplification, in vitro transcription and
XX translation, then protein detection.
XX
XX Claim 11; Fig 5; 62pp; German.
XX
XX The present invention relates to a method of detecting mutations in a
XX nucleic acid by amplifying the nucleic acid to produce a double-stranded
XX amplicon, in vitro transcription and translation of this amplicon, and
XX detection of the translated protein. The primers used for amplification
XX are designed to produce an amplicon that is translatable and allows
XX differentiation between translation products of wild-type and mutated
XX nucleic acids. The method is used to detect mutations in tumour
XX suppressor genes, for (early) diagnosis, monitoring and characterisation
XX of tumours (especially of bladder and intestines) and in the germ line
XX (using nucleic acids from embryos or blood cells). A new multi-tag vector
XX is used to detect or verify the reading frame of a nucleic acid cloned in
XX it, and to determine the suitability of detectable peptides for analysis
XX and/or purification of a recombinant protein, expressed from a sequence
XX cloned in the vector. The present sequence encodes a tag peptide and was
XX used in the invention
XX
XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 1 AAAAAAAAAAAAAA 15

RESULT 385
 AAD29506/c
 ID AAD29506 standard; DNA; 15 BP.
 XX
 AC AAD29506;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Primer used for the expression of adipocytes in human preadipose cells.
 XX
 KW Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;
 KW diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
 KW ss.
 XX
 OS Unidentified.
 XX
 PN W0200206450-A1.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-EP008165.
 XX
 PR 18-JUL-2000; 2000EP-00115489.
 XX
 PA (NEST) SOC PROD NESTLE SA.
 XX
 PI Darimont C, Mace K, Pfeifer A;
 XX
 DR WPI; 2002-188539/24.
 XX

New human pre-adipose cell line capable of differentiating to adipose cells, useful in developing drug, food ingredients, and supplements against obesity, diabetes and cardiovascular diseases.

Example 5; Page 10; 30pp; English.

The present invention relates to new human pre-adipose cell lines capable to differentiate to white adipose cells, exhibiting essentially the same cellular properties of normal white adipose cells. The human pre-adipose cell lines are useful for the identification of substances controlling the regulation of lipid uptake and release by human white adipocytes, and substances controlling the differentiation of preadipocytes into mature adipocytes. They are useful for screening compounds capable to regulate the secretion of any metabolites or hormones from human white adipocytes. Sequences of the invention are useful for developing drugs, food ingredients and supplements against obesity, diabetes and cardiovascular diseases. The present DNA sequence is a reverse transcription (RT)-PCR primer which is used for the expression of adipocytes in CC differentiated immortalised human preadipose cells. This primer is used CC in the exemplification of the invention

XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 386
 AAD22531
 ID AAD22531 standard; RNA; 15 BP.
 XX
 AC AAD22531;

XX
 DT 29-AUG-2003 (revised)
 DT 07-AUG-2003 (revised)
 DT 12-FEB-2002 (first entry)
 XX
 DE Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.
 XX
 KW RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
 KW virucide; oncogene; cancer; transcription; translation; leukaemia virus;
 KW hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A];
 KW poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.
 XX
 OS unidentified retrovirus.
 OS Unidentified.
 XX
 PN US6291438-B1.
 XX
 PD 18-SEP-2001.
 XX
 PF 06-OCT-1998; 98US-00167375.
 XX
 PR 24-FEB-1993; 93US-00022055.
 PR 23-FEB-1994; 94US-00200650.
 PR 22-FEB-1996; 96US-00604871.
 XX
 PA (WANG/) WANG J H.
 XX
 PI Wang JH;
 XX
 DR WPI; 2002-009339/01.
 XX

Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral reverse transcriptase comprises at the 2'-O position of the oligoribonucleotide, a hydrophobic carrier reagent containing a poly substituted phenyl compound.

Example 3; Col 24; 56pp; English.

The invention relates to derivatised antisense oligoribonucleotides with enhanced membrane permeability and stability. The derivatised antisense oligoribonucleotide complementary to a sequence of nucleotides found in a virus or a cell is useful for inhibiting e.g., viral reverse transcriptase. Derivatized antisense oligoribonucleotide is conjugated at the 2'-O position with a hydrophobic carrier reagent containing a poly substituted phenyl compound. The derivatised oligoribonucleotides are used to decrease the expression of oncogenes and thereby decrease the expression of cancer cells which rely upon oncogene expression for their phenotypic and pathological properties. The oligoribonucleotides are also used for increasing the effectiveness of antisense oligonucleotide targeted to a gene associated with a disease or a condition in an animal. To alter gene transcription and/or translation for any gene or gene segment responsible for expression, to inhibit viral reverse transcriptase, to inhibit the expression of leukaemia virus, hepatitis virus, oncogenes and human immunodeficiency virus. The present sequence is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment which is used in the treatment of moloney murine leukaemia virus (MuLV) in mammals. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to standardise OS field)

XX
 SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 1 AAAAAAAAAAAAAA 15

RESULT 387
 ABQ82140
 ID ABQ82140 standard; DNA; 15 BP.


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PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX
XX WPI; 2002-153821/20.
XX
PT New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
PS Disclosure; Col 68; 161pp; English.
XX
CC The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
XX Sequence 15 BP; 2 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1390 CATGCACCTGTCCTT 1404
DB 1 CATGCACCTGTCCTT 15
XX
RESULT 390
ABK32084
ID ABK32084 standard; DNA; 15 BP.
XX
AC ABK32084;
XX
XX 23-APR-2002 (first entry)
XX
DE Human colon cancer SAGE tag #185.
XX
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW serial analysis of gene expression; diagnostic; prognostic; probe;
XX cancer marker; ss.
XX
OS Homo sapiens.
XX
XX US6333152-B1.
XX
XX 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 25; 161pp; English.
XX
CC The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
XX Sequence 15 BP; 2 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1390 CATGCACCTGTCCTT 1404
DB 1 CATGCACCTGTCCTT 15
XX
RESULT 390
ABK32084
ID ABK32084 standard; DNA; 15 BP.
XX
AC ABK32084;
XX
XX 23-APR-2002 (first entry)
XX
DE Human colon cancer SAGE tag #185.
XX
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW serial analysis of gene expression; diagnostic; prognostic; probe;
XX cancer marker; ss.
XX
OS Homo sapiens.
XX
XX US6333152-B1.
XX
XX 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 25; 161pp; English.
XX
CC The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
XX Sequence 15 BP; 2 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1475 CATGCTAAAAA 1489
DB 1 CATGCTAAAAA 15
XX
RESULT 391
ABX00240/c
ID ABX00240 standard; RNA; 15 BP.
XX
XX ABX00240;
XX
XX 23-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.
XX
XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virocid;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX
XX US2002082225-A1.
XX
XX 27-JUN-2002.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (ROBE/) ROBERTS B.
XX (PAVC/) PAVCO P A.
XX (MACE/) MACEJACK D.
XX
XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
XX WPI; 2002-617759/66.
XX
XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX replication and are useful to treat hepatitis C virus infections and
XX cirrhosis, liver failure or hepatocellular carcinoma.
XX
XX Claim 1; Page 21; 80pp; English.
XX
XX The present invention relates to enzymatic nucleic acids which
XX specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX (HP) motif where the binding arms comprise sequences complementary to one
XX of the substrate sequences defined in the specification. The HCV
XX ribozymes are useful for modulating the expression and/or replication of
XX HCV. They can be used to treat cirrhosis, liver failure and/or
XX hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX a condition associated with HCV infection in conjunction with one or more
XX other drug therapies, particularly type I interferon, especially
XX interferon alpha, beta or gamma or consensus interferon. The present
XX sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
XX Some of the sequence data for this patent did not form part of the
XX printed specification. The complete sequence data for this patent was
XX obtained in electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/pslpsbIDentry.html
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
```

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 392
ABX03406/c
ID ABX03406 standard; RNA; 15 BP.
XX
AC ABX03406;
XX
DT 24-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.
XX
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 1; Page 64; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDentry.html
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 393
ABL57064/c
ID ABL57064 standard; DNA; 15 BP.
XX
AC ABL57064;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide precursor phosphoramidite oligonucleotide O35.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "Diethyl 5-(((2-cyanoethoxy) (diisopropylamino)
FT phosphanyloxy) methyl) isophthalate, synthetic branching
FT amidite"
FT modified_base 15
FT /tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PP 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TU, Greef CH, Wang D;
XX
DR WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorus containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 4; Page 44; 120pp; English.
XX
CC The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O35, which was produced in an
CC example from the invention and which includes a synthetic branching
CC amidite compound. The invention describes an improved process for
CC immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC multiple reactive sites, to a substrate surface or other conjugation
CC target. It also describes the preparation of oligos containing one or
CC more hydrazides, which can be used for conjugation to surface binding
CC moieties, or for other conjugation reactions. The process is useful e.g.
CC in nucleic acid hybridisation based assays, DNA chip technology and
CC biosensor applications
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

```
Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
    |||||
Db 15 AAAAAAAAAAAAAA 1
    |||||

RESULT 394
ABL57054/C
ID ABL57054 standard; DNA; 15 BP.
XX
AC ABL57054;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrizide phosphoramidite oligonucleotide O9.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /*note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl) benzoyloxy)-5
FT /*-(2'-cyanoethyl) (diisopropylamino) phosphanyloxymethyl)-
FT modified_base 15
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "3' Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
WPI; 2002-40476/43.
XX
Compound for binding macromolecule to substrate surface or conjugation
targets, contains phosphorous containing reactive group, hydrazide
protecting group and benzene ring, and has predefined formula.
XX
Example 2; Page 40; 120pp; English.
XX
The present sequence is of a trityl deprotected hydrazide phosphoramidite
15-mer, designated oligo O9, which was produced in an example from the
invention. The invention describes an improved process for immobilisation
of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
RNA and peptides, especially macromolecules containing multiple reactive
sites, to a substrate surface or other conjugation target. It also
describes the preparation of oligos containing one or more hydrazides,
which can be used for conjugation to surface binding moieties, or for
other conjugation reactions. The process is useful e.g. in nucleic acid
hybridisation based assays, DNA chip technology and biosensor
applications
XX
Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
    |||||
Db 15 AAAAAAAAAAAAAA 1
    |||||

RESULT 395
ABL57063/C
ID ABL57063 standard; DNA; 15 BP.
XX
AC ABL57063;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrizide precursor phosphoramidite oligonucleotide O39.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /*note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl) benzoyloxy)-5
FT /*-(2'-cyanoethyl) (diisopropylamino) phosphanyloxymethyl)-
FT modified_base 15
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "3' Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
WPI; 2002-40476/43.
XX
Compound for binding macromolecule to substrate surface or conjugation
targets, contains phosphorous containing reactive group, hydrazide
protecting group and benzene ring, and has predefined formula.
XX
Example 3; Page 43; 120pp; English.
XX
The present sequence is of a hydrazine treated hydrazide precursor
phosphoramidite 15-mer, designated oligo O39, which was produced in an
example from the invention. The invention describes an improved process
for immobilisation of macromolecules including DNA, RNA, peptide nucleic
acids, pyranosyl-RNA and peptides, especially macromolecules containing
multiple reactive sites, to a substrate surface or other conjugation
target. It also describes the preparation of oligos containing one or
more hydrazides, which can be used for conjugation to surface binding
moieties, or for other conjugation reactions. The process is useful e.g.
in nucleic acid hybridisation based assays, DNA chip technology and
biosensor applications
XX
Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
    |||||
```

```

Db      15 AAAAAAAAAAAAAA 1
RESULT 396
ABLS7066/c
ID      ABL57066 standard; DNA; 15 BP.
XX
XX
AC      ABL57066;
XX
XX      22-JUL-2002 (first entry)
XX
XX      Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
XX
XX      Macromolecule; hydrazide; immobilisation; ss.
XX
XX      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "Amino-C6 modification"
FT      modified_base 15
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "3' Cy3 dye"
XX
XX      WO200214558-A2.
XX
XX      21-FEB-2002.
XX
XX      10-AUG-2001; 2001WO-US041663.
XX
XX      11-AUG-2000; 2000WO-US022205.
XX
XX      (NANO-) NANOGEN INC.
XX
XX      Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI      Havens JR, Onofrey TU, Gref CH, Wang D;
XX      WPI; 2002-404476/43.
XX
XX      Compound for binding macromolecule to substrate surface or conjugation
PT      targets, contains phosphorous containing reactive group, hydrazide
PT      protecting group and benzene ring, and has predefined formula.
XX
PS      Example 12; Page 57; 120pp; English.
XX
XX      The present sequence is of an amino-C6-modified and Cy3 dye labeled T15
CC      oligonucleotide that was used in a comparison of hydrazine and amine
CC      attachment moieties on active ester surfaces in an example from the
CC      invention. The invention describes an improved process for immobilisation
CC      of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC      RNA and peptides, especially macromolecules containing multiple reactive
CC      sites, to a substrate surface or other conjugation target. It also
CC      describes the preparation of oligos containing one or more hydrazides,
CC      which can be used for conjugation to surface binding moieties, or for
CC      other conjugation reactions. The process is useful e.g. in nucleic acid
CC      hybridisation based assays, DNA chip technology and biosensor
CC      applications
XX
XX      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ      Query Match      1.0%; Score 15; DB 1; Length 15;
      Best Local Similarity 100.0%; Pred. No. 1.7e+02;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY      1481 AAAAAAAAAAAAAA 1495
      Db      15 AAAAAAAAAAAAAA 1
RESULT 397

```

```

ABLS7059/c
ID      ABL57059 standard; DNA; 15 BP.
XX
XX      ABL57059;
XX
XX      22-JUL-2002 (first entry)
XX
XX      Hydrazide precursor phosphoramidite oligonucleotide O33.
XX
XX      Macromolecule; hydrazide; immobilisation; ss.
XX
XX      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1
FT      /tag= b
FT      /note= "phosphoramidite linkage"
FT      modified_base 1
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "4-((2-cyanoethyl)(diisopropylamino)
FT      phosphanyloxyethyl)-benzoic acid methyl ester"
FT      modified_base 15
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "3' Cy3 dye"
XX
XX      WO200214558-A2.
XX
XX      21-FEB-2002.
XX
XX      10-AUG-2001; 2001WO-US041663.
XX
XX      11-AUG-2000; 2000WO-US022205.
XX
XX      (NANO-) NANOGEN INC.
XX
XX      Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI      Havens JR, Onofrey TU, Gref CH, Wang D;
XX      WPI; 2002-404476/43.
XX
XX      Compound for binding macromolecule to substrate surface or conjugation
PT      targets, contains phosphorous containing reactive group, hydrazide
PT      protecting group and benzene ring, and has predefined formula.
XX
PS      Example 3; Page 43; 120pp; English.
XX
XX      The present sequence is of a hydrazine treated hydrazide precursor
CC      phosphoramidite 15-mer, designated oligo O33, which was produced in an
CC      example from the invention. The invention describes an improved process
CC      for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC      acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC      multiple reactive sites, to a substrate surface or other conjugation
CC      target. It also describes the preparation of oligos containing one or
CC      more hydrazides, which can be used for conjugation to surface binding
CC      moieties, or for other conjugation reactions. The process is useful e.g.
CC      in nucleic acid hybridisation based assays, DNA chip technology and
CC      biosensor applications
XX
XX      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ      Query Match      1.0%; Score 15; DB 1; Length 15;
      Best Local Similarity 100.0%; Pred. No. 1.7e+02;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY      1481 AAAAAAAAAAAAAA 1495
      Db      15 AAAAAAAAAAAAAA 1
RESULT 398
ABLS7061/c

```

```
ID ABL57061 standard; DNA; 15 BP.
XX
AC ABL57061;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide precursor phosphoramidite oligonucleotide O37.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /*note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT phenylcarbonylamido)-2-((2'',-cyanoethyloxy)
FT (diisopropylamino)-phosphanyloxy)-propane"
FT modified_base 15
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "3' Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
DR WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 3; Page 43; 120pp; English.
XX
CC The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O37, which was produced in an
CC example from the invention. The invention describes an improved process
CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC multiple reactive sites, to a substrate surface or other conjugation
CC target. It also describes the preparation of oligos containing one or
CC more hydrazides, which can be used for conjugation to surface binding
CC moieties, or for other conjugation reactions. The process is useful e.g.
CC in nucleic acid hybridisation based assays, DNA chip technology and
CC biosensor applications
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 399
ABL57056/c

ID ABL57056 standard; DNA; 15 BP.
XX
AC ABL57056;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide phosphoramidite oligonucleotide O31.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /*note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "6-((2Cyanoethoxy)(diisopropylamino)
FT phosphanyloxy)-N'-tritylhexanohydrazide"
FT modified_base 15
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "3' Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
DR WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 2; Page 40; 120pp; English.
XX
CC The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC 15-mer, designated oligo O31, which was produced in an example from the
CC invention. The invention describes an improved process for immobilisation
CC of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC RNA and peptides, especially macromolecules containing multiple reactive
CC sites, to a substrate surface or other conjugation target. It also
CC describes the preparation of oligos containing one or more hydrazides,
CC which can be used for conjugation to surface binding moieties, or for
CC other conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
CC applications
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 400
ABL57060/c

ID ABL57060 standard; DNA; 15 BP.
```

```

XX AC ABL57060;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrizide precursor phosphoramidite oligonucleotide O34.
XX KW Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..15
XX FT /*tag= b
XX FT /note= "phosphoramidite linkage"
XX FT modified_base 1
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
XX FT phosphanyloxy)methyl) isophthalate"
XX FT modified_base 15
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "3' Cy3 dye"
XX PN WO200214558-A2.
XX DT 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US041663.
XX PR 11-AUG-2000; 2000WO-US022205.
XX PA (NANO-) NANOGEN INC.
XX PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
XX PI Havens JR, Onofrey IV, Greef CH, Wang D;
XX DR WPI; 2002-404476/43.
XX PT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX PT protecting group and benzene ring, and has predefined formula.
XX PS Example 3; Page 43; 120pp; English.
XX CC The present sequence is of a hydrazine treated hydrazide precursor
XX CC phosphoramidite 15-mer, designated oligo O34, which was produced in an
XX CC example from the invention. The invention describes an improved process
XX CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
XX CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX CC multiple reactive sites, to a substrate surface or other conjugation
XX CC target. It also describes the preparation of oligos containing one or
XX CC more hydrazides, which can be used for conjugation to surface binding
XX CC moieties, or for other conjugation reactions. The process is useful e.g.
XX CC in nucleic acid hybridisation based assays, DNA chip technology and
XX CC biosensor applications
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 401
ABK98141/C
ID ABK98141 standard; DNA; 15 BP.
XX

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```

AC ABK98141;
XX 07-OCT-2002 (first entry)
XX DE Triple helix forming associated oligonucleotide #26.
XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX KW pathogenic bacteria; virus; replication; virulence; cancer;
XX KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX OS Synthetic.
XX PN US6403302-B1.
XX PD 11-JUN-2002.
XX PF 16-DEC-1993; 93US-00168920.
XX PR 17-SEP-1992; 92US-00946976.
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX PI Dervan PB, Beal PA;
XX DR WPI; 2002-536030/57.
XX PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX PT oligonucleotide which binds in parallel and antiparallel orientation,
XX PT respectively, for targetting sequences on alternate strands of DHNA to
XX PT control gene expression.
XX PS Example 1; Fig 3B; 108pp; English.
XX CC The present invention relates to methods and oligonucleotides for forming
XX CC a triple-helix comprising a double helical nucleic acid comprising first
XX CC and second substantially complementary strands, and an oligonucleotide
XX CC bound to a purine-rich target sequence within the double helical nucleic
XX CC acid, where the oligonucleotide binds in a parallel and antiparallel
XX CC orientation, respectively, to target sequences on alternate strands of
XX CC the double helical nucleic acid. The method has therapeutic applications,
XX CC where gene expression is controlled by selective triple-helix formation
XX CC within expression regulatory sequences of a target gene. The
XX CC oligonucleotides can be used to form triple-helices, and are useful to
XX CC detect the presence or absence of specific sequences within genomic DNA
XX CC for diagnostic and therapeutic purposes. The oligonucleotides can be
XX CC selected to specifically bind to pathogenic double-stranded DNA including
XX CC specific sequences required by pathogenic bacteria or viruses for
XX CC replication or virulence, reducing their pathogenicity. Alternatively,
XX CC the oligonucleotide can be chosen to target a unique sequence of the
XX CC pathogen which is not found in the genome of pathogen's host. The
XX CC oligonucleotides can be used in cancer treatment by way of triple-helix
XX CC suppression of specific oncogenes including those of endogenous or viral
XX CC origin. Such therapeutic oligonucleotides are capable of forming triple-
XX CC helices with such sequences in cancerous cells containing the activated
XX CC oncogene, so preferentially killing or repressing the cancer causing
XX CC cell. The present sequence represents an oligonucleotide used in the
XX CC methods of the present invention
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 402
ABK98184/C
ID ABK98184 standard; DNA; 15 BP.
XX

```

XX ABK98184;
 XX AC
 XX DT
 XX DE
 XX DE Triple helix forming associated oligonucleotide #48.
 XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer; ss.
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
 XX OS Synthetic.
 XX PN US6403302-B1.
 XX PD 11-JUN-2002.
 XX PF 16-DEC-1993; 93US-00168920.
 XX PR 17-SEP-1992; 92US-00946976.
 XX PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 XX PI Dervan PB, Beal PA;
 XX DR WPI; 2002-536030/57.
 XX PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
 PT oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targetting sequences on alternate strands of DHNA to
 PT control gene expression.
 XX PS Example 7; Fig 24A; 108pp; English.
 XX CC The present invention relates to methods and oligonucleotides for forming
 CC a triple-helix comprising a double helical nucleic acid comprising first
 CC and second substantially complementary strands, and an oligonucleotide
 CC bound to a purine-rich target sequence within the double helical nucleic
 CC acid, where the oligonucleotide binds in a parallel and antiparallel
 CC orientation, respectively, to target sequences on alternate strands of
 CC the double helical nucleic acid. The method has therapeutic applications,
 CC where gene expression is controlled by selective triple-helix formation
 CC within expression regulatory sequences of a target gene. The
 CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic double-stranded DNA including
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1

RESULT 403
 ABZ37501/c

ID ABZ37501 standard; DNA; 15 BP.
 XX ABZ37501;
 XX DT 18-FEB-2003 (first entry)
 XX DE Oligonucleotide SEQ ID NO:622.
 KW Library; cleavage; display; diverse family; ss.
 XX OS Synthetic.
 XX PN WO200283872-A2.
 XX PD 24-OCT-2002.
 XX PF 17-APR-2002; 2002WO-US012405.
 XX PR 17-APR-2001; 2001US-00837306.
 XX PR 24-OCT-2001; 2001US-00000516.
 XX PR 25-OCT-2001; 2001US-00045674.
 XX PA (LADN/) LADNER R C.
 PA (COHE/) COHEN E H.
 PA (NAST/) NASTRI H G.
 PA (ROOK/) ROOKEY K L.
 PA (HOET/) HOET R.
 PA (HOOG/) HOOGENBOOM H R J M.
 XX PI Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;
 PI Hooogenboom HRJW;
 XX DR WPI; 2003-093015/08.
 XX CC Cleaving single-stranded nucleic acid sequences at a desired location by
 CC contacting the nucleic acid with an single strand oligonucleotide
 CC complementary to a nucleic acid region where cleavage is desired.
 XX PS Disclosure; Page 481; 485pp; English.
 XX CC The present invention describes a method for cleaving single-stranded
 CC nucleic acid sequences at a desired location. Also described: (1) methods
 CC for displaying or expressing a member of a diverse family of peptides,
 CC polypeptides or proteins on the surface of a genetic package and
 CC collectively displaying at least a part of the diversity of the family,
 CC where the displayed or expressed peptide, polypeptide or protein is
 CC encoded at least in part by a nucleic acid that has been cleaved at a
 CC desired location; (2) a method for preparing single-stranded nucleic
 CC acids; (3) a method for preparing a library comprising a collection of
 CC genetic packages that display a member of a diverse family of peptides,
 CC polypeptides or proteins and that collectively display at least a portion
 CC of the family; (4) a vector comprising a DNA sequence encoding an
 CC antibody variable region linked to a version of P11 anchor which does
 CC not mediate infection of phage particles, and wild-type gene III; (5) a
 CC method for producing a population or a library of immunoglobulin genes;
 CC and (6) a library of immunoglobulins that comprise members having at
 CC least one variable domain in which at least one of CDR1 and CDR2 contain
 CC synthetic diversity and CDR3 diversity is captured from B cells. The
 CC method is useful for cleaving single-stranded nucleic acid sequences at a
 CC desired location, which can be subsequently used to produce libraries or
 CC genetic packages that display and/or express a diverse family of
 CC peptides, polypeptides or proteins. ABZ36912 to ABZ37510 and ABP55464 to
 CC ABP55499 represent sequences used in the exemplification of the present
 CC invention
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 404
ABV74142
ID ABV74142 standard; DNA; 15 BP.
AC
XX ABV74142;
XX
XX 23-JAN-2003 (first entry)
XX
XX 5' End of cDNA library clone.
XX
XX G-protein coupled receptor; odourant; receptor; olfaction; array;
KW microarray; anosmia; attractant; aromatic; pesticide; ss.
XX
XX Synthetic.
XX
XX WO200277200-A2.
FN
XX
XX 03-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009559.
XX
XX 27-MAR-2001; 2001US-0279168P.
PR
XX 31-JAN-2002; 2002US-0353392P.
XX
XX (INSC-) INSCENT INC.
XX
XX Woods D, Dimitratos S;
PI
XX WPI; 2003-0299930/02.
XX
XX Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT receptors, useful for isolating odorant binding proteins or pesticide
PT alternatives, by analyzing sequences from a male- and female-specific
PT nucleic acid library.
XX
XX Disclosure; Fig 5; 83pp; English.
XX
XX The present sequence is that of the 5' end of a cDNA clone isolated from
CC a cDNA library e.g. a mosquito antenna library. A clone was isolated
CC using a method designed to rapidly array and normalize a complex cDNA
CC library obtained from a target species. Clones are arrayed into multi-
CC well plates. Each well contains 16 oligonucleotides (see ABV74137) with a
CC 5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail
CC and a unique 3' sequence, which allows an anchored oligonucleotide in
CC each well to selectively hybridise only to those cDNA clones with a
CC complementary 5' end. The unique 3' key sequences are designed to give a
CC comprehensive level of degeneracy since they are diverse and numerous
CC enough to ensure that every possible cDNA sequence can be bound by an
CC individual, specific oligonucleotide in a single well. The cDNA library
CC is heated to denature the clones into single stranded DNA, and an aliquot
CC is added to every well. The anchored oligonucleotide serves as the 3'
CC primer in PCR, and the common 5' region present in every cDNA clone
CC serves as the 5' priming site. Denaturing and washing leave anchored cDNA
CC in each well. The library is now arrayed and normalised. The method was
CC used to identify and isolate clones encoding G-protein coupled receptors,
CC especially odourant receptors, and active effectors involved in the
CC olfactory pathway of invertebrates and vertebrates, e.g. odourant binding
CC proteins, or other olfactory or neuronal proteins. The identified
CC receptors and proteins are useful for identifying compounds that reduce a
CC target animal's sensitivity to odours, for manufacturing compounds or
CC devices that mask odours, or trapping invertebrates with odourants.
CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
CC with desirable effects on specific species, for the development of pest
CC monitoring systems or non-toxic, species-specific pesticide alternatives,
CC for controlling insect feeding and breeding behaviour, detecting the
CC presence of small air-borne molecules, etc
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 1 AAAAAAAAAAAAAA 15

RESULT 405
ABV74141/c
ID ABV74141 standard; DNA; 15 BP.
XX
XX ABV74141;
XX
XX 23-JAN-2003 (first entry)
XX
XX Oligonucleotide used in cDNA library array.
DE
XX G-protein coupled receptor; odourant; receptor; olfaction; array;
KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5' polylinker"
XX
XX WO200277200-A2.
FN
XX
XX 03-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009559.
XX
XX 27-MAR-2001; 2001US-0279168P.
PR
XX 31-JAN-2002; 2002US-0353392P.
XX
XX (INSC-) INSCENT INC.
XX
XX Woods D, Dimitratos S;
PI
XX WPI; 2003-0299930/02.
XX
XX Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT receptors, useful for isolating odorant binding proteins or pesticide
PT alternatives, by analyzing sequences from a male- and female-specific
PT nucleic acid library.
XX
XX Disclosure; Fig 5; 83pp; English.
XX
XX The present sequence is that of a poly-T oligonucleotide used in a method
CC designed to rapidly array and normalize a complex cDNA library obtained
CC from a target species. Clones are arrayed into multi-well plates. Each
CC well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC which allows an anchored oligonucleotide in each well to selectively
CC hybridise only to those cDNA clones with a complementary 5' end. The
CC unique 3' key sequences are designed to give a comprehensive level of
CC degeneracy since they are diverse and numerous enough to ensure that
CC every possible cDNA sequence can be bound by an individual, specific
CC oligonucleotide in a single well. The cDNA library is heated to denature
CC the clones into single stranded DNA, and an aliquot is added to every
CC well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC the common 5' region present in every cDNA clone serves as the 5' priming
CC site. Denaturing and washing leave anchored cDNA in each well. The
CC library is now arrayed and normalised. The method was used to identify
CC and isolate clones encoding G-protein coupled receptors, especially
CC odourant receptors, and active effectors involved in the olfactory
CC pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC or other olfactory or neuronal proteins. The identified receptors and
CC proteins are useful for identifying compounds that reduce a target
CC animal's sensitivity to odours, for manufacturing compounds or devices

CC that mask odours, or trapping invertebrates with odourants.
 CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
 CC with desirable effects on specific species, for the development of pest
 CC monitoring systems or non-toxic, species-specific pesticide alternatives,
 CC for controlling insect feeding and breeding behaviour, detecting the
 CC presence of small air-borne molecules, etc
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 406
 ABV75865/C
 ID ABV75865 standard; DNA; 15 BP.

XX AC ABV75865;
 XX DT 05-FEB-2003 (first entry)
 XX DE Oligonucleotide T15-Q-CDPI3.
 XX KW Deprotection; phosphoramidite; ss.
 XX OS Synthetic.

FH Key Location/Qualifiers
 FT modified_base 1. .15
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphoramidite linkage"
 FT modified_base 15
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "3' Q-CDPI3"

PN WO200272864-A2.

XX PD 19-SEP-2002.

XX PF 04-MAR-2002; 2002WO-US006739.

XX PR 08-MAR-2001; 2001US-0274309P.

XX PA (PEKE) PE CORP NY.

XX PI Nelson J;

XX DR WPI; 2003-046740/04.

XX FT New oligonucleotide deprotection reagent useful for deprotecting
 PT oligonucleotide comprises an active methylene compound and an amine
 PT reagent.

PS Example 2; Page 25; 46pp; English.

XX CC The present invention provides a method for deprotection of an
 CC oligonucleotide. This involves reacting a protected oligonucleotide,
 CC which is preferably covalently attached to a solid support through a
 CC linkage, with a deprotection reagent comprising an active methylene
 CC compound and an amine reagent. The process and reagent minimise side-
 CC reactions leading to certain impurities that contaminate synthetic
 CC oligonucleotides. The present sequence is a T15 phosphoramidite
 CC oligonucleotide having a quencher moiety (Q) and minor groove binder
 CC (CDPI3) at the 3' end, which was synthesised in an example of the
 CC invention. This protected oligonucleotide was treated either with 15%
 CC ethanolic ammonia or with 3% diethylmalonate (DEM) dissolved in 15%

CC ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis showed that
 CC deprotection without DEM yielded a complex mixture of products containing
 CC only 26.5% of the desired product. When DEM was used, 76.8% of the
 CC desired product was obtained

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 407
 ADA14836
 ID ADA14836 standard; DNA; 15 BP.

XX AC ADA14836;

XX DT 06-NOV-2003 (first entry)

XX DE Hairpin target sequence, #1, used in an example of the invention.

XX KW Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
 XX quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
 XX rhodamine B-labelled dye; detection; gold support; ss.
 XX OS Synthetic.

FH Key Location/Qualifiers
 FT misc_binding 1. .15
 FT /*tag= a
 FT /bound_moiety= "Hairpin oligonucleotide #1"
 FT /note= "Forms a double-stranded region with the hairpin
 FT oligonucleotide shown in example 2"

XX PN US2003013109-A1.

XX PD 16-JAN-2003.

XX PF 21-JUN-2002; 2002US-00176055.

XX PR 21-JUN-2001; 2001US-0299460P.

XX PA (BALL/) BALLINGER C T.

XX PA (LOCA/) LOCASCIO M.

XX PA (LAND/) LANDRY D P.

XX PI Ballinger CT, Locascio M, Landry DP;

XX DR WPI; 2003-596312/56.

XX FT Hairpin sensor useful for detecting a target nucleotide sequence in a
 PT sample, comprises a hairpin loop assembly including a complementary probe
 PT and a quenchable fluorescing agent.

PS Example 2; Page 11; 16pp; English.

XX CC The invention discloses a hairpin sensor comprising a hairpin loop
 CC assembly including a complementary probe positioned between a first
 CC inverse repeat arm and a second inverse repeat arm, and a quenchable
 CC fluorescing agent joined, directly or indirectly, to the end of the
 CC second inverse repeat arm of the hairpin loop assembly opposite the
 CC complementary probe. Also claimed is a microarray comprising the hairpin
 CC sensor, where the end of the first inverse repeat arm opposite the
 CC complementary probe is bound, directly or indirectly, to a support, a kit
 CC for detecting a target nucleotide sequence in a sample comprising the
 CC hairpin sensor, and a support, and a hairpin sensor system, in which the
 CC particle is conductive or semi-conductive, including at least one of the
 CC above hairpin sensor assemblies. The hairpin sensor further comprises a

CC functional group joined to the end of the first inverse repeat arm
 CC opposite the complementary probe, or first spacer opposite the first
 CC inverse repeat arm, the functional group selected from amino, carboxyl,
 CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned
 CC between the second inverse repeat arm and the quenchable fluorescing
 CC agent, where the ligand is selected from mercapto, hydroxyl, amino,
 CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
 CC second spacer is positioned between the second inverse repeat arm and the
 CC quenchable fluorescing agent which comprises a semiconductor nanocrystal
 CC or rhodamine B-labelled dye. Within the microarray the support is capable
 CC of accepting a charge. At least one hairpin sensor comprises two or more
 CC hairpin sensors. The two or more hairpin sensors include complementary
 CC probes that are the same or different and respective quenchable
 CC fluorescing agents that are the same or different. The two or more
 CC hairpin sensors are arranged in a spatially-defined pattern. The sensor
 CC and system are useful for detecting a target nucleotide sequence in a
 CC sample. Further, the method involves identifying the target nucleotide
 CC sequence by the location of the complementary probe to which the target
 CC nucleotide sequence binds. The two or more hairpin sensors include
 CC complementary probes or quenchable fluorescing agents, that are
 CC different. The sequence presented is the hairpin oligonucleotide target
 CC sequence, #1, used in an example of the invention.

XX
 SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 1 AAAAAAAAAAAAAA 15

RESULT 408
 ADB68520/C
 ID ADB68520 standard; DNA; 15 BP.
 AC ADB68520;
 DT 04-DEC-2003 (first entry)
 XX Single-base mismatch oligonucleotide SEQ ID 10 DNA.
 XX hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
 KW gene expression; respiration; secretion; signalling;
 KW ion-channel activity; cell motility; developmental phenotype;
 KW tumour regression; single-base mismatch; ss;
 KW phosphono-peptide nucleic acid; ppNA.
 XX Synthetic.
 OS
 PN WO2003068798-A2.
 XX
 XX 21-AUG-2003.
 XX
 XX 07-FEB-2003; 2003WO-US003904.
 PF
 PR 09-FEB-2002; 2002US-00072975.
 XX
 PA (ACTI-) ACTIVE MOTIF.
 PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
 XX WPI; 2003-689653/65.
 XX Method of inhibiting expression of genes or RNA transcripts, useful for
 PT therapy and determining effects of genes, by administering oligomers
 PT containing hydroxyproline nucleic acid.
 XX
 PS Example 20; Page 234; 240pp; English.
 XX The invention relates to a novel method of inhibiting the expression of

CC one or more genes or RNA transcripts by administering at least one
 CC oligonucleotide analogue that includes at least one hydroxyproline
 CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. The
 CC oligonucleotides of the invention may be used to monitor properties
 CC including gene expression, respiration, secretion, signalling, ion-
 CC channel activity, cell motility, developmental phenotype and tumour
 CC regression. Furthermore, they may be utilised to determine the effects of
 CC particular genes, as antisense or homologous recombination constructs
 CC e.g. for creating animal models of disease and finally, for increasing
 CC the activity of some enzymes, such as polymerases. The current sequence
 CC is that of the single-base mismatch oligonucleotide SEQ ID 10 DNA of the
 CC invention. This sequence may also comprise a peptide nucleic acid (PNA),
 CC a phosphono-PNA (ppNA) or a HypNA.

XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 409
 ADC18592/C
 ID ADC18592 standard; DNA; 15 BP.
 AC ADC18592;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Annealing control primer Oligo-dT15 SEQ ID NO:54.
 XX annealing control primer; ACP; annealing specificity;
 KW nucleic acid amplification; hybridisation; DNA fingerprinting;
 KW genomic DNA; RNA fingerprint; primer; ss.
 XX Synthetic.
 OS
 PN WO2003050305-A1.
 XX
 XX 19-JUN-2003.
 XX 19-SEP-2002; 2002WO-KR001781.
 PF
 XX 08-DEC-2001; 2001WO-KR002133.
 PR
 PR 01-MAY-2002; 2002WO-KR000816.
 XX
 PA (SEEG-) SERGENE INC.
 XX
 XX Chun J;
 PI WPI; 2003-627256/59.
 XX

XX Annealing control primer to improve annealing specificity in nucleic acid
 PT amplification, has region complementary to target, arbitrary nucleotide
 PT sequence, regulator with universal base/non-discriminatory base analog.
 XX
 PS Example 2; SEQ ID NO 54; 190pp; English.
 XX The present invention describes an annealing control primer (ACP) (I) for
 CC improving the annealing specificity in nucleic acid amplification. (I)
 CC has a 3'-end portion with a nucleotide sequence complementary to a site
 CC on a template nucleic acid for hybridisation, a 5'-end portion having a
 CC pre-selected arbitrary nucleotide sequence, and a regulator portion
 CC between the 3' and 5'-end portions, comprising a universal or non-
 CC discriminatory base analogue, where the regulator portion is capable of
 CC regulating an annealing portion of the primer in association with
 CC annealing temperature. (I) is useful for improving annealing specificity
 CC in nucleic acid amplification. (I) is useful for amplifying a nucleic
 CC acid sequence from a DNA or a mixture of nucleic acids, for selectively

CC amplifying a target nucleic acid sequence from a DNA, and for selectively
CC amplifying a target nucleic acid sequence from a mRNA, by reverse
CC transcribing the mRNA and performing an amplification reaction using (I).
CC (I) is also useful for detecting DNA complementary to differentially
CC expressed mRNA in two or more nucleic acid samples, by reverse
CC transcribing the mRNA and performing an amplification reaction using (I).
CC (I) is also useful for rapidly amplifying a target cDNA fragment
CC comprising a cDNA region corresponding to the 3'-end or 5'-end region of
CC an mRNA, for amplifying a population of full-length double-stranded cDNAs
CC complementary to mRNAs, and amplifying 5'-enriched double-stranded cDNAs
CC complementary to mRNA. (I) is also useful for amplifying more than one
CC target nucleotide sequence simultaneously using more than one pair of
CC primers in the same reaction, where the primers are derived from (I), for
CC producing a DNA fingerprint of genomic DNA (gDNA), for producing a RNA
CC fingerprint of an mRNA sample, identifying conserved homology segments in
CC a multigene family from a mRNA sample, and for identifying conserved
CC homology segments in a multigene family from gDNA. (I) is also useful for
CC identifying a nucleotide variation in a target nucleic acid, and for
CC mutagenesis in a target nucleic acid. The present sequence represents a
CC primer which is used in the exemplification of the present invention.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 410
AA18369/C
ID AAX18369 standard; DNA; 16 BP.
XX
AC AAX18369;
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 10.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.

PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.

XX Disclosure; Page 10; 19pp; Japanese.
XX This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

SQ Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1494
DB 15 TAAAAAAAAAAAAA 1

RESULT 411
ABL57075
ID ABL57075 standard; DNA; 16 BP.
XX
AC ABL57075;
DT 22-JUL-2002 (first entry)
XX
DE Molecular beacon target sequence.
XX
KW Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS Synthetic.

XX FH Key Location/Qualifiers
FT misc_binding 1..16
FT /*tag= a
FT /bound_moiety= "Molecular beacon"
FT /note= "forms double-stranded region with bases 5-21 of
FT sequence in ABL57069"

XX W0200218951-A2.
PN
PD 07-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US041941.
XX
PR 29-AUG-2000; 2000US-0228728P.
PR 30-MAR-2001; 2001US-0280350P.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Dubertret B, Calame M, Libhaber A;

XX WPI; 2002-404569/43.
XX
PT Sensitive detecting proximity changes in a system that utilizes an
PT interacting fluorophore and quencher, for high sensitivity applications,
PT involves utilizing a metal surface as quencher.

PS Example 3; Page 30; 62pp; English.
XX
CC The present sequence is that of a perfectly matched target sequence for a
CC molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC a nanoparticle. In the native state, the probe forms a hairpin
CC conformation with hybridised termini. The proximity of the fluorophore
CC and quencher (gold nanoparticle) in the molecular beacon results in
CC little or no detectable fluorescence. Upon hybridisation of the central
CC complementary stretch of the probe to a target sequence, such as the
CC present sequence, the hairpin undergoes a conformational change resulting
CC in an increase in fluorescence, the extent of which is proportional to
CC the amount of target sequence present. Single mismatches can be detected.
CC The invention relates generally to the use of metal surface quenchers
CC such as particles or films for high sensitivity applications in, for
CC example, detection and diagnostic systems
XX
SQ Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

```

Query Match      1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 2 AAAAAAAAAAAAAA 16

RESULT 412
ABQ94572
ID ABQ94572 standard; DNA; 16 BP.
XX
AC ABQ94572;
XX
DT 28-OCT-2002 (first entry)
DE Tumour suppression-related oligonucleotide #223.
XX
KW Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW viral infection; cell degeneration disease; neurodegeneration; ds;
KW Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS Homo sapiens.
XX
PN FR2819824-A1.
XX
PD 26-JUL-2002.
XX
PF 23-JAN-2001; 2001FR-00000899.
XX
PR 23-JAN-2001; 2001FR-00000899.
PA (MOL-) MOLECULAR ENGINES LAB SA.
XX
PI Teleman A, Anson R, Tuijnder M, Susini L;
XX
DR WPI; 2002-610803/66.
XX
PT New nucleic acid implicated e.g. in tumor suppression, useful for
PT diagnosis of tumors, viral infection and cellular degeneration and for
PT drug screening.
XX
PS Claim 1; Page 90; 623pp; French.
XX
CC The present invention relates to novel human nucleic acid sequences (I).
CC The present sequence is one such nucleic acid sequence. Expression of (I)
CC are implicated in tumour suppression or reversion and apoptosis and viral
CC resistance. (I) are useful as probes or primers for detecting,
CC identifying, measuring and/or amplifying nucleic acid sequences, as
CC antisense reagents and for recombinant production of polypeptides. (I),
CC polypeptides (II) encoded by (I), vector containing (I), cells containing
CC these vectors and antibodies (AB) against (II) are all useful for
CC treatment/prevention of viral, tumour and cell degeneration diseases
CC (especially neurodegeneration, such as Alzheimer's disease and
CC schizophrenia). Analysing the expression of (I) is also useful for
CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC (I) are used for studying the aetiology of these diseases (also immune
CC and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC in the specification
XX
SQ Sequence 16 BP; 11 A; 1 C; 1 G; 3 T; 0 U; 0 Other;

Query Match      1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1477 TGCTAAAAAAAAAA 1491
DB 2 TGCTAAAAAAAAAA 16

RESULT 413
AAD57845
ID AAD57845 standard; DNA; 16 BP.
XX
AC AAD57845;
XX
DT 20-NOV-2003 (first entry)
DE Target oligonucleotide #2 used in nonlinear optical technique.
XX
KW Nonlinear optical technique; screening; ss.
XX
OS Unidentified.
XX
PN WO2003064991-A2.
XX
PD 07-AUG-2003.
XX
PF 17-JUL-2002; 2002WO-US022681.
XX
PR 17-JUL-2001; 2001US-0306040P.
PR 23-OCT-2001; 2001US-0347821P.
PR 06-FEB-2002; 2002US-0354668P.
XX
PA (SALA/) SALAFSKY J S.
XX
PI Salafsky JS;
XX
DR WPI; 2003-646172/61.
XX
PT Screening candidate binding partner(s) for binding to test molecule by
PT applying external force field to sample in homogeneous phase,
PT illuminating sample with light beam(s) at fundamental frequencies, and
PT measuring physical properties.
XX
PS Disclosure; Fig 20-B; 146pp; English.
XX
CC The present invention relates to a method for detecting interactions
CC between biological components using a nonlinear optical technique. The
CC invention is used for screening candidate binding partner(s) for binding
CC to test molecule. It can also be used to detect changes in orientation or
CC conformation of the probe and/or target. The present sequence is a target
CC oligonucleotide used in nonlinear optical technique
XX
SQ Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match      1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 2 AAAAAAAAAAAAAA 16

RESULT 414
ADB68508/c
ID ADB68508 standard; DNA; 16 BP.
XX
AC ADB68508;
XX
DT 04-DEC-2003 (first entry)
DE PNA-HypNA hybridisation oligomer.
XX
KW hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW gene expression; respiration; secretion; signalling;
KW ion-channel activity; cell motility; developmental phenotype;
KW tumour regression; hybridisation; ss; serine nucleic acid; SerNA;
KW phosphono-peptide nucleic acid; pPNA.
XX
OS Synthetic.

```



```

PI XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
DR XX WPI; 1997-259017/23.
XX
PT XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX
PS PS Claim 4; Page 79; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 417
AAV37934/c
ID AAV37934 standard; cDNA; 17 BP.
XX
AC AAV37934;
XX
DT 05-OCT-1998 (first entry)
XX
DE Primer of the specification.
XX
KW Leukocyte; IgA nephropathy; diagnosis; treatment; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9824815-A1.
XX
PD 11-JUN-1998.
XX
PF 05-DEC-1997; 97WO-JP004469.
XX
PR 05-DEC-1996; 96JP-00325752.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA (KAZU-) KAZUSA DNA RES INST FOUND.
XX
PI Ishiwata T, Sakurada M, Nishimura A, Nakagawa S, Kuga T, Nishi T;
PI Nomura N, Nagase T, Sawada S, Takei M;
XX
DR WPI; 1998-333259/29.
XX
PT Protein from leukocytes and DNA encoding it - useful as reagents for
PT diagnosing and treating IgA nephropathy.
XX
PS Example 2; Page 33; 41pp; Japanese.
XX
CC PCR primers AAV37933-39 are used in the course of the invention. The
CC specification describes a novel protein isolated from leukocytes of
CC patients with IgA nephropathy. Oligonucleotides based on the DNA sequence
CC encoding this protein are useful as reagents for diagnosing and treating
CC IgA nephropathy
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 418
AAA30181/c
ID AAA30181 standard; DNA; 17 BP.
XX
AC AAA30181;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15G used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP005506.
XX
PR 06-OCT-1998; 98JP-00284610.
XX
XX (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
DR WPI; 2000-317712/27.
XX
PT Gene highly expressed in patients with high cedar pollen-specific IgE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
PS Example 6; Page 38; 44pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 419
AAA30180/c
ID AAA30180 standard; DNA; 17 BP.
XX
AC AAA30180;
XX

```

DT	16-AUG-2000	(first entry)
XX		
DE	PCR primer GT15C used in pollenosis associated gene identification.	
XX		
KW	Pollenosis-associated protein; high pollen-specific immunoglobulin E;	
KW	IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200020575-A1.	
XX		
PD	13-APR-2000.	
XX		
PF	06-OCT-1999; 99WO-JP005506.	
XX		
PR	06-OCT-1998; 98JP-00284610.	
XX		
PA	(GENO-) GENOX RES INC.	
XX		
PI	Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;	
PI	Obayashi I, Imai Y, Lu N, Ogawa K;	
XX		
DR	WPI; 2000-317712/27.	
XX		
PT	Gene highly expressed in patients with high cedar pollen-specific IgE	
PT	levels, useful for diagnosing pollenosis, and screening candidate	
PT	compounds for pollenosis treatment.	
XX		
PS	Example 6; Page 38; 44pp; Japanese.	
XX		
CC	This sequence represents a PCR primer used in the identification of a	
CC	human pollenosis associated gene. The gene is highly expressed in	
CC	individuals with high pollen-specific immunoglobulin E (IgE) levels	
CC	invention relates to the nucleotide sequence encoding the pollenosis	
CC	associated protein, diagnosing pollenosis and screening candidate	
CC	compounds for treating pollenosis. The gene can be used in diagnosing	
CC	pollenosis, particularly cedar pollenosis, and screening candidate	
CC	compounds for pollenosis treatment	
XX		
SO	Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;	

```
Query Match      1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1481 AAAAAAAAAAAAAA 1495
|||
Db 16 AAAAAAAAAAAAAA 2

RESULT 420
AAZ35714/C
ID AAZ35714 standard; DNA; 17 BP.
XX
XX AAZ35714;
XX AC
XX AC
XX 31-JAN-2000 (first entry)
XX
XX
DE Murine gene anchor PCR primer SEQ ID NO:3.

Rare expressed gene; analysis; expression; nucleic acid sample;
 PCR primer; ss.

XX (HITA) HITACHI LTD.
XX PA
XX XX
XX PI Muramatsu T, Fujita T, Kiyama M, Irie T, Okano K;
XX XX
XX DR WPI; 2000-001284/01.
XX XX
XX PT Preparation of nucleic acid sample, useful for analysis of rare expressed
XX PT genes.
XX XX
XX PS Disclosure; Page 11; 22pp; English.

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 421
AAX82722/C
ID AAX82722 standard; DNA: 17 BP.

DT 10-NOV-2000 (first entry)
 XX
 DE Human Iga nephropathy-associated cDNA primer #63.
 XX
 KW Iga nephropathy-associated protein; diagnosis; treatment; antisense;
 KW human; primer; ss.


```

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
XX PI Sawada S, Takei M, Shibata K, Furuya A;
XX DR WPI; 2000-097328/08.
XX PT DNA sequences preferentially expressed in IgA nephropathy patients,
XX PT proteins encoded by them, and antibodies to those proteins.
XX PS Claim 3; Page 170; 180pp; Japanese.
XX CC This invention describes novel DNA sequences preferentially expressed in
XX CC IgA nephropathy patients, and DNA sequences stringently hybridizing to
XX CC them. Independent claims cover diagnostic reagents for IgA nephropathy
XX CC incorporating the antisense sequences; the treatment of IgA nephropathy
XX CC using the antisense sequences for mRNA inhibition; proteins associated
XX CC with IgA nephropathy, containing sequences encoded by the DNA sequences;
XX CC antibodies recognizing these proteins; the production of the proteins by
XX CC culture of host cells transformed with DNA encoding them; diagnostic
XX CC reagents for IgA nephropathy containing the antibodies; and compositions
XX CC for the treatment of IgA nephropathy which contain the antibodies. The
XX CC products of the invention can be used for the diagnosis and treatment of
XX CC IgA nephropathy. This sequence represents a primer used in the isolation
XX CC and identification of the human IgA nephropathy-associated proteins
XX CC described in the method of the invention
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db |||||
16 AAAAAAAAAAAAAA 2

RESULT 422
AAZ36740/C
ID AAZ36740 standard; DNA; 17 BP.
XX AC AAZ36740;
XX DT 13-MAR-2000 (first entry)
XX DE Anchored oligo(dT) primer GT15G used for modified differential display.
XX KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
XX KW differentially expressed nucleic acid; disease state; cancer;
XX KW autoimmune disease; infectious disease; aging; developmental disorder;
XX KW proliferative disorder; neurological disorder; toxicity; primer;
XX KW treatment resistance; differential expression; drug discovery;
XX KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX OS Synthetic.
XX PN WO955913-A2.
XX PD 04-NOV-1999.
XX PF 27-APR-1999; 99WO-US009119.
XX PR 27-APR-1998; 98US-0083331P.
XX PR 27-AUG-1998; 98US-0098070P.
XX PR 04-FEB-1999; 99US-0118624P.
XX PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX PI McClelland M, Welsh J, Trenkle T;
XX DR WPI; 2000-086388/07.
XX PT Measuring expression of low abundance reduced complexity target nucleic
XX PT acid molecules.
XX PS Example 3; Page 91; 187pp; English.
XX CC AAZ36739-41 represent oligo(dT) primers used for modified differential
XX CC display, in the method of the invention. The specification describes a
XX CC method for measuring the level of two or more nucleic acid molecules in a
XX CC target. The method comprises contacting a probe with an arbitrarily or
XX CC statistically sampled target and detecting the amount of specific binding
XX CC of the target to the probe. The methods can be used to identify

```

CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
xx Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Len

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels

Qy 1481 AAAAAAAAAAAAAAAAAA 1495
Db 17 AAAAAAAAAAAAAAAAAA 3

RESULT 425
AAA25452/C
ID AAA25452 standard; DNA: 17 BP.

DT 19-JUL-20

DE Oestrogen receptor hammerh

DE	Oestrogen receptor	hammerhead ribozyme	target sequence	SEQ ID NO:1950
DE	Oestrogen receptor	hammerhead ribozyme	target sequence	SEQ ID NO:1950

KW
KW
KW
KW
KW

nanomead ribozyme; hairpin ribozyme; antitense oligonucleotide;
gene expression modification; cancer; phosphorothioate; endonuclease
anticancer; breast cancer; endometrium cancer; ss.

XX PN WO9954459-A2.

28-OCT-1999.

19-APR-1999:

XX
PR 20-APR-1998: 98US-0082404P-

XX
PR 23-JUN-1998; 9805-00103636.

PA (RIBO-) RIBOZYME PHARM INC.
XX

PI Thompson JD, Beigelman L,
PI Rembold M, Zwick M, Jern

PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.

PT New nucleic acids th

XX
PS Claim 77; Page 79; 148pp; English.

CC The present invention describes nu

The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphorodithioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), *in vivo* or by transforming cells *ex vivo* and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and

CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention

XX SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 426
 AAC64203/C
 ID AAC64203 standard; DNA; 17 BP.
 XX AC AAC64203;
 XX DT 21-FEB-2001 (first entry)
 XX DE PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.
 XX KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KW drug screening; allergic disease; PCR primer; ss.
 XX OS Synthetic.
 XX PN WO200065046-A1.
 XX PD 02-NOV-2000.
 XX PF 26-APR-2000; 2000WO-JP002730.
 XX PR 27-APR-1999; 99JP-00120489.
 XX PA (GENO-) GENOX RES INC.
 XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687339/67.

XX Pollinosis-associated gene 373 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
 PT in diagnosis of allergic diseases and screening drug candidates.
 XX Example 6; Page 70; 80pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 373 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates also relates
 CC to the protein encoded by pollinosis gene 373; expression constructs and
 CC host cells comprising pollinosis-associated gene 373 nucleic acids;
 CC pollinosis-associated gene 373 primers and probes; antibodies against the
 CC protein encoded by the gene; methods of detection of pollinosis-
 CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
 CC diseases via the detection of pollinosis-associated gene 373 nucleic
 CC acids. The invention additionally encompasses methods of screening drug
 CC candidates for the treatment of allergic disease by measuring the
 CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
 CC T-cells in the presence of a test compound relative to a control.
 CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
 CC diseases and in the screening of drug candidates for the treatment of
 CC such diseases. The present sequence represents a PCR primer used in the

CC isolation of human pollinosis-associated gene 373 cDNA .
 XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 16 AAAAAAAAAAAAAA 2

RESULT 427
 AAC64204/C
 ID AAC64204 standard; DNA; 17 BP.
 XX AC AAC64204;
 XX DT 21-FEB-2001 (first entry)
 XX DE PCR anchor primer, SEQ ID NO:5, used in human gene 373 isolation.
 XX KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KW drug screening; allergic disease; PCR primer; ss.
 XX OS Synthetic.
 XX PN WO200065046-A1.
 XX PD 02-NOV-2000.
 XX PF 26-APR-2000; 2000WO-JP002730.
 XX PR 27-APR-1999; 99JP-00120489.
 XX PA (GENO-) GENOX RES INC.
 XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687339/67.

XX Pollinosis-associated gene 373 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
 PT in diagnosis of allergic diseases and screening drug candidates.
 XX Example 6; Page 70; 80pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 373 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates also relates
 CC to the protein encoded by pollinosis gene 373; expression constructs and
 CC host cells comprising pollinosis-associated gene 373 nucleic acids;
 CC pollinosis-associated gene 373 primers and probes; antibodies against the
 CC protein encoded by the gene; methods of detection of pollinosis-
 CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
 CC diseases via the detection of pollinosis-associated gene 373 nucleic
 CC acids. The invention additionally encompasses methods of screening drug
 CC candidates for the treatment of allergic disease by measuring the
 CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
 CC T-cells in the presence of a test compound relative to a control.
 CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
 CC diseases and in the screening of drug candidates for the treatment of
 CC such diseases. The present sequence represents a PCR primer used in the
 CC isolation of human pollinosis-associated gene 373 cDNA

XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0

QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2

RESULT 428
AAC64183/c
ID AAC64183 standard; DNA; 17 BP.
XX
AC AAC64183;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PP 27-APR-1999; 99JP-00120490.
XX
PR (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsu K;
XX
DR WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 50; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis-associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2

RESULT 429
AAC64182/c
ID AAC64182 standard; DNA; 17 BP.
XX
AC AAC64182;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PP 27-APR-1999; 99JP-00120490.
XX
PR (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsu K;
XX
DR WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 49; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis-associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2

```

XX DE
XX DE
XX KW Human; pollinosis-associated gene 513; IGE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
XX KW drug screening; allergic disease; PCR primer; ss.
XX OS Synthetic.
XX PN WO200065049-A1.
XX XX
XX PD 02-NOV-2000.
XX XX
XX PF 26-APR-2000; 2000WO-JP002733.
XX XX
XX PR 27-APR-1999; 99JP-00120491.
XX XX
XX PA (GENO-) GENOX RES INC.
XX XX
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX XX
XX DR WPI; 2000-687342/67.
XX XX
XX PT Pollinosis-associated gene 513 undergoing significantly low expression in
XX PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
XX PT of allergic diseases and screening drug candidates.
XX XX
XX PS Example 6; Page 38; 46pp; Japanese.
XX CC The invention relates to the human pollinosis-associated gene 513 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen using
XX CC the differential display method. The invention also relates to methods of
XX CC detection of pollinosis-associated gene 513 nucleic acids; a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 513 nucleic acids; and methods of screening drug candidates for the
XX CC treatment of allergic disease by measuring the expression of pollinosis-
XX CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
XX CC of a test compound relative to a control. Pollinosis-associated gene 513
XX CC is useful in the diagnosis of allergic diseases and in the screening of
XX CC drug candidates for the treatment of such diseases. The present sequence
XX CC represents a PCR primer used in the isolation of human pollinosis-
XX CC associated gene 513 cDNA
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 432
AAC64163/c
ID AAC64163 standard; DNA; 17 BP.
XX XX
XX AC AAC64163;
XX XX
XX DT 21-FEB-2001 (first entry)
XX DE
XX DE PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation.
XX KW Human; pollinosis-associated gene 581; IGE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
XX KW drug screening; allergic disease; PCR primer; ss.
XX OS Synthetic.
XX PN WO200065049-A1.
XX XX
XX PD 02-NOV-2000.
XX XX
XX PF 26-APR-2000; 2000WO-JP002733.
XX XX
XX PR 27-APR-1999; 99JP-00120491.
XX XX
XX PA (GENO-) GENOX RES INC.
XX XX
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX XX
XX DR WPI; 2000-687342/67.
XX XX
XX PT Pollinosis-associated gene 513 undergoing significantly low expression in
XX PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
XX PT of allergic diseases and screening drug candidates.
XX XX
XX PS Example 6; Page 39; 46pp; Japanese.
XX CC The invention relates to the human pollinosis-associated gene 513 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen using
XX CC the differential display method. The invention also relates to methods of
XX CC detection of pollinosis-associated gene 513 nucleic acids; a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 513 nucleic acids; and methods of screening drug candidates for the
XX CC treatment of allergic disease by measuring the expression of pollinosis-
XX CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
XX CC of a test compound relative to a control. Pollinosis-associated gene 513
XX CC is useful in the diagnosis of allergic diseases and in the screening of
XX CC drug candidates for the treatment of such diseases. The present sequence
XX CC represents a PCR primer used in the isolation of human pollinosis-
XX CC associated gene 513 cDNA
XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 431
AAC64172/c
ID AAC64172 standard; DNA; 17 BP.
XX XX
XX AC AAC64172;
XX XX
XX DT 21-FEB-2001 (first entry)

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PN WO200065048-A1.
XX
XX
PD 02-NOV-2000.
XX
XX
PF 26-APR-2000; 2000WO-JP002732.
XX
XX
PR 27-APR-1999; 99JP-00120492.
XX
XX
PA (GENO-) GENOX RES INC.
XX
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX
DR WPI; 2000-687341/67.
XX
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
XX
XX
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
XX
XX
RESULT 433
AAC64162/c
ID AAC64162 standard; DNA; 17 BP.
XX
XX
AC AAC64162;
XX
XX
DT 21-FEB-2001 (first entry)
XX
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO200065048-A1.
XX
XX
PD 02-NOV-2000.
XX
XX
PF 26-APR-2000; 2000WO-JP002732.
XX
XX
PR 27-APR-1999; 99JP-00120493.
XX
XX
PA (GENO-) GENOX RES INC.
XX
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX
DR WPI; 2000-687341/67.
XX
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
XX
XX
RESULT 434
AAC64215/c
ID AAC64215 standard; DNA; 17 BP.
XX
XX
AC AAC64215;
XX
XX
DT 21-FEB-2001 (first entry)
XX
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 627 isolation.
XX
XX
KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO200065051-A1.
XX
XX
PD 02-NOV-2000.
XX
XX
PF 26-APR-2000; 2000WO-JP002735.
XX
XX
PR 27-APR-1999; 99JP-00120493.
XX
XX
PA (GENO-) GENOX RES INC.
XX
XX

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PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687344/67.
 XX Pollinosis-associated gene 627 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.
 XX
 XX Example 6; Page 42; 51pp; Japanese.
 XX The invention relates to the human pollinosis-associated gene 627 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates to methods of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 627 nucleic acids; and a method of screening drug candidates for the
 CC treatment of allergic diseases associated with the expression of pollinosis-
 CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 627
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 627 cDNA
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 16 AAAAAAAAAAAAAA 2

RESULT 435
 AAC64214/C
 ID AAC64214 standard; DNA; 17 BP.
 XX
 AC AAC64214;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.
 XX
 KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KW drug screening; allergic disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200065051-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-JP002735.
 XX
 PR 27-APR-1999; 99JP-00120493.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687344/67.
 XX Pollinosis-associated gene 627 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.

XX The invention relates to the human pollinosis-associated gene 795 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. Pollinosis-associated gene 795 has

PS Example 6; Page 42; 51pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 627 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates to methods of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 627 nucleic acids; and a method of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-
 CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 627
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 627 cDNA

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 16 AAAAAAAAAAAAAA 2

RESULT 436
 AAC64231/C
 ID AAC64231 standard; DNA; 17 BP.

XX
 AC AAC64231;

DT 21-FEB-2001 (first entry)

DE PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.

XX Human; pollinosis-associated gene 795; vimentin homologue; IgE;
 KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
 KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

XX Synthetic.

PN WO200065050-A1.

XX PD 02-NOV-2000.

XX PF 26-APR-2000; 2000WO-JP002734.

XX PR 27-APR-1999; 99JP-00120494.

XX (GENO-) GENOX RES INC.
 XX (BISA) BISA CO LTD.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
 PI Yokoi A;

XX WPI; 2000-687343/67.

XX Pollinosis-associated gene 795 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.

XX Page 45; Example 6; 73pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 795 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. Pollinosis-associated gene 795 has

CC homology with the human vimentin gene. The invention also relates also
 CC relates to the protein encoded by pollinosis gene 795; to expression
 CC constructs and host cells comprising pollinosis-associated gene 795
 CC nucleic acids; pollinosis-associated gene 795 primers and probes;
 CC antibodies against the protein encoded by the gene; methods of detection
 CC of pollinosis-associated gene 795 nucleic acids; and a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 795 nucleic acids. The invention additionally encompasses methods of
 CC screening drug candidates for the treatment of allergic disease by
 CC measuring the expression of pollinosis-associated gene 795 in pollen
 CC antigen-stimulated T-cells in the presence of a test compound relative to
 CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
 CC allergic diseases and in the screening of drug candidates for the
 CC treatment of such diseases. The present sequence represents a PCR primer
 CC used in the isolation of human pollinosis-associated gene 795 cDNA
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 RESULT 437
 AAC64232/C
 ID AAC64232 standard; DNA; 17 BP.
 XX
 AC AAC64232;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation.
 XX
 KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;
 KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
 KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200065050-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-JP002734.
 XX
 PR 27-APR-1999; 99JP-00120494.
 XX
 PA (GENO-) GENOX RES INC.
 PA (EISA) EISAI CO LTD.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
 PI Yokoi A;
 XX
 DR WPI; 2000-687343/67.
 XX
 PT Pollinosis-associated gene 795 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.
 XX
 PS Page 46; Example 6; 73pp; Japanese.
 XX
 CC The invention relates to the human pollinosis-associated gene 795 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. Pollinosis-associated gene 795 has
 CC homology with the human vimentin gene. The invention also relates also
 CC relates to the protein encoded by pollinosis gene 795; to expression

CC constructs and host cells comprising pollinosis-associated gene 795
 CC nucleic acids; pollinosis-associated gene 795 primers and probes;
 CC antibodies against the protein encoded by the gene; methods of detection
 CC of pollinosis-associated gene 795 nucleic acids; and a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 795 nucleic acids. The invention additionally encompasses methods of
 CC screening drug candidates for the treatment of allergic disease by
 CC measuring the expression of pollinosis-associated gene 795 in pollen
 CC antigen-stimulated T-cells in the presence of a test compound relative to
 CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
 CC allergic diseases and in the screening of drug candidates for the
 CC treatment of such diseases. The present sequence represents a PCR primer
 CC used in the isolation of human pollinosis-associated gene 795 cDNA
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 RESULT 438
 AAC92294/C
 ID AAC92294 standard; DNA; 17 BP.
 XX
 AC AAC92294;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:4.
 XX
 KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
 KW allergic disease; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073439-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 18-MAY-2000; 2000WO-JP003191.
 XX
 PR 27-MAY-1999; 99JP-00148784.
 XX
 PA (GENO-) GENOX RES INC.
 PA (EISA) EISAI CO LTD.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
 PI Yokoi A;
 XX
 DR WPI; 2001-061528/07.
 XX
 PT Pollinosis-associated gene 465 undergoing significantly low expression in
 PT subjects after pollen scattering, useful in diagnosis of allergic
 PT diseases and screening candidate compounds to regulate response of T
 PT cells to antigen stimulus.
 XX
 PS Example 6; Page 44; 61pp; Japanese.
 XX
 CC The present invention describes the human pollinosis-associated gene 465
 CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
 CC (AAC92291), that undergoes significantly low expression in subjects after
 CC pollen scattering, and is useful in the diagnosis of allergic diseases
 CC and screening candidate compounds for remedies capable of regulating the
 CC response of T cells to the stimulus by an antigen. The gene is useful in
 CC the diagnosis of allergic diseases and screening candidate compounds for
 CC remedies capable of regulating the response of T cells to the stimulus by
 CC an antigen. The present sequence represents a PCR primer which is used in


```

CC  an example from the present invention
XX
SQ  Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

    Query Match      1.0%; Score 15; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 2.1e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAAA 1495
Db  16 AAAAAAAAAAAAAA 2

RESULT 439
AAC92293/c
ID  AAC92293 standard; DNA; 17 BP.
XX
AC  AAC92293;
XX
DT  22-MAR-2001 (first entry)
XX
DE  Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:3.
XX
KW  Human; pollinosis-associated gene 465; pollen scattering; allergy;
XX  allergic disease; PCR primer; ss.
XX
OS  Homo sapiens.
XX
PN  WO200073439-A1.
XX
PD  07-DEC-2000.
XX
PF  18-MAY-2000; 2000WO-JP003191.
XX
PR  27-MAY-1999; 99JP-00148784.
XX
PA  (GENO-) GENOX RES INC.
PA  (EISA) EISAI CO LTD.
XX
PI  Nagasu T, Sugita Y, Kaishwabara T, Oshida T, Obayaehi M, Gunji S;
PI  Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI  Yokoi A;
XX
XX  WPI; 2001-061528/07.
XX
DR  Pollinosis-associated gene 465 undergoing significantly low expression in
PT  subjects after pollen scattering, useful in diagnosis of allergic
PT  diseases and screening candidate compounds to regulate response of T
PT  cells to antigen stimulus.
XX
PS  Example 6; Page 44; 61pp; Japanese.
XX
CC  The present invention describes the human pollinosis-associated gene 465
CC  which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC  (AAC92291), that undergoes significantly low expression in subjects after
CC  pollen scattering, and is useful in the diagnosis of allergic diseases
CC  and screening candidate compounds for remedies capable of regulating the
CC  response of T cells to the stimulus by an antigen. The gene is useful in
CC  the diagnosis of allergic diseases and screening candidate compounds for
CC  remedies capable of regulating the response of T cells to the stimulus by
CC  an antigen. The present sequence represents a PCR primer which is used in
CC  an example from the present invention
XX
SQ  Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

    Query Match      1.0%; Score 15; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 2.1e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAAA 1495
Db  16 AAAAAAAAAAAAAA 2

an example from the present invention
AAC91720/c
ID  AAC91720 standard; DNA; 17 BP.
XX
AC  AAC91720;
XX
DT  27-MAR-2001 (first entry)
XX
DE  PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.
XX
KW  Human; pollinosis-associated gene 787; pollen allergy; T-cell;
XX  reduced expression; detection; diagnosis; drug screening;
XX  allergic disease; PCR primer; ss.
XX
OS  Synthetic.
XX
PN  WO200073440-A1.
XX
PD  07-DEC-2000.
XX
PF  18-MAY-2000; 2000WO-JP003192.
XX
PR  27-MAY-1999; 99JP-00148785.
XX
PA  (GENO-) GENOX RES INC.
PA  (EISA) EISAI CO LTD.
XX
PI  Nagasu T, Sugita Y, Kaishwabara T, Oshida T, Obayaehi M, Gunji S;
PI  Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI  Yokoi A;
XX
XX  WPI; 2001-032159/04.
XX
DR  Pollinosis-associated gene 787 undergoing significantly low expression in
PT  subjects after pollen scattering, useful in diagnosis of allergic
PT  diseases and screening candidate compounds to regulate response of T
PT  cells to antigen stimulus.
XX
PS  Example 6; Page 40; 54pp; Japanese.
XX
CC  The invention relates to the human pollinosis-associated gene 787 which
CC  exhibits significantly reduced expression in the T-cells of individuals
CC  after the pollen-scattering season, relative to expression levels in T-
CC  cells before the pollen-scattering season. The gene was isolated from T-
CC  cells from individuals allergic to pollen using the differential display
CC  method. The invention also relates to pollinosis-associated gene 787
CC  primers and probes; methods of detection of pollinosis-associated gene
CC  787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC  detection of pollinosis-associated gene 787 nucleic acids. The invention
CC  additionally encompasses a method of screening drug candidates for the
CC  treatment of allergic disease by measuring the expression of pollinosis-
CC  associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC  of a test compound relative to a control. Pollinosis-associated gene 787
CC  is useful in the diagnosis of allergic diseases and in the screening of
CC  drug candidates for the treatment of such diseases. The present sequence
CC  represents a PCR primer used in the isolation of human pollinosis-
CC  associated gene 787 cDNA
XX
SQ  Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

    Query Match      1.0%; Score 15; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 2.1e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAAA 1495
Db  16 AAAAAAAAAAAAAA 2

an example from the present invention
AAC91721/c
ID  AAC91721 standard; DNA; 17 BP.

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XX AAC91721;
AC
XX
DT 27-MAR-2001 (first entry)
DE PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.
XX
XX Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
XX allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO200073440-A1.
PN
XX
PD 07-DEC-2000.
XX
XX 18-MAY-2000; 2000WO-JP003192.
XX
XX 27-MAY-1999; 99JP-00148785.
XX
XX (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
XX WPI; 2001-032159/04.
DR
XX
XX Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
XX Example 6; Page 41; 54pp; Japanese.
PS
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2

RESULT 442
AAC82876/c
ID AAC82876 standard; DNA; 17 BP.
XX
AC AAC82876;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 441 primer #2.
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200073435-A1.
PN
XX
PD 07-DEC-2000.
XX
XX 18-MAY-2000; 2000WO-JP003190.
XX
XX 27-MAY-1999; 99JP-00148783.
XX
XX (GENO-) GENOX RES INC.
PA
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI

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XX Human pollinosis-associated gene 441 primer #3.
DE
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200073435-A1.
PN
XX
PD 07-DEC-2000.
XX
XX 18-MAY-2000; 2000WO-JP003190.
XX
XX 27-MAY-1999; 99JP-00148783.
XX
XX (GENO-) GENOX RES INC.
PA
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX WPI; 2001-061526/07.
DR
XX
XX Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
XX Example 6; Page 36; 42pp; Japanese.
PS
XX
CC This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2

RESULT 443
AAC82875/c
ID AAC82875 standard; DNA; 17 BP.
XX
AC AAC82875;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 441 primer #2.
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200073435-A1.
PN
XX
PD 07-DEC-2000.
XX
XX 18-MAY-2000; 2000WO-JP003190.
XX
XX 27-MAY-1999; 99JP-00148783.
XX
XX (GENO-) GENOX RES INC.
PA
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI

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PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2001-061526/07.
XX
XX Pollinosis-associated gene 441 which undergoes lower expression in
XX subjects after pollen scattering, useful in diagnosis of allergic
XX diseases and screening candidate compounds to regulate response of T
XX cells to antigen stimulus.
XX
XX Example 6; Page 35; 43pp; Japanese.
XX
XX This invention describes a novel nucleic acid molecule comprising a
XX sequence (I) which undergoes significantly low expression in subjects
XX after pollen scattering, and is useful in diagnosis of allergic diseases
XX and screening candidate compounds for remedies capable of regulating the
XX response of T cells to the stimulus by an antigen
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 444
AAH47128/C
XX AAH47127;
XX AC
XX 30-NOV-2001 (first entry)
XX DT
XX DE Nucleotide sequence of primer GT15C.
XX KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
XX KW PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200165259-A1.
XX PD 07-SEP-2001.
XX PF 23-FEB-2001; 2001WO-JP001372.
XX PR 02-MAR-2000; 2000JP-00061832.
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX WPI; 2001-557789/62.
XX DR
XX PT Diagnosis of allergies including atopic dermatitis.
XX PS Example 6; Page 66; 83pp; Japanese.
XX CC The invention provides a method of diagnosis of allergies that involves:
XX assaying the levels of expression of genes B1001, B1466, B1072 or B1151
XX in T-cells; and comparing them with the level of expression in healthy T-
XX cells. The method is useful for diagnosing allergies, particularly atopic
XX dermatitis. The present sequence represents a PCR primer used for
XX analysis of the expression of the above genes
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 446
ABK49636/C
XX ABK49636;
XX AC
XX 15-JUL-2002 (first entry)
XX DT
XX DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15G.
XX KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
XX KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15G.
XX OS Homo sapiens.

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XX PN WO200224903-A1.
XX PD
XX PF 28-MAR-2002.
XX PR 21-SEP-2001; 2001WO-JP008246.
XX PR 25-SEP-2000; 2000JP-00291318.
XX PR (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PA (EISA ) EISAI CO LTD.
XX PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
XX PI Takahashi E;
XX DR WPI; 2002-315738/35.
XX PT Examining allergic diseases by differential display of gene showing
XX PT different expression particularly increased expression in remission stage
XX PT in eosinophils of patients, also applicable in screening candidate
XX PT compounds for remedies.
XX PS Example 1; Page 57; 72pp; Japanese.
XX CC The invention relates to a method for examining allergic diseases
XX CC comprises determining the expression level of a gene containing, the
XX CC human cDNA appearing as ABK49633 which has homology with
XX CC acetyltransferases in the eosinophils of a patient and comparing the
XX CC expression level with that in the eosinophils of a healthy individual
XX CC (i.e. differential display). Also included are methods of screening for
XX CC candidate compounds which affect the expression level of the gene or the
XX CC activity of the protein encoded by the gene (including related proteins
XX CC and mutants), the use of probes based on the gene sequence in the
XX CC examination of allergic diseases, the use of reporter constructs in the
XX CC screening of candidate compounds, a vector containing a the transcription
XX CC -controlling region of the gene, cells transformed with the vector, an
XX CC antibody against the protein and a model animal for allergic diseases
XX CC which is a transgenic non-human vertebrate with lowering of expression
XX CC intensity of the gene in eosinophils. The method is examining allergic
XX CC diseases particularly atopic dermatitis which is also applicable in
XX CC screening candidate compounds for remedies. Such method can be performed
XX CC in high throughput, at low cost. The present sequence is a differential
XX CC display PCR primer for the cDNA encoding the human acetyltransferase-like
XX CC protein 20-90-05
XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 447
ABK49635/c
ID ABK49635 standard; DNA; 17 BP.
XX AC ABK49635;
XX DT 15-JUL-2002 (first entry)
XX DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.
XX KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
XX KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15C.
XX OS Homo sapiens.
XX PN WO200224903-A1.
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```
XX XX 28-MAR-2002.
XX PD
XX PF 21-SEP-2001; 2001WO-JP008246.
XX PR 25-SEP-2000; 2000JP-00291318.
XX PR (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PA (EISA ) EISAI CO LTD.
XX PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
XX PI Takahashi E;
XX DR WPI; 2002-315738/35.
XX PT Examining allergic diseases by differential display of gene showing
XX PT different expression particularly increased expression in remission stage
XX PT in eosinophils of patients, also applicable in screening candidate
XX PT compounds for remedies.
XX PS Example 1; Page 56; 72pp; Japanese.
XX CC The invention relates to a method for examining allergic diseases
XX CC comprises determining the expression level of a gene containing, the
XX CC human cDNA appearing as ABK49633 which has homology with
XX CC acetyltransferases in the eosinophils of a patient and comparing the
XX CC expression level with that in the eosinophils of a healthy individual
XX CC (i.e. differential display). Also included are methods of screening for
XX CC candidate compounds which affect the expression level of the gene or the
XX CC activity of the protein encoded by the gene (including related proteins
XX CC and mutants), the use of probes based on the gene sequence in the
XX CC examination of allergic diseases, the use of reporter constructs in the
XX CC screening of candidate compounds, a vector containing a the transcription
XX CC -controlling region of the gene, cells transformed with the vector, an
XX CC antibody against the protein and a model animal for allergic diseases
XX CC which is a transgenic non-human vertebrate with lowering of expression
XX CC intensity of the gene in eosinophils. The method is examining allergic
XX CC diseases particularly atopic dermatitis which is also applicable in
XX CC screening candidate compounds for remedies. Such method can be performed
XX CC in high throughput, at low cost. The present sequence is a differential
XX CC display PCR primer for the cDNA encoding the human acetyltransferase-like
XX CC protein 20-90-05
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 448
ABL59040/c
ID ABL59040 standard; DNA; 17 BP.
XX AC ABL59040;
XX DT 20-AUG-2002 (first entry)
XX DE Nucleotide sequence of PCR primer GT15G.
XX KW Human; allergosis; eosinophil; PCR; primer; ss.
XX OS Homo sapiens.
XX PN JP2002095500-A.
XX XX 02-APR-2002.
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PF 25-SEP-2000; 2000JP-00291316.
 XX
 PR 25-SEP-2000; 2000JP-00291316.
 XX
 PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
 PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
 XX
 XX WPI; 2002-439993/47.
 DR
 XX Examining allergosis, involves measuring the expression levels of a
 PT specific gene, and comparing it to the levels in the eosinophils of a
 PT healthy control.
 XX
 XX Example 1; Page 17; 20pp; Japanese.
 PS
 CC The specification describes a method for examining allergosis. The method
 CC comprises measuring the expression level of the gene given in ABL59037,
 CC and comparing it with the expression level of the gene in the eosinophils
 CC of a healthy person. The method is used for the examination of
 CC allergosis. The present sequence represents a PCR primer, which is used
 CC in the course of the invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 RESULT 449
 ABL59039/c
 ID ABL59039 standard; DNA; 17 BP.
 XX
 AC ABL59039;
 XX
 XX 20-AUG-2002 (first entry)
 DT
 XX Nucleotide sequence of PCR primer GT15C.
 DE
 XX Human; allergosis; eosinophil; PCR; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX JP2002095500-A.
 PN
 XX 02-APR-2002.
 PD
 XX 25-SEP-2000; 2000JP-00291316.
 PF
 XX 25-SEP-2000; 2000JP-00291316.
 PR
 XX (GENO-) GENOX SOYAKU KENKYUSHO KK.
 PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
 PA
 XX WPI; 2002-439993/47.
 DR
 XX Examining allergosis, involves measuring the expression levels of a
 PT specific gene, and comparing it to the levels in the eosinophils of a
 PT healthy control.
 XX
 XX Example 1; Page 17; 20pp; Japanese.
 PS
 CC The specification describes a method for examining allergosis. The method
 CC comprises measuring the expression level of the gene given in ABL59037,
 CC and comparing it with the expression level of the gene in the eosinophils
 CC of a healthy person. The method is used for the examination of
 CC allergosis. The present sequence represents a PCR primer, which is used
 CC in the course of the invention
 XX

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 RESULT 450
 ABN99831/c
 ID ABN99831 standard; DNA; 17 BP.
 XX
 AC ABN99831;
 XX
 DT 15-AUG-2002 (first entry)
 DT
 XX Human allergic disease related PCR primer SEQ ID NO: 20.
 DE
 XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
 KW primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200233069-A1.
 PN
 XX 25-APR-2002.
 PD
 XX 28-SEP-2001; 2001WO-JP008574.
 PF
 XX 13-OCT-2000; 2000JP-00314093.
 PR
 XX (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 PA
 XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
 PI WPI; 2002-372311/40.
 DR
 XX Method for examining allergic diseases by differential display of
 PT seventeen genes showing different expression particularly significant
 PT increase in eosinophils in patients with mild atopic dermatitis, also
 PT applicable in screening compounds.
 XX
 XX Example 1; Page 110; 165pp; Japanese.
 PS
 CC The present invention relates to a method for examining allergic diseases
 CC which involves determining the expression level of a gene, having one of
 CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
 CC eosinophils in a patient and comparing the expression level with that in
 CC the eosinophils of a healthy individual. The method can be used to
 CC examine allergic diseases, particularly atopic dermatitis, and its early
 CC diagnosis, which is also applicable in screening candidate compounds for
 CC remedies. The present sequence is a PCR primer described in the
 CC exemplification of the invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 RESULT 451
 ABN99830/c
 ID ABN99830 standard; DNA; 17 BP.
 XX

XX The present invention relates to a method of examining allergic diseases
 CC which comprises comparing the expression level of gene B1153 in allergy
 CC patients with the expression level in healthy subjects. The method is
 CC useful for the treatment, prevention, diagnosis and study of allergic
 CC diseases including atopic skin inflammation and asthma. The present
 CC sequence is a PCR primer described in the exemplification of the
 CC invention
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 |||||
 RESULT 454
 AAL47236/c
 ID AAL47236 standard; DNA; 17 BP.
 XX
 AC AAL47236;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Allergic disease examination method related anchor primer SEQ ID NO: 4.
 XX
 DE Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
 KW atopic dermatitis; human; PCR; primer; ss.
 KW
 XX Unidentified.
 OS
 XX
 PN WO200233122-A1.
 XX
 PD 25-APR-2002.
 XX
 XX 11-OCT-2001; 2001WO-JP008937.
 XX
 PR 13-OCT-2000; 2000JP-00314093.
 XX
 PA (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 PA (EISA) EISAI CO LTD.
 XX
 PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
 PI Takahashi E;
 PI
 DR WPI; 2002-372313/40.
 XX
 PD 25-APR-2002.
 XX
 PF 11-OCT-2001; 2001WO-JP008937.
 XX
 PR 13-OCT-2000; 2000JP-00314093.
 XX
 PA (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 PA (EISA) EISAI CO LTD.
 XX
 PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
 PI Takahashi E;
 PI
 DR WPI; 2002-372313/40.
 XX
 XX Method for examining allergic diseases by differential display of
 FT intersectin 2 gene showing different expression particularly significant
 PT increase in eosinophils in patients.
 XX
 PS Example 1; Page 53; 90pp; Japanese.
 XX
 CC The present invention relates to a method for examining allergic diseases
 CC with intersectin 2 gene or a gene with equivalent function of intersectin
 CC 2 as an indicator gene, which comprises determining the expression level
 CC of the gene in the eosinophils in a patient, and comparing the expression
 CC level with that in the eosinophils of a healthy individual. The method is
 CC for examining allergic diseases, particularly atopic dermatitis, which is
 CC also applicable in screening candidate compounds for remedies. The
 CC present sequence is an anchor primer described in the exemplification of
 CC the invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 |||||
 RESULT 455
 AAL47235/c
 ID AAL47235 standard; DNA; 17 BP.
 XX
 AC AAL47235;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Allergic disease examination method related anchor primer SEQ ID NO: 3.
 DE Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
 KW atopic dermatitis; human; PCR; primer; ss.
 KW
 XX Unidentified.
 OS
 XX
 PN WO200233122-A1.
 XX
 PD 25-APR-2002.
 XX
 XX 11-OCT-2001; 2001WO-JP008937.
 XX
 PR 13-OCT-2000; 2000JP-00314093.
 XX
 PA (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 PA (EISA) EISAI CO LTD.
 XX
 PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
 PI Takahashi E;
 PI
 DR WPI; 2002-372313/40.
 XX
 PD 25-APR-2002.
 XX
 PF 11-OCT-2001; 2001WO-JP008937.
 XX
 PR 13-OCT-2000; 2000JP-00314093.
 XX
 PA (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 PA (EISA) EISAI CO LTD.
 XX
 PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
 PI Takahashi E;
 PI
 DR WPI; 2002-372313/40.
 XX
 XX Method for examining allergic diseases by differential display of
 FT intersectin 2 gene showing different expression particularly significant
 PT increase in eosinophils in patients.
 XX
 PS Example 1; Page 53; 90pp; Japanese.
 XX
 CC The present invention relates to a method for examining allergic diseases
 CC with intersectin 2 gene or a gene with equivalent function of intersectin
 CC 2 as an indicator gene, which comprises determining the expression level
 CC of the gene in the eosinophils in a patient, and comparing the expression
 CC level with that in the eosinophils of a healthy individual. The method is
 CC for examining allergic diseases, particularly atopic dermatitis, which is
 CC also applicable in screening candidate compounds for remedies. The
 CC present sequence is an anchor primer described in the exemplification of
 CC the invention
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 |||||
 RESULT 456
 ABK49757/c
 ID ABK49757 standard; DNA; 17 BP.
 XX
 AC ABK49757;
 XX
 DT 15-JUL-2002 (first entry)
 XX

```
DE Human atopic dermatitis cDNA related PCR primer GT15c.
XX
XX Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; GT15c.
XX
XX Synthetic.
OS
XX WO200226962-A1.
XX
XX 04-APR-2002.
PD
XX
XX 21-SEP-2001; 2001WO-JP008247.
PF
XX
XX 26-SEP-2000; 2000JP-00293021.
XX
XX (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
PI WPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
XX Example 1; Page 55; 74pp; Japanese.
PS
XX This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15c PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
AAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAA
RESULT 457
ID ABK49758/c
XX ABK49758 standard; DNA; 17 BP.
XX
XX ABK49758;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Human atopic dermatitis cDNA related PCR primer GT15g.
DE
XX
XX Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; GT15g.
XX
XX Synthetic.
OS
XX WO200226962-A1.
XX
XX 04-APR-2002.
PD
XX
XX 21-SEP-2001; 2001WO-JP008247.
PF
```

```
XX
XX 26-SEP-2000; 2000JP-00293021.
XX
XX (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
PI WPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
XX Example 1; Page 55; 74pp; Japanese.
PS
XX This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15g PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
AAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAA
RESULT 458
ID AAD44151/c
XX AAD44151 standard; DNA; 17 BP.
XX
XX AAD44151;
AC
XX
XX 13-DEC-2002 (first entry)
DT
XX
XX Oligo-AT PCR primer #2 used to illustrate the method of the invention.
DE
XX
XX Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX
XX Unidentified.
OS
XX
XX US6277571-B1.
PN
XX
XX 21-AUG-2001.
PD
XX
XX 30-SEP-1998; 98US-00163485.
PF
XX
XX 03-OCT-1997; 97US-00943162.
PR
XX 03-OCT-1997; 97US-0108152P.
XX
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
PA
XX
XX Fillmore H, Broadus W, Gillies G;
PI
XX
XX WPI; 2002-412824/44.
DR
XX
XX Sequential consensus region-directed amplification for sorting mixture of
PT
```


PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
 PT 2 samples, useful for disease diagnosis and gene analysis.

XX Example; Fig 1D; 19pp; English.

XX The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
 CC for disease diagnosis and gene analysis. The present sequence is oligo A1
 CC PCR primer used to illustrate the method of the invention

XX Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAAAAAAAAA 1495

DB 17 AAAAAAAAAAAAAA 3

RESULT 459

ID ABX79793/c

XX ABX79793 standard; cDNA; 17 BP.

XX AC ABX79793;

XX DT 17-APR-2003 (first entry)

XX EST polymorphic DNA repeat polynucleotide #118.

XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX Homo sapiens.

XX US6472154-B1.

XX 29-OCT-2002.

XX 31-DEC-1999; 99US-00475947.

XX 31-DEC-1999; 99US-00475947.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Garner HR, Wren JD, Minna JD, Fondon JW;

XX WPI; 2003-208818/20.

XX Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.

XX Example; Col 483; 588pp; English.

XX The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods to identify a
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic

CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs

XX Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAAAAAAAAA 1495

DB 15 AAAAAAAAAAAAAA 1

RESULT 460

ADB04270/c

XX ID ADB04270 standard; DNA; 17 BP.

XX AC ADB04270;

XX DT 20-NOV-2003 (first entry)

XX Human MDZ7 scanning oligonucleotide SEQ ID 5256.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.

XX Homo sapiens.

XX PN EP1281758-A2.

XX PD 05-FEB-2003.

XX PF 30-JUL-2002; 2002EP-00016874.

XX PR 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 5256; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences; MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
| | | | | | | | | | | | | | | | | |
Db 17 AAAAAAAAAAAAAA 3

RESULT 461
ID ABZ61566/c
AC ABZ61566;
XX
XX
DT 21-MAR-2003 (first entry)
XX
DE Human H-Ras DNazyme target #357.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

Claim 58; Page 117; 185pp; English.
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytosstatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX
SQ Sequence 17 BP; 2 A; 4 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1228 CTGCTCAGCCAGGCC 1242
| | | | | | | | | | | | | | | | | |
Db 17 CTGCTCAGCCAGGCC 3

RESULT 462

ABZ64568
ID ABZ64568 standard; RNA; 17 BP.
XX
AC ABZ64568;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HER2 DNazyme substrate #25.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
Claim 4; Page 133; 185pp; English.
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytosstatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX
SQ Sequence 17 BP; 1 A; 12 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CCCCCGCCCCCGCC 104
| | | | | | | | | | | | | | | | | |
Db 3 CCCCCGCCCCCGCC 17

RESULT 463
ADC84469/c
ID ADC84469 standard; DNA; 17 BP.
XX
AC ADC84469;
XX
DT 01-JAN-2004 (first entry)
XX
DE PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 2.
XX
KW Plant blastogenesis; transformation; gene expression; tissue specific;
KW PCR; primer; ss.


```
Query Match      1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
    |||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 466
ID ABN87920/c
XX ABN87920 standard; DNA; 15 BP.
AC ABN87920;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human GSR allele specific oligonucleotide primer SEQ ID NO:39.
XX
KW Human; glutathione reductase; GSR; enzyme; haemolytic anaemia; SNP;
KW gene therapy; antianaemic; polymorphic; single nucleotide polymorphism;
KW primer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 14
FT FT /*tag= a
FT FT /note= "polymorphic base"
XX
PN W020024320-A2.
XX
PD 30-MAY-2002.
XX
XX 13-NOV-2001; 2001WO-US046473.
XX
XX 10-NOV-2000; 2000US-0247202P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
XX Bieglecki KM, Sanchis A, Sausker EA, Sun X;
XX WPI; 2002-471719/50.
XX
PT New genetic variants of Glutathione reductase isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT hemolytic anemia.
XX
PS Claim 14; Page 14; 137pp; English.
XX
CC The present invention describes genetic variants of the human glutathione
CC reductase (GSR) gene (1). (1) has antianaemic activity and can be used in
CC gene therapy. (1) can be used in screening for drugs targeting (1) that
CC are useful for treating haemolytic anaemia. Methods from the present
CC invention can be used for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with GSR activity; for haplotyping, which is also
CC used by the pharmaceutical research scientist to validate GSR as a
CC candidate target for treating a specific condition or disease predicted
CC to be associated with GSR activity, e.g. haemolytic anaemia, and in the
CC design of clinical trials for treating a specific condition of disease
CC associated with GSR activity; and for screening compounds targeting GSR.
CC (1) is useful in studying the expression and function of GSR, and in
CC expressing GSR protein for use in screening for candidate drugs to treat
CC diseases related to GSR activity. (1) is also useful in studying the
CC effect of the variation on the biological activity of GSR as well as on
CC the binding affinity of candidate drugs targeting GSR for the treatment
CC of haemolytic anaemia. The present sequence represents an allele specific
CC oligonucleotide (ASO) primer for the human GSR gene, which is given in
CC the exemplification of the present invention. N.B. The polymorphic base
CC (showing a single nucleotide polymorphism) in the ASO primer is shown
CC using an IUPAC ambiguity code (as given in the present invention)
```

```
XX
SQ Sequence 15 BP; 1 A; 0 C; 0 G; 13 T; 0 U; 0 Other;

Query Match      1.0%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1494
    |||||
Db 15 TAAAAAAAAAAAAA 1

RESULT 467
ID AAT44591/c
XX AAT44591 standard; DNA; 16 BP.
AC AAT44591;
XX
DT 03-JUL-1997 (first entry)
XX
DE Cryptosporidium parvum 18S rRNA gene primer/probe.
XX
KW Cryptosporidium parvum; 18S rRNA; ribosomal RNA; detection; diagnosis;
KW polymerase chain reaction; hybridisation probe; ss.
XX
OS Synthetic.
XX
PN W09634978-A1.
XX
PD 07-NOV-1996.
XX
XX 06-MAY-1996; 96WO-AU000274.
XX
XX 05-MAY-1995; 95AU-00002831.
XX
PA (MACQ-) MACQUARIE RES LTD.
PA (SYDN-) SYDNEY WATER CORP LTD.
XX
PI Vesey G, Veal D, Williams KL, Ashbolt NJ, Dorsch M;
XX WPI; 1996-506178/50.
XX
XX Oligonucleotide for detection of viable Cryptosporidium parvum cells -
XX hybridises with unique sequences in 18S rRNA, useful as probe or primer
XX for PCR amplification.
XX
PS Claim 4; Page 15; 22pp; English.
XX
CC The present sequence is for detecting viable Cryptosporidium parvum cells
CC by hybridising specifically to unique 18S rRNA sequences of C. parvum. It
CC can be used when labelled as a probe or as a primer for PCR amplification
CC of 18S rRNA. It can detect live C. parvum oocysts, or other cells,
CC particularly in water but also in other environmental or clinical samples
CC such as animal or human body fluids or excretions. It does not detect
CC dead cells, because RNA degrades too quickly in such cells, or cells of
CC other Cryptosporidium species that are not pathogenic to humans
XX
SQ Sequence 16 BP; 2 A; 0 C; 1 G; 13 T; 0 U; 0 Other;

Query Match      1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1476 ATGCTAAAAA 1491
    |||||
Db 16 ATACTAAAAA 1

RESULT 468
ID AAX18365/c
XX AAX18365 standard; DNA; 16 BP.
XX
AC AAX18365;
```


CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences

XX Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAA 1495

Db 16 TCAAAAAAAAAAAAAAAAA 1

RESULT 471

AA18366/c

ID AAX18366 standard; DNA; 16 BP.

XX

AC AAX18366;

XX

DT 11-MAY-1999 (first entry)

XX

DE RT-PCR primer of the invention SEQ ID 7.

XX

KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX

OS Synthetic.

XX

PN JP11032765-A.

XX

PD 09-FEB-1999.

XX

PF 18-JUL-1997; 97JP-00208312.

XX

PR 18-JUL-1997; 97JP-00208312.

XX

PA (TAKI) TAKARA SHUZO CO LTD.

XX

DR WPI; 1999-183822/16.

XX

PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.

XX

PS Disclosure; Page 10; 19pp; Japanese.

XX

CC This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta

CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or

CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;

CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene

CC sequences

XX

SQ Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.0%; Score 14.4; DB 1; Length 16;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAA 1495

Db 16 TCAAAAAAAAAAAAAAAAA 1

RESULT 472

AA18367/c

ID AAX18367 standard; DNA; 16 BP.

XX

AC AAX18367;

XX

DT 11-MAY-1999 (first entry)

XX

DE RT-PCR primer of the invention SEQ ID 8.

XX

KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX

OS Synthetic.

XX

PN JP11032765-A.

XX

PD 09-FEB-1999.

XX

PF 18-JUL-1997; 97JP-00208312.

XX

PR 18-JUL-1997; 97JP-00208312.

XX

PA (TAKI) TAKARA SHUZO CO LTD.

XX

DR WPI; 1999-183822/16.

XX

PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.

XX

PS Disclosure; Page 10; 19pp; Japanese.

XX

CC This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta

CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or

CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;

CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene

CC sequences

XX

SQ Sequence 16 BP; 0 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.0%; Score 14.4; DB 1; Length 16;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAA 1496

Db 16 ACAAAAAAAAAAAAAAAA 1

RESULT 473

AA18363/c

ID AAX18363 standard; DNA; 16 BP.

XX

AC AAX18363;

XX

DT 11-MAY-1999 (first entry)

XX

DE RT-PCR primer of the invention SEQ ID 4.

XX

KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX

OS Synthetic.

XX

PN JP11032765-A.

XX

PD 09-FEB-1999.

XX

PF 18-JUL-1997; 97JP-00208312.

XX

PR 18-JUL-1997; 97JP-00208312.

XX

PA (TAKI) TAKARA SHUZO CO LTD.
 XX WPI; 1999-183822/16.
 XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.
 PT
 PS Disclosure; Page 10; 19pp; Japanese.
 XX
 CC This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences
 CC
 XX Sequence 16 BP; 0 A; 1 C; 0 G; 15 T; 0 U; 0 Other;
 SQ
 Query Match 1.0%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 DB 16 AAAAAAAAAAAAAA 1
 RESULT 474
 AAH27758/C
 ID AAH27758 standard; DNA; 16 BP.
 AC AAH27758;
 XX
 XX 15-AUG-2001 (first entry)
 DE Primer used in human LUNX cDNA isolation.
 XX
 XX LUNX; human; cancer; micrometastatic cancer; primer; ss.
 XX Homo sapiens.
 XX
 XX JP2001078772-A.
 XX
 XX 27-MAR-2001.
 XX
 XX 07-SEP-1999; 99JP-00253186.
 XX
 XX 07-SEP-1999; 99JP-00253186.
 XX
 XX (SAKA) OTSUKA PHARM CO LTD.
 XX
 XX WPI; 2001-313367/33.
 XX
 XX Polynucleotide encoding LUNX gene product useful for the detection of cancer especially micrometastatic cancer.
 XX
 XX Example 1; Page 27; 30pp; Japanese.
 XX
 CC This invention relates to the human LUNX protein and the polynucleotide sequence encoding it. The invention includes a vector containing a LUNX polynucleotide, a host cell transformed with the vector, and an antibody that binds to LUNX. The gene can be used for cancer diagnosis and diagnosis of micrometastatic cancer and for the production of the LUNX gene product. The present sequence represents a primer used in the isolation of cDNA encoding human LUNX
 CC
 XX Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
 SQ
 Query Match 1.0%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 DB 16 AAAAAAAAAAAAAA 1
 RESULT 476
 ADE86353
 ID ADE86353 standard; DNA; 16 BP.
 XX
 XX ADE86353;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 Query Match 1.0%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 DB 16 AAAAAAAAAAAAAA 1
 RESULT 476
 ADE86353
 ID ADE86353 standard; DNA; 16 BP.
 XX
 XX ADE86353;
 XX
 XX 29-JAN-2004 (first entry)
 DT

```
XX DE Human PTPN11 PCR primer SEQ ID NO:34.
XX AC
KW Noonan syndrome; protein tyrosine phosphatase 11; PTPN11; mutant;
XX variant; mutation; chromosome 12; enzyme; PCR primer; ss.
XX OS
XX Synthetic.
OS Homo sapiens.
XX PN WO2003029422-A2.
XX PD
XX 10-APR-2003.
XX PF
XX 01-OCT-2002; 2002WO-US031290.
XX PR
XX 01-OCT-2001; 2001US-0326532P.
XX PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX PI Gelb BD, Tartaglia M;
XX XX
XX WPI; 2003-381624/36.
XX
XX Diagnosing and treating Noonan syndrome in a subject using a mutation in
PT a protein tyrosine phosphatase 11 gene with increased expression or
PT activity.
XX
XX Example 4; SEQ ID NO 34; 262pp; English.
XX
XX The present invention describes a method for diagnosing Noonan syndrome
CC in a subject. The method comprises detecting a mutation in the protein
CC tyrosine phosphatase 11 (PTPN11) gene in a subject, where the mutation
CC results in increased PTPN11 expression or activity as compared to
CC control. The human PTPN11 gene is located on chromosome 12, more
CC specifically to 12q24. Also described: (1) a kit for diagnosing Noonan
CC syndrome, comprising an oligonucleotide that specifically hybridises to
CC or adjacent to a site of mutation of a PTPN11 gene that results in
CC increased activity of a PTPN11 protein encoded by the gene or an antibody
CC that specifically recognises a mutation in a PTPN11 protein, and
CC instructions for use; (2) diagnosing Noonan syndrome in a subject,
CC comprising assessing the level of expression or activity of a PTPN11
CC protein in the test subject, and comparing it to the level of expression
CC or activity in a control subject, where an increased expression or basal
CC activity of the PTPN11 protein in the test subject compared to the
CC control is indicative of Noonan syndrome; (3) treating Noonan syndrome in
CC a patient, comprising administering an agent that modulates the
CC expression or activity of a PTPN11 protein in association with a carrier;
CC (4) an isolated PTPN11 variant comprising a mutation resulting in
CC increased level of PTPN11 activity; (5) an isolated cell comprising a
CC vector comprising a nucleic acid encoding the PTPN11 variant of (4),
CC operatively associated with an expression control sequence; (6) an
CC isolated nucleic acid encoding the PTPN11 variant of (4); and (7) an
CC isolated oligonucleotide which specifically hybridises to the nucleic
CC acid of (6). The methods and compositions of the present invention are
CC useful for diagnosing and treating a disorder associated with the
CC aberrant expression and/or activity of the PTPN11 gene, specifically
CC Noonan syndrome. The present sequence represents a PCR primer used in the
CC amplification of human PTPN11, which is given in the exemplification of
XX the present invention.
XX
XX Sequence 16 BP; 0 A; 12 C; 4 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 16;
XX Best Local Similarity 93.8%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 221 CCGCGCGCGCGCGCGCG 236
XX
XX 1 CCGCGCGCGCGCGCGCG 16
XX
XX RESULT 477
XX AAAA7676/c
```

```
ID AAAA7676 standard; cDNA; 15 BP.
XX
AC AAAA7676;
XX
XX 08-NOV-2000 (first entry)
DT
XX
XX Oligo d(T) primer for human DDAH1.
DE
XX
XX Dimethylarginine dimethylaminohydrolase; DDAH; DDAH1; DDAH2;
KW arginine deaminase; hyperlipidemia; renal failure; hypertension;
KW restenosis; atherosclerosis; schizophrenia; multiple sclerosis; cancer;
KW ischemia reperfusion injury; septic shock; multi organ failure;
KW arthritis; skin disorders; inflammatory cardiac disease; migraine;
KW infection; ss.
XX
XX Homo sapiens.
OS
XX WO200044888-A2.
XX PN
XX
XX 03-AUG-2000.
PD
XX
XX 26-JAN-2000; 2000WO-GB000226.
PF
XX
XX 26-JAN-1999; 99GB-00001705.
XX PR
XX 04-JUN-1999; 99GB-00013066.
XX
XX (UNLO ) UNIV COLLEGE LONDON.
PA
XX
XX Vallance PJT, Leiper JM, Whitley GSJ, Charles IG;
XX WPI; 2000-543392/49.
XX
XX Novel methylarginase polypeptides and polynucleotides, used to identify
PT modulators of them, which are used in the treatment of e.g. cancer,
PT hypertension, and bacterial infections.
XX
XX Example 1; Page 33; 68pp; English.
XX
XX Nucleotides encoding methylarginase polypeptides, vectors comprising
CC these nucleotides and the polypeptides themselves can be used in
CC medicaments for the treatment of hyperlipidemia, renal failure,
CC hypertension, restenosis after angioplasty, atherosclerosis,
CC complications of heart failure, schizophrenia, multiple sclerosis or
CC cancer. Modulators of the enzyme can be used in medicaments for the
CC treatment of ischemia-reperfusion injury of the brain or heart, cancer,
CC lethal hypertension in severe inflammatory conditions such as septic
CC shock or multi-organ failure, or local and systemic inflammatory
CC disorders including arthritis, skin disorders, inflammatory cardiac
CC disease, migraine, or microbial or bacterial infection. The sequence of
CC human DDAH1 was obtained by data base searching. The EST's used in the
CC process are given in GENESEQ records AAA47661-A47677
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
XX
XX Query Match 0.9%; Score 14.2; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 2.4e+02;
XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1480 TAAAAAATAAAAAA 1494
XX :|||||
XX 15 BAAAAAATAAAAAA 1
XX
XX RESULT 478
XX AAD44150
XX ID AAD44150 standard; DNA; 15 BP.
XX
XX AAD44150;
AC
XX
XX 13-DEC-2002 (first entry)
DT
XX
XX Oligo-AT PCR primer #1 used to illustrate the method of the invention.
DE
XX
```


KW Sequential consensus region-directed amplification; gene expression; PCR;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
 KW primer; ss.
 XX Unidentified.
 XX US6277571-B1.
 XX 21-AUG-2001.
 XX 30-SEP-1998; 98US-00163485.
 XX 03-OCT-1997; 97US-00943162.
 PR 03-OCT-1997; 97US-0108152P.
 XX (UVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
 XX Fillmore H, Broadus W, Gillies G;
 XX WPI; 2002-412824/44.
 XX Sequential consensus region-directed amplification for sorting mixture of
 PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
 PT 2 samples, useful for disease diagnosis and gene analysis.
 XX Example; Fig 1D; 19pp; English.
 XX The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
 CC for disease diagnosis and gene analysis. The present sequence is oligo AT
 CC PCR primer used to illustrate the method of the invention
 XX Sequence 15 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
 SQ Query Match 0.9%; Score 14.2; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 2.4e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 1 AAAAAAAAAAAAAA 15
 RESULT 479
 AAX18387/c
 ID AAX18387 standard; DNA; 15 BP.
 AC AAX18387;
 XX 11-MAY-1999 (first entry)
 DT RT-PCR primer of the invention SEQ ID 28.
 DE RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 KW Synthetic.
 XX JPI1032765-A.
 XX 09-FEB-1999.
 XX 18-JUL-1997; 97JP-00208312.
 XX 18-JUL-1997; 97JP-00208312.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX WPI; 1999-183822/16.
 XX Peptides having at least two new nucleotides - useful as primers in RT-

PT PCR.
 XX Example 1; Page 12; 19pp; Japanese.
 CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 XX sequences
 SQ Sequence 16 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 2 Other;
 Query Match 0.9%; Score 14.2; DB 1; Length 16;
 Best Local Similarity 93.3%; Pred. No. 2.7e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAAAAAAAAA 1494
 Db 15 BAAAAAAAAAAAAA 1
 RESULT 480
 AAX333508
 ID AAX333508 standard; DNA; 14 BP.
 AC AAX333508;
 XX 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX Sequence of microsatellite from clone AGLA206.
 DE PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX Bos taurus.
 XX WO9213102-A1.
 XX 06-AUG-1992.
 XX 15-JAN-1992; 92WO-US000340.
 XX 15-JAN-1991; 91US-00642342.
 XX (GENM-) GENMARK.
 XX Georges M, Massey JM;
 XX WPI; 1992-284684/34.
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.
 XX Table 7; Page 131; 517pp; English.
 CC The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a genomic library of bovine MboI DNA fragments of between 250
 CC and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of
 CC 50 clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.

CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494
 Db 1 AAAAAAAAAAAAAA 14

RESULT 481

AAT36896/C
 ID AAT36896 standard; DNA; 14 BP.

XX AC AAT36896;

XX DT 23-OCT-1996 (first entry)

XX DE Candida albicans leukotriene A4 hydrolase cDNA PCR primer.

XX KW Leukotriene A4 hydrolase; pro-inflammatory; reduced;
 KW 5,6-dihydroxy-7,9,11,14-eicosatetraenoic acid; immune response;
 KW expression vector; recombinant production; antibody generation;
 KW diagnostic agent; passive immunisation; vaccine; treatment; prevention;
 KW infection; reagent; detection; modulation; inflammatory response;
 KW antisense; prevention; PCR; primer; polymerase chain reaction; ss.

XX OS Synthetic.

XX PN US5529916-A.

XX PD 25-JUN-1996.

XX PF 01-NOV-1994; 94US-00332838.

XX PR 01-NOV-1994; 94US-00332838.

XX PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX PI Falkow S, Cormack BP;

XX DR WPI; 1996-308739/31.

XX PT Recombinant DNA encoding yeast leukotriene A4 hydrolase - and related
 PT vectors and transformed cells, producing yeast hydrolase useful, e.g. as
 PT vaccine against Candida infection and as diagnostic reagent.

XX PS Example 1; Col 23-24; 24pp; English.

XX CC The present sequence is a primer for the C. albicans leukotriene A4
 CC (LTA4) hydrolase, cDNA. The hydrolase converts LTA4 to (probably) 5,6-
 CC dihydroxy-7,9,11,14-eicosatetraenoic acid, which is less pro-inflammatory
 CC than the LTB4 produced by the mammalian enzyme, therefore reducing the
 CC immune response to C. albicans. An expression vector contg. the hydrolase
 CC cDNA can be used to produce the hydrolase, which can be used to generate
 CC antibodies (as diagnostic agents, or for passive immunisation), as a
 CC vaccine to treat or prevent Candida infection, as a reagent to detect
 CC antibodies and to reduce/modulate an inflammatory response by systemic or
 CC topical application. Nucleic acid antisense to the hydrolase cDNA may
 CC prevent hydrolase expression

XX SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1479 CTAATAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAA 1

RESULT 482

AAT75017/C
 ID AAT75017 standard; DNA; 14 BP.

XX AC AAT75017;

XX DT 06-OCT-1997 (first entry)

XX DE Breast tumour cDNA primer (T)12AG.

XX KW Breast cancer; tumour; B18Ag1; prognosis; diagnosis; vaccine; retrovirus;
 KW polymerase chain reaction; PCR; primer; ss.

XX OS Synthetic.

XX PN W09725431-A1.

XX PD 17-JUL-1997.

XX PF 10-JAN-1997; 97WO-US000398.

XX PR 10-JAN-1996; 96US-00587329.

XX PA (CORI-) CORIXA CORP.

XX PI Frudakis TN, Smith JM;

XX DR WPI; 1997-384982/35.

XX PT Endogenous human tumour-associated retroviral element, B18Ag1 - used for
 PT the prognosis, diagnosis and monitoring of human cancers, especially
 PT breast cancer.

XX PS Example 3; Page 21; 74pp; English.

XX CC Primer (T)12AG (AAT75017) is used for first strand cDNA synthesis from
 CC RNA prepd. from human breast tumour tissue. The cDNA can subsequently be
 CC amplified using primers B18Ag1-2 and B18Ag1-3 (see also AAT75013 and
 CC AAT75014) to isolate tumour-associated retroviral element B18Ag1 (see
 CC also AAT75002)

XX SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTAATAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAA 1

RESULT 483

AAX83329/C
 ID AAX83329 standard; DNA; 14 BP.

XX AC AAX83329;

XX DT 31-AUG-1999 (first entry)

XX DE Breast cancer tumour specific cDNA anchored primer.

XX KW Breast cancer; tumour; gene expression; genome; diagnosis; mammal;
 KW human endogenous retrovirus; vaccine; primer; PCR; amplification; ss.
 XX OS Synthetic.

```

OS Homo sapiens.
XX WO9725426-A2.
XX
XX
XX
XX 17-JUL-1997.
XX
XX 10-JAN-1997; 97WO-US0000485.
XX
XX 11-JAN-1996; 96US-00585392.
XX
XX 20-AUG-1996; 96US-00700014.
XX
XX (CORI-) CORIXA CORP.
XX
XX Prudakis TN, Smith JM, Reed SG;
XX WPI; 1997-372865/34.
XX
XX
XX Breast cancer-related DNA from retrovirus antigen (s) - useful for
XX diagnosis and treatment of breast cancer.
XX
XX Example 1; Page 24; 221pp; English.
XX
XX Primers AAX83286-X83329 were used to PCR amplify breast cancer tumour
XX specific clones (AAX83201-X83285 and AAX83331-X83415) which are expressed
XX from a genomic region containing a human endogenous retrovirus
XX (AAX83330). Detection of the clone sequences allows determination of the
XX presence of breast cancer in a mammal. Progression of breast cancer can
XX be monitored by detecting the level of clone expression. Polypeptides
XX encoded by the clones can be used in vaccines to inhibit or prevent
XX breast cancer
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Example 1; Page 50; 113pp; English.
XX
XX This is a 3' poly(T) PCR primer used in the amplification of the
XX inducible cytochrome P450RAI gene which specifically metabolises a
XX derivative of the retinoic acid (RA). The cytochrome P450 gene in general
XX produces enzymes involved in the oxidative metabolism of endogenous and
XX exogenous compounds. The cytochrome P450 nucleotide sequence can be used
XX to induce or suppress the expression of its protein. P450RAI is highly
XX induced by RA in cell lines and tissues. This allows for the development
XX of a drug screen using promoters and nucleotide sequences to identify
XX drugs which are useful for reducing the catabolism of RA
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAAGAAAAA 1492
XX DB 14 CTAAGAAAAA 1
XX
XX RESULT 485
XX AAV12221/c
XX ID AAV12221 standard; DNA; 14 BP.
XX
XX AC AAV12221;
XX
XX XX 22-JUN-1998 (first entry)
XX
XX DE Poly(T) oligonucleotide used in differential display PCR.
XX
XX KW Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid;
XX zebrafish; inhibitor; antisense; cancer; actinic keratosis;
XX oral leukoplakia; head tumour; neck tumour;
XX KW non-small cell lung carcinoma; basal cell carcinoma;
XX KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis;
XX therapy; diagnosis; screening; differential display; PCR; primer; ss.
XX
XX OS Synthetic.
XX
XX XX WO9749815-A1.
XX
XX PD 31-DEC-1997.
XX
XX PF 23-JUN-1997; 97WO-CA000440.
XX
XX PR 21-JUN-1996; 96US-00667546.
XX
XX PR 01-OCT-1996; 96US-00724466.
XX
XX XX (TOOH) UNIV QUEENS KINGSTON.
XX
XX PI Petkovich PM, White JA, Beckett BR, Jones G;
XX
XX DR WPI; 1998-077178/07.
XX
XX PT Retinoid metabolising protein - useful to develop products to treat, e.g.
XX cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
XX PT ichthyosis.
XX
XX PS Disclosure; Page 14; 110pp; English.
XX
XX CC Poly(T) oligonucleotides (see AAV12217-28) were used in reverse
XX transcription reactions on poly(A) RNA isolated from the fins of control
XX or retinoic acid-treated zebrafish (Danio rerio). Several combinations of
XX the poly(T) primers were used with degenerate upstream primers (see
XX AAV12229-33) for differential display PCR. Bands demonstrating
XX reproducible differential amplifications were found using the primers
XX given in AAV12221 and AAV12231. This PCR product was reamplified (see

```

CC AAV12234-35). A differential display product (see AAV12213) which
 CC exhibited a dependence on the presence of retinoic acid for its
 CC expression was isolated, and was used to isolate a full-length clone (see
 CC AAV12203) coding for a novel retinoid metabolising protein (see
 CC AAW44159), designated ZP450RA1
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
 |||||
 Db 14 CTAATAAAAAAAAAA 1

RESULT 486
 AAV69039/c
 ID AAV69039 standard; DNA; 14 BP.
 XX
 AC AAV69039;
 XX
 DT 22-JAN-1999 (first entry)
 XX
 DE Human breast tumour RNA anchor primer #1.
 XX
 KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
 KW vaccine; epitope; endogenous; retroviral element; primer; ss.
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9845328-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 09-APR-1998; 98WO-US006939.
 XX
 PR 09-APR-1997; 97US-00838762.
 PR 11-DEC-1997; 97US-00991789.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Frudakis TN, Smith JM, Reed SG;
 XX
 DR WPI; 1998-557473/47.
 XX

XX New DNA sequences isolated from endogenous human retroviral element - and
 PT related vectors, transformed cells, proteins and antibodies, useful for
 PT diagnosis, treatment and prevention of breast cancer.
 XX
 PS Example 1; Page 76; 173pp; English.
 XX
 CC The present sequence represents an anchor primer used to convert normal
 CC breast and tumour RNA to cDNA. The present invention describes nucleotide
 CC sequences which encode human breast cancer specific polypeptides.
 CC Detection or measurement of human breast tumour specific polypeptides and
 CC nucleotide sequences, or the corresponding RNA in a sample, is used for
 CC diagnosis and monitoring of breast cancer. Human breast tumour specific
 CC polypeptides and nucleotide sequences, and the vectors containing the
 CC DNAs, are also useful in vaccines for inhibiting development (for
 CC prevention or therapy) of breast cancer. The polypeptides may also be
 CC used to raise monoclonal antibodies, used as immunoassay reagents
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
 |||||

Db 14 CTAATAAAAAAAAAA 1
 RESULT 487
 AAX02695/c
 ID AAX02695 standard; DNA; 14 BP.
 XX
 AC AAX02695;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Barley HPPD primer #1.
 XX
 KW HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation;
 KW transgenic; plant cell; callus tissue; protoplast; electroporation;
 KW particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
 KW sunflower; tobacco; ss.
 XX
 OS Hordeum vulgare.
 XX
 PN DE19730066-A1.
 XX
 PD 21-JAN-1999.
 XX
 PF 14-JUL-1997; 97DE-01030066.
 XX
 PR 14-JUL-1997; 97DE-01030066.
 XX
 PA (BADI) BASF AG.
 XX
 PI Seuberger H, Lerchl J, Schmidt R, Kurpinska K, Falk J;
 XX
 DR WPI; 1999-096742/09.
 XX

XX DNA encoding barley hydroxyphenylpyruvate dioxygenase - for producing
 PT plants with increased vitamin E content, etc.
 XX
 PS Example 1; Page 9; 26pp; German.
 XX
 CC AAX02695-X02708 are primers used in the isolation of a novel barley
 CC (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This
 CC protein is useful for plant transformation to produce transgenic plants
 CC especially where an expression cassette is introduced into a plant cell,
 CC callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens
 CC transformation, electroporation or particle bombardment and where the
 CC plants are selected from soya, barley, wheat, oilseed rape, maize and
 CC sunflower, or where the DNA is expressed in tobacco plants, especially in
 CC leaves or seeds
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
 |||||
 Db 14 CTAATAAAAAAAAAA 1

RESULT 488
 AAX14689/c
 ID AAX14689 standard; DNA; 14 BP.
 XX
 AC AAX14689;
 XX
 DT 24-MAR-1999 (first entry)
 XX
 DE Triple helix third strand of Esterase D gene nucleotides 962-975.
 XX
 KW Triplex formation; DNA detection; triple helix; identification; bacteria;
 KW oncogene; virus; ss.
 XX

```

OS Synthetic.
OS Homo sapiens.
XX
XX US5861244-A.
XX
XX 19-JAN-1999.
XX
XX 22-DEC-1993; 93US-00173489.
XX
XX 29-OCT-1992; 92US-00968436.
XX
XX (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
XX Hepburn AG, Wang C;
XX WPI; 1999-130384/11.
XX
XX Assay of genetic sequences based on triplex formation from double
XX stranded analyte - and hybrid of anchor and reporter sequences, with
XX reporter released if triplex formation occurs, used e.g. to identify
XX bacteria.
XX
XX Disclosure; Col 15-16; 168pp; English.
XX
XX The present sequence represents a polynucleotide that is able to form a
XX triple helix with a double stranded sequence. Cytosine bases in the
XX present can be replaced with 5-methylcytosine for increased triplex
XX stability. The present sequence is used in the assay of the invention,
XX where it can be part of the anchor DNA or reporter DNA sequence. The
XX assay comprises adding a sample containing double-stranded DNA test
XX sequences to an aqueous medium containing at least one complex of anchor
XX DNA, attached to a solid support, and reporter DNA, where either a part
XX of the anchor DNA or reporter DNA is designed to form a triple-strand
XX structure with part of the test sequence. Triplex formation results in
XX displacement of the reporter DNA which is detected as an indication of
XX the presence of the DNA test sequence. The method is used to detect DNA
XX sequences, particularly for identification of bacteria (by detecting
XX genes for ribosomal RNA) in clinical samples, but also detection of
XX oncogenes and Hepatitis B virus
XX
XX Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1
XXXXXXXXXXXXXXXXXXXX

RESULT 489
AAX14688
ID AAX14688 standard; DNA; 14 BP.
XX
XX AAX14688;
XX
XX 24-MAR-1999 (first entry)
XX
XX Triple helix forming nucleotides 962-975 of Esterase D gene.
XX
XX Triple-helix forming region; Triplex formation; DNA detection;
XX identification; bacteria; oncogene; virus; ds.
XX
XX Homo sapiens.
XX
XX US5861244-A.
XX
XX 19-JAN-1999.
XX
XX 22-DEC-1993; 93US-00173489.
XX
XX 29-OCT-1992; 92US-00968436.
XX
XX (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
XX Hepburn AG, Wang C;
XX WPI; 1999-130384/11.
XX
XX Assay of genetic sequences based on triplex formation from double
XX stranded analyte - and hybrid of anchor and reporter sequences, with
XX reporter released if triplex formation occurs, used e.g. to identify
XX bacteria.
XX
XX Disclosure; Col 15-16; 168pp; English.
XX
XX The present sequence represents a potential triple-helix forming region.
XX It can be used to demonstrate the assay of the invention. The assay
XX comprises adding a sample containing double-stranded DNA test sequences,
XX e.g. containing the present sequence, to an aqueous medium containing at
XX least one complex of anchor DNA, attached to a solid support, and
XX reporter DNA, where either a part of the anchor DNA or reporter DNA is
XX designed to form a triple-strand structure with part of the test
XX sequence. Triplex formation results in displacement of the reporter DNA
XX which is detected as an indication of the presence of the DNA test
XX sequence. The method is used to detect DNA sequences, particularly for
XX identification of bacteria (by detecting genes for ribosomal RNA) in
XX clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
XX Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1481 AAAAAAAAAAAAAA 1494
Db 1 AAAAAAAAAAAAAA 14
XXXXXXXXXXXXXXXXXXXX

RESULT 490
AAX57019/C
ID AAX57019 standard; DNA; 14 BP.
XX
XX AAX57019;
XX
XX 19-JUL-1999 (first entry)
XX
XX WO9923258 oligonucleotide primer 1.
XX
XX Visual; nucleic acid detection; target; hybridisation; probe; primer;
XX agglutination; bridging molecule; ss.
XX
XX Synthetic.
XX
XX WO9923258-A1.
XX
XX 14-MAY-1999.
XX
XX 30-OCT-1998; 98WO-US023267.
XX
XX 31-OCT-1997; 97US-0063969P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Weisburg WG, Stull PD, Reshatoff MR;
XX WPI; 1999-326994/27.
XX
XX Optical detection of hybridization complexes for specific target nucleic
XX acid sequences.
XX
XX Example 1; Page 40; 46pp; English.
XX
XX This invention describes a novel method for the visual detection of

```

CC target nucleic acid presence in a sample. A preferred target is a
 CC Mycobacterium complex nucleic acid sequence. The detection method uses
 CC visual detection of a change in the hybridization without aid of
 CC instrumentation. Multiple copies of a target nucleic acid sequence are
 CC mixed with first and second detectable probes under hybridizing
 CC conditions favouring particle agglutination via a bridging molecule
 CC allowing for visual detection of the target nucleic acid sequence. The
 CC bridging molecule enhances or inhibits formation of a hybridization
 CC complex
 XX
 SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
 Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1494
 Db 14 AAAAAAAAAAAAAA 1
 RESULT 491
 AAX19468/c
 ID AAX19468 standard; DNA; 14 BP.
 XX
 AC AAX19468;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Human senescence factor p23 T12 anchor primer SEQ ID NO:10.
 XX
 DE Human; senescence factor; p23; cancer; persistent inflammation;
 KW proliferative disorder; degenerative disorder; primer; ss.
 KW
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX W09907893-A1.
 XX
 PD 18-FEB-1999.
 XX
 XX 05-AUG-1998; 98WO-US016343.
 PF
 XX 08-AUG-1997; 97US-00908873.
 PR
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX
 XX Swisselhm K, Hosier S, Kubbies M;
 PI
 XX WPI; 1999-167454/14.
 DR
 XX
 PT Newly isolated nucleic acid molecule (designated p23) encoding a p23
 PT polypeptide - useful for inducing a senescence phenotype in a cell.
 XX
 XX Example 1; Page 18; 44pp; English.
 PS
 XX
 CC The present invention describes human senescence factor p23. An
 CC expression vector for p23 is useful for inducing a senescent phenotype in
 CC a cell (preferably eukaryotic). This may help in regulating diseases,
 CC including cancer, persistent inflammation, and various proliferative and
 CC degenerative disorders. These transgenic cells are useful in gene therapy
 CC for treating cancer, particularly where antisense oligonucleotides are
 CC useful for blocking normal or mutant p23 expression in cancer cells or
 CC other proliferating cells. Transgenic cells are also useful for producing
 CC the p23 polypeptide in large quantities. The antibodies are useful for
 CC raising antiserum against p23, and for identifying senescent cells in
 CC culture and tissue biopsies. The p23 polynucleotides are useful for
 CC modulating or altering p23 activity in a cell, and for identifying and
 CC isolating the whole gene encoding p23, and variants of p23. Assays based
 CC on p23 elements, which detect p23 levels and activity are useful as
 CC diagnostic markers for staging tumours, determining prognosis, and/or
 CC predicting therapeutic success. These elements also provide an assay for
 CC detecting chromosomal rearrangements in chromosome 3 in a human cell. The

CC isolation of the p23 polynucleotide permits the manipulation of malignant
 CC growth in cancer. The present sequence represents a primer used in an
 CC example from the present invention
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
 Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1479 CTAATAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAA 1
 RESULT 492
 AAZ08326/c
 ID AAZ08326 standard; DNA; 14 BP.
 XX
 AC AAZ08326;
 XX
 DT 13-OCT-1999 (first entry)
 XX
 DE Human lung tumour RNA conversion primer (dT)12AG anchored 3' primer.
 XX
 DE Human; lung tumour protein; therapy; diagnosis; lung cancer; vaccine;
 KW immunotherapy; detection; inhibition; primer; ss.
 KW
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX W09938973-A2.
 PN
 XX 05-AUG-1999.
 PD
 XX 26-JAN-1999; 99WO-US001642.
 PF
 XX 28-JAN-1998; 98US-00015022.
 PR
 XX 28-JAN-1998; 98US-00015029.
 PR
 XX 18-MAR-1998; 98US-00040828.
 PR
 XX 18-MAR-1998; 98US-00040831.
 PR
 XX 23-JUL-1998; 98US-00122191.
 PR
 XX 23-JUL-1998; 98US-00122192.
 PR
 XX 22-DEC-1998; 98US-00219245.
 PR
 XX (CORI-) CORIXA CORP.
 PA
 XX
 XX Reed SG, Lodes MJ, Frudakis TN, Mohamath R;
 PI
 XX WPI; 1999-479187/40.
 DR
 XX
 PT Lung tumor specific polynucleotides for inhibiting the development of
 PT lung cancer.
 XX
 XX Example 1; Page 82; 171pp; English.
 PS
 XX
 CC The present invention describes lung tumour specific polynucleotides and
 CC tumour antigens. AAZ07144 to AAZ07246 and AAZ08301 to AAZ08325 represent
 CC specifically claimed polynucleotides, and AAZ29486 to AAZ29571 represent
 CC amino acid sequences from the present invention. The lung tumour specific
 CC polynucleotides and polypeptides can be used in pharmaceutical
 CC compositions and vaccines to inhibit the development of lung cancer. They
 CC can also be used to detect lung cancer in a patient. Probes and
 CC antibodies derived from the lung tumour sequences are useful in detection
 CC of lung cancer. The present sequence represents a primer used in an
 CC example from the present invention
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
 Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1479 CTAACAAAAA 1492
Db 14 CTAACAAAAA 1

RESULT 493
AAC80852/c
ID AAC80852 standard; DNA; 14 BP.
XX AC AAC80852;
XX AC
DT 13-FEB-2001 (first entry)
XX
DE Human B18Ag1 cDNA anchored 3' PCR primer.
XX
DE Human; breast tumour-specific antigen; cytostatic; vaccine;
KW breast cancer; B18Ag1; B11Ag1; B15Ag1; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200061753-A2.
XX
XX 19-OCT-2000.
XX
XX 07-APR-2000; 2000WO-US009312.
XX
XX 09-APR-1999; 99US-00289198.
XX
XX 28-OCT-1999; 99US-00429755.
XX
XX 23-MAR-2000; 2000US-00534825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
PI WPI; 2000-628403/60.
XX
XX An isolated polypeptide comprising an immunogenic portion of a breast
PT tumour protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient.
XX
XX Example 1; Page 33; 187pp; English.
XX
XX The present sequence is a PCR primer which was used in the isolation of
CC human breast tumour-specific antigens. Methods for the treatment and
CC diagnosis of breast cancer are disclosed. Nucleotide sequences that are
CC preferentially expressed in breast tumour tissue, and the polypeptides
CC encoded by such nucleotide sequences, are used in compositions and
CC vaccines to inhibit the development of cancer, especially breast cancer.
CC The progression of a cancer may be monitored by carrying out detection of
CC tumour-specific antigens at subsequent time points and comparing the
CC results from the different time points. CD4+ and/or CD8+ T-Cells isolated
CC from the cancer patient may be treated with tumour-specific polypeptides,
CC polynucleotides encoding the polypeptides or antigen presenting cells
CC expressing the polypeptides. The cells are then administered to the
CC patient to inhibit development of cancer
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTAACAAAAA 1492
Db 14 CTAACAAAAA 1

RESULT 495
AAC62349/c
ID AAC62349 standard; DNA; 14 BP.
XX AC AAC62349;
XX AC
DT 06-NOV-2000 (first entry)
XX
DE Oligonucleotide #1 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX
KW Conformationally-locked oligonucleotide; antisense inhibitor;
KW bicyclic sugar nucleoside analogue; gene probe; ds.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT modified_base 3
FT /*tag= b
FT /mod_base= OTHER

```

```
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 5
FT /*tag= c
FT /mod_base= OTHER
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 7
FT /*tag= d
FT /mod_base= OTHER
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 9
FT /*tag= e
FT /mod_base= OTHER
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 10
FT /*tag= f
FT /mod_base= OTHER
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 12
FT /*tag= g
FT /mod_base= OTHER
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 14
FT
FT US6083482-A.
FT
FT
FT 04-JUL-2000.
FT
FT 11-MAY-1999; 99US-00309742.
FT
FT 11-MAY-1999; 99US-00309742.
FT (ICNC ) ICN PHARM INC.
FT
FT Wang G;
FT
FT WPI; 2000-451496/39.
FT
FT New conformationally restricted 3',5'-bridged nucleosides and
FT oligonucleotides useful as antisense therapeutics or as gene-specific
FT diagnostics.
FT
FT Example 20; Col 16; 10pp; English.
FT
FT The present sequence is an oligonucleotide containing 3'-C-amino-5' (S) -
FT C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
FT the sequence were incorporated by phosphoramidite chemistry using a DNA
FT synthesiser. Bicyclic sugar nucleosides are conformationally restricted
FT 3',5'-bridged nucleosides which can be used as building blocks for
FT oligonucleotides. Oligonucleotides can be produced that have certain,
FT desired, geometrical shapes and entropy advantages. They may have
FT superior hybridisation to DNA and RNA, and excellent biological
FT stability. The conformationally-modified oligonucleotides may be useful
FT as antisense inhibitors of gene expression or as gene probes, and may
FT therefore be used in antisense therapeutics or gene-specific diagnostics
FT
FT Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
FT
FT Query Match 0.9%; Score 14; DB 1; Length 14;
FT Best Local Similarity 100.0%; Pred. No. 2.3e+02;
FT Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT QY 1481 AAAAAAAAAAAAAA 1494
FT |||||
FT Db 14 AAAAAAAAAAAAAA 1
FT
FT RESULT 496
FT AAD23152/c
FT ID AAD23152 standard; DNA; 14 BP.
FT
FT AC AAD23152;
FT
FT 26-FEB-2002 (first entry)
FT
FT XX
```

```
DE Human lung tumour-specific cDNA synthesising 3' RT-PCR anchored primer.
XX
XX Human; lung tumour protein; immunostimulant; cytostatic; gene therapy;
XX antisense-therapy; vaccine; immune response; lung cancer; RT-PCR primer;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200172295-A2.
XX
XX 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US009991.
XX
XX 29-MAR-2000; 2000US-00538037.
XX 05-JUN-2000; 2000US-00588937.
XX 18-AUG-2000; 2000US-00640878.
XX 22-SEP-2000; 2000US-0234517P.
XX 01-NOV-2000; 2000US-00704512.
XX 14-DEC-2000; 2000US-00738973.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Lodes MJ, Mohamath R, Secrist H, Benson DR, Indrias CV;
XX Henderson RA, Fling SP, Algate PA, Elliot M, Mannion J, Kalos MD;
XX WPI; 2001-639201/73.
XX
XX New human lung-specific polynucleotides and polypeptides for the
XX diagnosis and treatment of disease e.g. lung cancer.
XX
XX Example 1; Page 162; 378pp; English.
XX
XX The invention relates to isolated lung tumour-specific proteins and their
XX corresponding cDNA molecules. Lung tumour-specific proteins and their
XX antigen-presenting cells are useful for stimulating and/or expanding T
XX cells specific for a tumour protein, and for inhibiting the development
XX of cancer. The invention also relates to a composition useful for
XX stimulating an immune response, and for treating cancer. The lung tumour
XX specific oligonucleotide is useful in gene therapy and for diagnosis,
XX detection and treatment of lung cancer. The present DNA sequence is 3' RT
XX (reverse transcriptase)-PCR anchored primer which is used for
XX synthesising human lung tumour-specific cDNA
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAATAAAAAAAAA 1492
XX |||||
XX Db 14 CTAATAAAAAAAAA 1
XX
XX RESULT 497
XX AAF84160/c
XX ID AAF84160 standard; DNA; 14 BP.
XX
XX AC AAF84160;
XX
XX 08-JUN-2001 (first entry)
XX
XX Oligonucleotide #2.
XX
XX Light responsive oligonucleotide; light irradiation; gene therapy; ss.
XX
XX Unidentified.
XX
XX WO200121637-A1.
XX
XX 29-MAR-2001.
XX
```


PF 20-SEP-2000; 2000WO-JP006415.
 XX
 PR 20-SEP-1999; 99JP-00304479.
 XX
 PA (KOMI/) KOMIYAMA M.
 XX
 PI Komiyama M, Asanuma H, Yoshida T;
 XX
 DR WPI; 2001-266061/27.
 XX
 PT Light-responsive oligonucleotides, useful in controlling DNA synthesis
 PT and gene expression, have structural isomerization on irradiation, and
 PT reversible change in melting temperature of the formed double or triple
 PT strands.
 XX
 XX Example 3; Page 20; 43pp; Japanese.
 PS
 XX The present invention relates to light responsive oligonucleotide, which
 CC contain one or more organic groups which can undergo structural
 CC isomerisation upon irradiation at a specific wavelength. The melting
 CC temperature of a double-strand formed by the light-responsive
 CC oligonucleotide, and another oligonucleotide complementary to the light-
 CC responsive oligonucleotide, reversibly changes depending on light
 CC irradiation. The oligonucleotides are useful in biotechnology, e.g. in
 CC controlling DNA elongation, gene expression, amplification and
 CC transcription, and for efficient gene diagnosis and gene therapy. The
 CC present sequence is an oligonucleotide used in the present invention
 XX
 XX Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
 SQ
 Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Example 11; Page 56; 79pp; English.
 PS
 XX The present invention relates to an oligomer comprising L-ribo-
 CC configured Locked Nucleoside Analogues (L-ribo-LNA analogues). The
 CC present sequence is an RNA oligonucleotide. Binding studies of the L-ribo
 CC -LNA analogues towards the present sequence were carried out, to
 CC determine the thermostability of the L-ribo-LNA analogues. The analogs of
 CC the present invention have a variety of uses e.g. in the preparation of
 CC conjugates of the L-ribo-LNA modified oligonucleotides (oligomers)
 XX
 XX Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Example 1; Page 93; 245pp; English.
 PS
 XX The invention relates to novel breast tumour polynucleotides and
 CC polypeptides. The polypeptides and polynucleotides are useful in
 CC pharmaceutical compositions for treating and/or preventing cancer,
 CC particularly breast cancer, and for eliciting an immune response,
 CC may be used as probes or primers for nucleic acid hybridisation, in the
 CC design and preparation of ribozyme molecules for inhibiting expression of
 CC tumour polypeptides and proteins, and in recombinant DNA molecules to
 CC direct expression of a polypeptide in host cells. AAS99570-AAS99888
 CC represent novel human breast cancer protein coding sequences and PCR
 CC primers of the invention
 XX

XX 1481 AAAAAAAAAAAAAA 1494
 Db 1 AAAAAAAAAAAAAA 14
 RESULT 499
 AAS99698/C
 ID AAS99698 standard; DNA; 14 BP.
 XX
 XX AAS99698;
 AC
 XX 12-MAR-2002 (first entry)
 DT
 XX Breast tumour-specific cDNA B18A1, RT-PCR primer.
 DE
 XX Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
 XX tumour; vaccine; immunogenic.
 KW
 XX Homo sapiens.
 OS
 XX WO200190152-A2.
 PN
 XX 29-NOV-2001.
 PD
 XX 22-MAY-2001; 2001WO-US016776.
 PF
 XX 24-MAY-2000; 2000US-00577505.
 PR 08-JUN-2000; 2000US-00590583.
 PR 26-OCT-2000; 2000US-00699295.
 PR 16-MAR-2001; 2001US-00810936.
 XX
 XX (CORI-) CORIXA CORP.
 PA
 XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
 PI Wang A, Skeiky YAW, Harlocker SL, Day CH;
 PI
 XX WPI; 2002-089919/12.
 DR
 XX New breast tumor proteins and polynucleotides encoding them, useful for
 XX treating and/or preventing cancer, particularly breast cancer, and for
 XX eliciting humoral and/or cellular immune response.
 PT
 XX Example 1; Page 93; 245pp; English.
 PS
 XX The invention relates to novel breast tumour polynucleotides and
 CC polypeptides. The polypeptides and polynucleotides are useful in
 CC pharmaceutical compositions for treating and/or preventing cancer,
 CC particularly breast cancer, and for eliciting an immune response,
 CC may be used as probes or primers for nucleic acid hybridisation, in the
 CC design and preparation of ribozyme molecules for inhibiting expression of
 CC tumour polypeptides and proteins, and in recombinant DNA molecules to
 CC direct expression of a polypeptide in host cells. AAS99570-AAS99888
 CC represent novel human breast cancer protein coding sequences and PCR
 CC primers of the invention
 XX

PF 20-SEP-2000; 2000WO-JP006415.
 XX
 PR 20-SEP-1999; 99JP-00304479.
 XX
 PA (KOMI/) KOMIYAMA M.
 XX
 PI Komiyama M, Asanuma H, Yoshida T;
 XX
 DR WPI; 2001-266061/27.
 XX
 PT Light-responsive oligonucleotides, useful in controlling DNA synthesis
 PT and gene expression, have structural isomerization on irradiation, and
 PT reversible change in melting temperature of the formed double or triple
 PT strands.
 XX
 XX Example 3; Page 20; 43pp; Japanese.
 PS
 XX The present invention relates to light responsive oligonucleotide, which
 CC contain one or more organic groups which can undergo structural
 CC isomerisation upon irradiation at a specific wavelength. The melting
 CC temperature of a double-strand formed by the light-responsive
 CC oligonucleotide, and another oligonucleotide complementary to the light-
 CC responsive oligonucleotide, reversibly changes depending on light
 CC irradiation. The oligonucleotides are useful in biotechnology, e.g. in
 CC controlling DNA elongation, gene expression, amplification and
 CC transcription, and for efficient gene diagnosis and gene therapy. The
 CC present sequence is an oligonucleotide used in the present invention
 XX
 XX Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
 SQ
 Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Example 11; Page 56; 79pp; English.
 PS
 XX The present invention relates to an oligomer comprising L-ribo-
 CC configured Locked Nucleoside Analogues (L-ribo-LNA analogues). The
 CC present sequence is an RNA oligonucleotide. Binding studies of the L-ribo
 CC -LNA analogues towards the present sequence were carried out, to
 CC determine the thermostability of the L-ribo-LNA analogues. The analogs of
 CC the present invention have a variety of uses e.g. in the preparation of
 CC conjugates of the L-ribo-LNA modified oligonucleotides (oligomers)
 XX
 XX Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Example 1; Page 93; 245pp; English.
 PS
 XX The invention relates to novel breast tumour polynucleotides and
 CC polypeptides. The polypeptides and polynucleotides are useful in
 CC pharmaceutical compositions for treating and/or preventing cancer,
 CC particularly breast cancer, and for eliciting an immune response,
 CC may be used as probes or primers for nucleic acid hybridisation, in the
 CC design and preparation of ribozyme molecules for inhibiting expression of
 CC tumour polypeptides and proteins, and in recombinant DNA molecules to
 CC direct expression of a polypeptide in host cells. AAS99570-AAS99888
 CC represent novel human breast cancer protein coding sequences and PCR
 CC primers of the invention
 XX

XX 1481 AAAAAAAAAAAAAA 1494
 Db 1 AAAAAAAAAAAAAA 14
 RESULT 498
 AAC83821
 ID AAC83821 standard; RNA; 14 BP.
 XX
 XX AAC83821;
 AC
 XX 28-FEB-2001 (first entry)
 DT
 XX RNA oligonucleotide #1 used in a binding assay.
 DE
 XX L-ribo-configured Locked Nucleoside Analogue; L-ribo-LNA analogue; ss.
 KW
 XX Unidentified.
 OS
 XX WO200066604-A2.
 PN
 XX 09-NOV-2000.
 PD
 XX 04-MAY-2000; 2000WO-DK000225.
 PF
 XX 04-MAY-1999; 99DK-00000603.
 PR 01-SEP-1999; 99DK-00001225.
 PR 11-JAN-2000; 2000DK-00000032.
 XX
 XX (EXIQ-) EXIQON AS.
 PA
 XX Wengel J;
 PI
 XX WPI; 2001-060972/07.
 DR
 XX Oligomers comprising L-ribo-Locked Nucleic Acid (LNA) nucleosides, useful
 PT for therapeutic purposes e.g. in the construction of oligonucleotides, as
 PT substrates for nucleic acids polymerases and in RNA mediated catalytic
 PT processes.
 PT

```
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
  Query Match      0.9%; Score 14; DB 1; Length 14;
  Best Local Similarity 100.0%; Pred. No. 2.3e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 500
ABK46742/c
ID ABK46742 standard; DNA; 14 BP.
AC ABK46742;
XX
XX 05-JUN-2002 (first entry)
DE Human breast tumour-specific cDNA B18Ag1, RT-PCR primer.
XX
XX Human; breast tumour-specific protein; vaccine; breast cancer; primer;
KW ss.
XX
XX Homo sapiens.
XX
XX US6344550-B1.
XX
XX 05-FEB-2002.
XX
XX 17-APR-1998; 98US-00062451.
XX
XX 01-JAN-1996; 96US-00585392.
XX
XX 20-AUG-1996; 96US-00700014.
XX
XX 10-JAN-1997; 97WO-US000485.
XX
XX 09-APR-1997; 97US-00838762.
XX
XX 11-DEC-1997; 97US-00991789.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TN, Smith JM, Reed SG;
XX
XX WPI; 2002-215084/27.
XX
XX Polynucleotide encoding breast-specific tumor polypeptides useful as
PT vaccine for preventing and treating breast cancer in a subject.
XX
XX Example 1; Col 16; 128pp; English.
XX
XX The invention relates to an isolated DNA molecule (I) encoding breast-
CC tumour-specific polypeptides. (I) is useful as a vaccine for preventing
CC and treating breast cancer in a subject. The polypeptide encoded by (I)
CC is used for production of compounds such as antibodies useful in
CC diagnosing and monitoring the progression of breast cancer. ABK46614-
CC ABK46899 represent human breast tumour-specific coding sequences and
CC related PCR primers of the invention
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
  Query Match      0.9%; Score 14; DB 1; Length 14;
  Best Local Similarity 100.0%; Pred. No. 2.3e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 501
ABQ83278/c
ID ABQ83278 standard; DNA; 14 BP.
XX
XX ABQ83278;
AC

SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
  Query Match      0.9%; Score 14; DB 1; Length 14;
  Best Local Similarity 100.0%; Pred. No. 2.3e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
DB 14 AAAAAAAAAAAAAA 1

RESULT 502
ABQ83275/c
ID ABQ83275 standard; DNA; 14 BP.
XX
XX ABQ83275;
AC
XX
XX 18-JAN-2003 (first entry)
DE EGI cDNA tag related oligonucleotide SEQ ID NO:48.
XX
XX cDNA tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
XX Synthetic.
```

```
XX WO200274951-A1.
XX
XX
XX PD 26-SEP-2002.
XX
XX 13-MAR-2002; 2002WO-JP002338.
XX
XX 15-MAR-2001; 2001JP-00073959.
XX
XX (KURE ) KUREHA CHEM IND CO LTD.
XX PA (YAMA/) YAMAMOTO M.
XX PA (YAMA/) YAMAMOTO N.
XX
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX WPI; 2002-759896/82.
XX
XX Construction of cDNA tags for identifying expressed genes with specific
XX linkers and recognition sequences, applicable in gene expression
XX analysis, disease diagnosis and identifying target for gene therapy.
XX
XX Example 1; Page 24; 59pp; Japanese.
XX
XX The present invention describes a method for constructing a cDNA tag for
XX identifying an expressed gene. The method comprises: (a) preparation of
XX complementary deoxyribonucleic acid; (b) producing cDNA fragment by
XX cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX linker Y ligated material; and (e) cleaving the amplification product.
XX The method can be used for the construction of cDNA tags for identifying
XX expressed genes, which is applicable in gene expression analysis, disease
XX diagnosis and identifying target for gene therapy, including the
XX clarification of difference in function or morphology of cells under
XX physiological or pathological conditions. The cDNA or cells for assay can
XX be specifically expressed, with reproducibility and accuracy in the
XX detection of genes. The present sequence represents an expressed gene
XX identification (EGI) cDNA tag related oligonucleotide which is used in an
XX example from the present invention
XX
XX Sequence 14 BP; 1 A; 0 C; 0 G; 13 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1480 TAAAAAATAAAAAA 1493
XX Db |||||
XX 14 TAAAAAATAAAAAA 1
XX
XX RESULT 503
XX ABQ83269
XX ID ABQ83269 standard; DNA; 14 BP.
XX
XX AC ABQ83269;
XX
XX DT 18-JAN-2003 (first entry)
XX
XX DE EGI cDNA tag related oligonucleotide SEQ ID NO:42.
XX
XX cDNA tag; identification; gene expression analysis; linker;
XX expressed gene identification; EGI; ss.
XX
XX OS Synthetic.
XX
XX FN WO200274951-A1.
XX
XX PD 26-SEP-2002.
XX
XX 13-MAR-2002; 2002WO-JP002338.
XX
XX 15-MAR-2001; 2001JP-00073959.
XX
```

```
PA (KURE ) KUREHA CHEM IND CO LTD.
PA PA (YAMA/) YAMAMOTO M.
XX PA (YAMA/) YAMAMOTO N.
XX
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX WPI; 2002-759896/82.
XX
XX Construction of cDNA tags for identifying expressed genes with specific
XX linkers and recognition sequences, applicable in gene expression
XX analysis, disease diagnosis and identifying target for gene therapy.
XX
XX Example 1; Page 24; 59pp; Japanese.
XX
XX The present invention describes a method for constructing a cDNA tag for
XX identifying an expressed gene. The method comprises: (a) preparation of
XX complementary deoxyribonucleic acid; (b) producing cDNA fragment by
XX cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX linker Y ligated material; and (e) cleaving the amplification product.
XX The method can be used for the construction of cDNA tags for identifying
XX expressed genes, which is applicable in gene expression analysis, disease
XX diagnosis and identifying target for gene therapy, including the
XX clarification of difference in function or morphology of cells under
XX physiological or pathological conditions. The cDNA or cells for assay can
XX be specifically expressed, with reproducibility and accuracy in the
XX detection of genes. The present sequence represents an expressed gene
XX identification (EGI) cDNA tag related oligonucleotide which is used in an
XX example from the present invention
XX
XX Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1481 AAAAAAATAAAAAA 1494
XX Db |||||
XX 1 AAAAAAATAAAAAA 14
XX
XX RESULT 504
XX ABS54141/c
XX ID ABS54141 standard; DNA; 14 BP.
XX
XX AC ABS54141;
XX
XX DT 25-NOV-2002 (first entry)
XX
XX DE Oligo-dT primer #2.
XX
XX KW PCR; primer; Zis-SR; neuroendocrine phenotype; diabetes; ss;
XX Parkinson's disease; Alzheimer's disease; neurodegenerative disease;
XX zinc finger splicing with extended Ser-Arg domain; secretory pathway;
XX zinc finger protein.
XX
XX OS Synthetic.
XX
XX FN WO200261082-A2.
XX
XX PD 08-AUG-2002.
XX
XX 29-JAN-2002; 2002WO-CA000101.
XX
XX 29-JAN-2001; 2001US-0264296P.
XX
XX (UYSH ) UNIV SHERBROOKE.
XX
XX Day R;
XX
XX WPI; 2002-682683/73.
XX
XX New Zis-SR nucleic acid molecules and polypeptides, useful for restoring
```

PT or increasing the secretory properties of a cell, or for treating
 PT diseases or conditions associated with a loss of function, e.g. diabetes
 PT or Parkinson's disease.
 XX

PS Disclosure; Page 35; 70pp; English.

XX The invention relates to an isolated nucleic acid molecule, Zis-SR,
 CC encoding a protein involved in the secretory pathway in a cell (or its
 CC homologue or variant) or nucleic acid molecules that hybridise under high
 CC stringency condition to the Zis-SR nucleic acid. Also included are an
 CC isolated polypeptide involved in the formation of secretory granules in
 CC cells comprising the amino acid sequence spanning amino acids 243-310 of
 CC the Zis-SR protein, restoring the neuroendocrine differentiation of a
 CC cell using the nucleic acid molecule or polypeptide cited above,
 CC identifying a gene and/or protein involved in inducing regulated
 CC secretion comprising a comparison at the molecular level of a secretion-
 CC defective cell line under conditions that restore differentiation of the
 CC secretion-defective cell, such that secretion is restored, and the
 CC secretion-defective cell line in the absence of the conditions cited.
 CC Also included are modulating the secretory properties of a cell
 CC comprising modulating the activity and/or level of Zis-SR and an assay to
 CC identify a modulator of regulated secretion in a cell comprising an
 CC assessment of a biological activity of Zis-SR, its part or derivative in
 CC the presence of a candidate agent, where a modulator of regulated
 CC secretion is selected when the biological activity of Zis-SR, its part or
 CC derivative is measurably different in the presence of the candidate
 CC compound as compared in its absence. The nucleic acid molecules or
 CC polypeptides are useful for restoring or increasing the secretory
 CC properties of a cell, for regulating neuroendocrine phenotype, and for
 CC long term therapies to treat diseases or conditions associated with a
 CC loss of function, e.g. diabetes, neurodegenerative diseases such as
 CC Alzheimer's disease or Parkinson's disease. The assay is useful for
 CC screening compounds for treating diseases or conditions associated with a
 CC defect in the regulated secretory pathways in cells. The nucleic acid
 CC molecules can also be used to locate gene regions associated with genetic
 CC diseases. The present sequence is an oligo-dT PCR primer used to isolate
 CC the cDNA encoding mouse Zis-SR (zinc finger splicing with extended Ser-
 CC Arg domain)
 XX

SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
 |||||
 Db 14 CTAATAAAAAAAAAA 1

RESULT 505
 AAD24491/c
 ID AAD24491 standard; DNA; 14 BP.

XX AAD24491;

XX 07-MAR-2002 (first entry)

XX Retinoid-regulated gene isolating poly(T) PCR primer #5.

XX Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
 KW cytochrome P450; prostate cancer; drug screening; PCR primer;
 KW retinoid-regulated gene; ss.

XX Unidentified.

XX US6306624-B1.

XX 23-OCT-2001.

XX 25-JUN-1997; 97US-00882164.

XX 21-JUN-1996; 96US-00667546.

PR 01-OCT-1996; 96US-00724466.
 PR 23-JUN-1997; 97WO-CA000440.

XX (TOOH) UNIV QUEENS KINGSTON.

PI Petkovich PM, White JA, Beckett BR, Jones G;

XX WPI; 2002-033254/04.

XX New DNA fragments having promoter activity, useful in retinoid
 PT metabolism, as well as in producing retinoic acid metabolizing cytochrome
 PT P450s that are useful as targets for the treatment of certain cancers.

PS Disclosure; Col 13; 75pp; English.

XX The present invention relates to retinoid (e.g., retinoic acid (RA),
 CC vitamin A) metabolising proteins and nucleic acid sequences encoding
 CC them. RA metabolising proteins contain a haeme-binding motif which is
 CC characteristic of the group of proteins known as cytochrome P450s. The
 CC sequences of the invention are useful in retinoid metabolism and in
 CC producing retinoic acid metabolising cytochrome P450s. They are
 CC particularly useful as targets for the treatment of certain cancers such
 CC as prostate cancer. The invention also relates to a method of screening
 CC drugs for their effect on activity of RA inducible proteins. The present
 CC DNA sequence is poly(T) PCR primer which is used for isolating retinoid
 CC regulating genes by differential display of mRNAs. Note: This sequence is
 CC incorrectly referred as SEQ ID NO: 6 in column 14 of the specification
 XX

SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
 |||||
 Db 14 CTAATAAAAAAAAAA 1

RESULT 506
 ABA93701/c
 ID ABA93701 standard; DNA; 14 BP.

XX ABA93701;

XX 30-APR-2002 (first entry)

XX Light responsive oligonucleotide (X1)T14.

XX Light responsive; detection; single nucleotide polymorphism; SNP;
 KW irradiation; ss.

XX Synthetic.

XX JP2001346579-A.

XX 18-DEC-2001.

XX 02-JUN-2000; 2000JP-00165441.

XX 02-JUN-2000; 2000JP-00165441.

XX (KOMI/) KOMIYAMA S.

XX (ASAN/) ASANUMA H.

XX WPI; 2002-145181/19.

XX Detecting single nucleotide polymorphism for expressing sensitivity
 PT information of diseases and drugs, comprises using a new oligonucleotide.

XX Example 3; Page 11; 14pp; Japanese.

XX The present invention describes a method for detecting single nucleotide

CC polymorphisms (SNPs). Also described is an oligonucleotide used in the
 CC detection of an SNP, prepared by binding an oligonucleotide having a
 CC complementary sequence or those devoid of up to several bases with 1 or
 CC more organic group(s) to be tested by light irradiation of a specific
 CC wave length to vary a double strand formation property of the
 CC oligonucleotide to be tested. The method is used for detecting SNPs. The
 CC present sequence represents a light responsive oligonucleotide which is
 CC used in an example from the present invention

XX
 SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494
 Db 14 AAAAAAAAAAAAAA 1

RESULT 507
 ABZ23321/c
 ID ABZ23321 standard; DNA; 14 BP.
 XX AC ABZ23321;
 XX DT 07-APR-2003 (first entry)
 XX DE Reverse transcription primer used to produce human cDNA for PCR.
 XX
 KW IRS-1, insulin receptor substrate-1; angiogenesis; capillary tube;
 KW endothelial cell; retinopathy; rheumatoid arthritis; Crohn's disease;
 KW atherosclerosis; ovarian hyperstimulation; psoriasis; endometriosis;
 KW restenosis; wound healing; peripheral vascular disease; hypertension;
 KW vascular inflammation; Raynaud disease; aneurysm; arterial restenosis;
 KW thrombophlebitis; lymphagitis; lymphodema; ischemia; angina;
 KW myocardial infarction; chronic heart disease; macular degeneration;
 KW osteoporosis; cell multiplication; antitumor; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W02002103014-A2.
 XX
 PD 27-DEC-2002.
 XX
 PP 14-JUN-2002; 2002WO-FR002067.
 XX
 PR 14-JUN-2001; 2001FR-00007805.
 XX
 PA (ALMA/) AL-MAHMOOD S.
 XX
 PI Al-Mahmood S;
 XX
 DR WPI; 2003-167520/16.
 XX
 PT Angiogenesis-modifying composition, useful for treatment or diagnosis of
 PT e.g. retinopathy, comprises inhibitor of expression of the insulin
 PT receptor substrate-1 gene.
 XX
 PS Example 1; Page 12; 52pp; French.
 XX
 CC The present sequence represents a primer used to produce human CDNA for
 CC amplification of cDNA encoding IRS-1 (insulin receptor substrate-1). IRS-
 CC 1 is used to produce the compositions of the invention. The specification
 CC describes an angiogenesis-modifying composition, containing at least one
 CC nucleic acid selected from the gene encoding IRS-1 or a molecule that
 CC inhibits expression of that nucleic acid. The composition inhibits the
 CC formation of capillary tubes by endothelial cells. The composition is
 CC used to treat and diagnose diseases associated with angiogenesis,
 CC particularly retinopathy, rheumatoid arthritis, Crohn's disease,
 CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis,
 CC restenosis after balloon angioplasty, overproduction of tissue during
 CC wound healing, peripheral vascular diseases, hypertension, vascular

CC inflammation, Raynaud disease, aneurysm, arterial restenosis,
 CC thrombophlebitis, lymphagitis, lymphodema, ischemia, angina, myocardial
 CC infarction, chronic heart disease, (congestive) cardiac insufficiency,
 CC age-related macular degeneration and osteoporosis. It is also used to
 CC prevent cell multiplication, especially as antitumor agents, and as
 CC research reagents for in vitro or in vivo studies on signalling pathways

XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTAATAAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAAA 1

RESULT 508
 ADAL1209/c
 ID ADAL1209 standard; DNA; 14 BP.
 XX AC ADAL1209;
 XX DT 06-NOV-2003 (first entry)
 XX DE Differential display Oligo-dT primer.
 XX KW ss; PCR; breast cancer; cytostatic; tumour; gene therapy; primer;
 KW differential display.
 XX OS Synthetic.
 XX PN US2002165371-A1.
 XX PD 07-NOV-2002.
 XX PF 07-AUG-2001; 2001US-00924400.
 XX
 PR 11-JAN-1996; 96US-00585392.
 PR 10-JAN-1997; 97WO-US000485.
 PR 09-APR-1997; 97US-00838762.
 PR 11-DEC-1997; 97US-00991789.
 PR 17-APR-1998; 98US-00062451.
 PR 09-APR-1999; 99US-00289198.
 PR 28-OCT-1999; 99US-00429755.
 PR 23-MAR-2000; 2000US-00534825.
 PR 24-MAY-2000; 2000US-00577505.
 PR 08-JUN-2000; 2000US-00590583.
 PR 26-OCT-2000; 2000US-00699295.
 PR 16-MAR-2001; 2001US-00810936.
 XX
 PA (FRUD/) FRUDAKIS T N.
 PA (REED/) REED S G.
 PA (SMIT/) SMITH J M.
 PA (MISH/) MISHNER L E.
 PA (DILL/) DILLON D C.
 PA (RETT/) RETTER M W.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HARL/) HARLOCKER S L.
 PA (DAYC/) DAY C H.
 PA (LISX/) LI S X.
 PA (DENG/) DENG T.
 XX
 PI Prudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
 PI Wang A, Skeiky YAW, Harlocker SL, Day CH, Li SX, Deng T;
 XX
 DR WPI; 2003-247262/24.
 XX
 PT New breast tumor proteins nucleic acids encoding such proteins, useful in
 PT diagnosing, preventing and/or treating diseases such as cancer,
 PT particularly breast cancer, and as markers for detecting the presence of

```

PT a cancer.
XX
PS Example 1; Page 32; 190pp; English.
XX
CC The invention relates to a breast tumour polynucleotide selected from one
CC of the 275 fully defined nucleotide sequences (a) given in the
CC specification, including their complements, sequences consisting of at
CC least 20 contiguous residues of a sequence in (a), sequences that
CC hybridise to a sequence in (a) under moderately stringent conditions,
CC sequences having at least 75% or 90% identity to a sequence in (a), or
CC degenerate variants of a sequence in (a). Also included are an isolated
CC polypeptide (II) (comprising an amino acid sequence selected from
CC sequences encoded by (a), sequences having at least 70% or 90% identity
CC to a sequence encoded by (a), sequences of 30 fully defined amino acid
CC sequences (c), and sequences having at least 70% or 90% identity to a
CC sequence in (c)), expression vectors comprising (a), a host cell
CC transformed or transfected with the expression vector, an isolated
CC antibody or its antigen-binding fragment that specifically binds to (II),
CC a method for detecting the presence of a cancer in a patient, a fusion
CC protein comprising at least one polypeptide (II), an oligonucleotide that
CC hybridises to (a), under moderately stringent conditions, a method for
CC stimulating and/or expanding T cells specific for a tumour protein (by
CC contacting T cells with at least one component selected from (a), (II)
CC and antigen-presenting cells that express (II)), an isolated T cell
CC population comprising T cells prepared from as detailed above, a method
CC for stimulating an immune response or treating cancer in a patient by
CC administering a composition comprising (a), (II), the vector, cells or
CC the antibodies, and a method for inhibiting the development of a cancer
CC in a patient. The polynucleotides may be used in the design and
CC preparation of ribzyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in tumour cells. The breast tumour proteins are
CC useful as markers to indicate the presence or absence of a cancer, such
CC as breast cancer, and in the detection of other cancers. Compositions
CC comprising the breast tumour proteins are useful in diagnosing,
CC preventing and/or treating diseases such as cancer, particularly breast
CC cancer. The present sequence is a differential display random PCR primer
CC used in the isolation of breast cancer specific cDNAs of the invention.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAA 1492
Db 14 CTAAAAAATAAAAA 1

RESULT 509
ADCL5182/c
ID ADC15182 standard; DNA; 14 BP.
XX
AC ADC15182;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human breast tumour protein primer, SEQ ID 130.
XX
KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
KW primer; ss.
XX
OS Homo sapiens.
XX
FN WO2003013431-A2.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024917.
XX
PR 07-AUG-2001; 2001US-00924400.
PR 20-FEB-2002; 2002US-00079137.
PR 02-AUG-2002; 2002US-00212679.

(CORI-) CORIXA CORP.
Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
Kalos MD;
WPI; 2003-342398/32.
New polynucleotide, useful for preparing a composition for diagnosing,
treating or preventing cancer.
Example 1; SEQ ID NO 130; 308pp; English.
The present invention relates to compositions and methods for the therapy
and diagnosis of cancer, particularly breast cancer. The method for
detecting the presence of a cancer in a patient comprises: obtaining a
biological sample from the patient; contacting the biological sample with
a binding agent that binds to the polypeptide; detecting in the sample an
amount of the polypeptide that binds to the binding agent; and comparing
the amount of the polypeptide to a predetermined cut-off value. Treating
breast cancer comprises administering a composition comprising breast
tumour proteins and nucleic acids, which simulates and/or expands T cells
specific for the tumour protein. The present sequence was used to
illustrate the invention.
Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAA 1492
Db 14 CTAAAAAATAAAAA 1

RESULT 510
AD66355/c
ID ADD66355 standard; DNA; 14 BP.
XX
AC ADD66355;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human lung tumour-specific DNA related primer, SEQ ID NO 47.
XX
KW expression control; cancer; T cell; tumour; immune; cytostatic; vaccine;
KW human; lung tumour-specific; PCR; primer; ss.
XX
OS Homo sapiens.
XX
FN WO200292001-A2.
XX
PD 21-NOV-2002.
XX
PF 10-MAY-2002; 2002WO-US014975.
XX
PR 11-MAY-2001; 2001US-00854133.
XX
(CORI-) CORIXA CORP.
Lodes MJ, Wang T, Fan L, Algate PA, Mcneill PD;
WPI; 2003-120592/11.
New polynucleotide and polypeptide, useful for preparing a composition
for diagnosing, treating or preventing cancer.
Example 1; SEQ ID NO 47; 494pp; English.
The invention relates to a novel isolated polynucleotide comprising one
of 32 47-6080 base pair sequences, given in the specification, or their
complements or degenerate variants, at least 20 contiguous residues of a

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CC sequence in, or having at least 75 or 90 % identity with the isolated
 CC polynucleotide, or that hybridise with the polynucleotide. The invention
 CC further comprises: an isolated polypeptide; an expression vector
 CC comprising the polynucleotide operably linked to an expression control
 CC sequence; a host cell transformed or transfected with the expression
 CC vector; an isolated antibody or its antigen-binding fragment that
 CC specifically binds to the polypeptide; a method for detecting the
 CC presence of a cancer in a patient; a fusion protein comprising the
 CC polypeptide; an oligonucleotide that hybridises to the isolated
 CC polynucleotide under moderately stringent conditions; a method for
 CC stimulating and/or expanding T cells specific for a tumour protein; an
 CC isolated T cell population; a composition comprising a first component
 CC consisting of carriers and immunostimulants and a second component; a
 CC method for stimulating an immune response in a patient; a method for
 CC treating cancer in a patient; a method for determining cancer in a
 CC patient; a diagnostic kit comprising at least one oligonucleotide or
 CC antibody and a detection reagent comprising a reporter group; and a
 CC method for inhibiting the development of cancer in a patient. The
 CC compositions of the invention have cytostatic activity and can be used to
 CC create a vaccine. The isolated polynucleotide is useful for preparing a
 CC composition for diagnosing, treating or preventing cancer. This
 CC polynucleotide sequence represents a primer relating to the human lung
 CC tumour-specific cDNA sequences of the invention.

XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTAATAAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAAA 1

RESULT 511
 ADE87609/c
 ID ADE87609 standard; DNA; 14 BP.
 XX
 AC ADE87609;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human lung tumour antigen cDNA PCR primer #1.
 XX
 KW Human; lung tumour antigen; PCR; ss; cancer; lung cancer; CD4+; CD8+;
 KW T cell; immune response; immunostimulant; cytostatic; primer.
 XX
 OS Homo sapiens.
 XX
 PN US2003118599-A1.
 XX
 PD 26-JUN-2003.
 XX
 PF 10-MAY-2002; 2002US-0014649.
 XX
 PR 02-APR-1999; 99US-00285323.
 PR 09-AUG-1999; 99US-00370838.
 PR 30-DEC-1999; 99US-00476235.
 PR 03-MAR-2000; 2000US-00518809.
 PR 29-MAR-2000; 2000US-00538037.
 PR 05-JUN-2000; 2000US-00588937.
 PR 18-AUG-2000; 2000US-00640878.
 PR 20-SEP-2000; 2000US-00657170.
 PR 01-NOV-2000; 2000US-00704512.
 PR 14-DEC-2000; 2000US-00738973.
 PR 11-MAY-2001; 2001US-00854133.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Algate PA, Lodes MJ, Wang T, Fan L, Mcneill PD;
 XX WPI; 2003-897103/82.
 DR

XX New polynucleotides encode lung tumor antigens and are useful to
 PT stimulate an immune response or detect or treat a cancer in a patient,
 PT particularly lung cancer.
 XX
 PS Example 1; SEQ ID NO 47; 63pp; English.
 XX
 CC The invention relates to polynucleotides encoding lung tumour antigens.
 CC The invention also relates to the polypeptides encoded by the
 CC polynucleotides, isolated antibodies or antigen-binding fragments that
 CC specifically bind the polypeptides and a method for detecting cancer in a
 CC patient, comprising obtaining a biological sample from the patient,
 CC contacting the sample with a binding agent that binds a polypeptide of
 CC the invention, detecting in the sample an amount of polypeptide that
 CC binds to the binding agent, and comparing the amount of polypeptide to a
 CC predetermined cut-off value. T cells specific for a tumour protein can be
 CC stimulated and/or expanded by contacting the T cells with a polypeptide,
 CC polynucleotide or an antigen-presenting cell that expresses a
 CC polypeptide. Cancer development can be inhibited by incubating CD4+
 CC and/or CD8+ T cells isolated from a patient with a polypeptide,
 CC polynucleotide or an antigen-presenting cell that expresses a
 CC polypeptide, so that the T cells proliferate. The invention is used to
 CC stimulate an immune response or to detect or treat a cancer in a patient,
 CC particularly lung cancer. This sequence represents a PCR primer used to
 CC amplify human lung tumour antigen cDNA of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html.

SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTAATAAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAAA 1

RESULT 512
 AAT52140/c
 ID AAT52140 standard; RNA; 15 BP.
 XX
 AC AAT52140;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-MAR-1997 (first entry)
 XX
 DE Human ICAM hammerhead ribozyme target sequence (nt. position 2912).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 SS.
 XX
 KW Homo sapiens.
 OS
 XX
 PN W09523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-IB000156.
 XX
 PR 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR

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PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291433.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00293620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Dorenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
XX Ribozyymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 15 BP; 0 A; 1 C; 0 G; 0 T; 14 U; 0 Other;
Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1
RESULT 513
AAAT52134/c
ID AAAT52134 standard; RNA; 15 BP.
XX
AC AAAT52134;
XX
XX 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
XX Human ICAM hammerhead ribozyme target sequence (nt. position 2909).
DE

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XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX ss.
XX Homo sapiens.
XX WO9523225-A2.
XX
XX 31-AUG-1995.
XX
XX 23-FEB-1995; 95WO-IB000156.
XX
XX 23-FEB-1994; 94US-00201109.
XX 29-MAR-1994; 94US-00218934.
XX 04-APR-1994; 94US-00222795.
XX 07-APR-1994; 94US-00224483.
XX 15-APR-1994; 94US-00227958.
XX 15-APR-1994; 94US-00228041.
XX 18-MAY-1994; 94US-00245736.
XX 06-JUL-1994; 94US-00271280.
XX 15-AUG-1994; 94US-00291932.
XX 16-AUG-1994; 94US-00291433.
XX 17-AUG-1994; 94US-00292620.
XX 19-AUG-1994; 94US-00293520.
XX 02-SEP-1994; 94US-00300000.
XX 08-SEP-1994; 94US-00303039.
XX 23-SEP-1994; 94US-00311486.
XX 23-SEP-1994; 94US-00311749.
XX 28-SEP-1994; 94US-00314397.
XX 03-OCT-1994; 94US-00316771.
XX 07-OCT-1994; 94US-00319492.
XX 11-OCT-1994; 94US-00321993.
XX 04-NOV-1994; 94US-00334847.
XX 10-NOV-1994; 94US-00337608.
XX 28-NOV-1994; 94US-00345516.
XX 16-DEC-1994; 94US-00357577.
XX 23-DEC-1994; 94US-00363233.
XX 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Dorenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozyymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 15 BP; 0 A; 1 C; 0 G; 0 T; 14 U; 0 Other;
Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1
RESULT 513
AAAT52134/c
ID AAAT52134 standard; RNA; 15 BP.
XX
AC AAAT52134;
XX
XX 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
XX Human ICAM hammerhead ribozyme target sequence (nt. position 2909).
DE

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CC correct PI field.)

XX Sequence 15 BP; 1 A; 0 C; 0 G; 0 T; 14 U; 0 Other;

SQ

Query Match 0.9%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
 |||||
 Db 15 AAAAAAAAAAAAAA 2

RESULT 514
 AAF49041/c
 ID AAF49041 standard; DNA; 15 BP.
 XX
 AC AAF49041;
 XX
 DT 30-MAR-2001 (first entry)
 DE IGF-I oligonucleotide #1.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 CC Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 60; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or [IGFBP3], which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present invention is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
 |||||
 Db 14 AAAAAAAAAAAAAA 1

RESULT 515
 ABK98169/c
 ID ABK98169 standard; DNA; 15 BP.
 XX
 AC ABK98169;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Triple helix forming associated oligonucleotide #39.
 XX
 KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
 XX
 OS Synthetic.
 XX
 PN US6403302-B1.
 XX
 PD 11-JUN-2002.
 XX
 PF 16-DEC-1993; 93US-00168920.
 XX
 PR 17-SEP-1992; 92US-00946976.
 XX
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 XX
 PI Dervan PB, Beal PA;
 XX
 DR WPI; 2002-536030/57.
 XX
 CC A triple-helix comprising a double helical nucleic acid (DHNA) and an
 CC oligonucleotide which binds in parallel and antiparallel orientation,
 CC respectively, for targeting sequences on alternate strands of DHNA to
 CC control gene expression.
 XX
 PS Example 6; Fig 20A; 108pp; English.
 XX
 CC The present invention relates to methods and oligonucleotides for forming
 CC a triple-helix comprising a double helical nucleic acid comprising first
 CC and second substantially complementary strands, and an oligonucleotide
 CC bound to a purine-rich target sequence within the double helical nucleic
 CC acid, where the oligonucleotide binds in a parallel and antiparallel
 CC orientation, respectively, to target sequences on alternate strands of
 CC the double helical nucleic acid. The method has therapeutic applications,
 CC where gene expression is controlled by selective triple-helix formation
 CC within expression regulatory sequences of a target gene. The
 CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic double-stranded DNA including
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
||||| |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 516
ABK98187/c
ID ABK98187 standard; DNA; 15 BP.

XX ABK98187;

DT 07-OCT-2002 (first entry)

DE Triple helix forming associated oligonucleotide #51.

XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

OS Synthetic.

XX US6403302-B1.

PN 11-JUN-2002.

XX 16-DEC-1993; 93US-00168920.

XX 17-SEP-1992; 92US-00946976.

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX Dervan PB, Beal PA;

XX WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targeting sequences on alternate strands of DHNA to
PT control gene expression.

XX Example 7; Fig 24A; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
||||| |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 517

ABK98168/c
ID ABK98168 standard; DNA; 15 BP.

XX ABK98168;

DT 07-OCT-2002 (first entry)

DE Triple helix forming associated oligonucleotide #38.

XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

OS Synthetic.

XX US6403302-B1.

PN 11-JUN-2002.

XX 16-DEC-1993; 93US-00168920.

XX 17-SEP-1992; 92US-00946976.

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX Dervan PB, Beal PA;

XX WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targeting sequences on alternate strands of DHNA to
PT control gene expression.

XX Example 6; Fig 20A; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention

```

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 518
ABK98167/c
XX ID ABK98167 standard; DNA; 15 BP.
XX AC ABK98167;
XX DT 07-OCT-2002 (first entry)
XX DE Triple helix forming associated oligonucleotide #37.
XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX OS Synthetic.
XX PN US6403302-B1.
XX PD 11-JUN-2002.
XX PF 16-DEC-1993; 93US-00168920.
XX PR 17-SEP-1992; 92US-00946976.
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX PI Dervan PB, Beal PA;
XX WPI; 2002-536030/57.

A triple-helix comprising a double helical nucleic acid (DHNA) and an
oligonucleotide which binds in parallel and antiparallel orientation,
respectively, for targetting sequences on alternate strands of DHNA to
control gene expression.

Example 6; Fig 20A; 108pp; English.

The present invention relates to methods and oligonucleotides for forming
a triple-helix comprising a double helical nucleic acid comprising first
and second substantially complementary strands, and an oligonucleotide
bound to a purine-rich target sequence within the double helical nucleic
acid, where the oligonucleotide binds in a parallel and antiparallel
orientation, respectively, to target sequences on alternate strands of
the double helical nucleic acid. The method has therapeutic applications,
where gene expression is controlled by selective triple-helix formation,
within expression regulatory sequences of a target gene. The
oligonucleotides can be used to form triple-helices, and are useful to
detect the presence or absence of specific sequences within genomic DNA
for diagnostic and therapeutic purposes. The oligonucleotides can be
selected to specifically bind to pathogenic bacteria or viruses for
specific sequences required by pathogenic bacteria or viruses for
replication or virulence, reducing their pathogenicity. Alternatively,
the oligonucleotide can be chosen to target a unique sequence of the
pathogen which is not found in the genome of pathogen's host. The
oligonucleotides can be used in cancer treatment by way of triple-helix
suppression of specific oncogenes including those of endogenous or viral
origin. Such therapeutic oligonucleotides are capable of forming triple-
helices with such sequences in cancerous cells containing the activated
oncogene, so preferentially killing or repressing the cancer causing
cell. The present sequence represents an oligonucleotide used in the

```

```

CC methods of the present invention
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 519
ABK98186/c
XX ID ABK98186 standard; DNA; 15 BP.
XX AC ABK98186;
XX DT 07-OCT-2002 (first entry)
XX DE Triple helix forming associated oligonucleotide #50.
XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX OS Synthetic.
XX PN US6403302-B1.
XX PD 11-JUN-2002.
XX PF 16-DEC-1993; 93US-00168920.
XX PR 17-SEP-1992; 92US-00946976.
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX PI Dervan PB, Beal PA;
XX WPI; 2002-536030/57.

A triple-helix comprising a double helical nucleic acid (DHNA) and an
oligonucleotide which binds in parallel and antiparallel orientation,
respectively, for targetting sequences on alternate strands of DHNA to
control gene expression.

Example 7; Fig 24A; 108pp; English.

The present invention relates to methods and oligonucleotides for forming
a triple-helix comprising a double helical nucleic acid comprising first
and second substantially complementary strands, and an oligonucleotide
bound to a purine-rich target sequence within the double helical nucleic
acid, where the oligonucleotide binds in a parallel and antiparallel
orientation, respectively, to target sequences on alternate strands of
the double helical nucleic acid. The method has therapeutic applications,
where gene expression is controlled by selective triple-helix formation,
within expression regulatory sequences of a target gene. The
oligonucleotides can be used to form triple-helices, and are useful to
detect the presence or absence of specific sequences within genomic DNA
for diagnostic and therapeutic purposes. The oligonucleotides can be
selected to specifically bind to pathogenic bacteria or viruses for
specific sequences required by pathogenic bacteria or viruses for
replication or virulence, reducing their pathogenicity. Alternatively,
the oligonucleotide can be chosen to target a unique sequence of the
pathogen which is not found in the genome of pathogen's host. The
oligonucleotides can be used in cancer treatment by way of triple-helix
suppression of specific oncogenes including those of endogenous or viral
origin. Such therapeutic oligonucleotides are capable of forming triple-
helices with such sequences in cancerous cells containing the activated
oncogene, so preferentially killing or repressing the cancer causing
cell. The present sequence represents an oligonucleotide used in the

```

CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.9%; Score 14; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 520

ABX79833/c

ID ABX79833 standard; cDNA; 15 BP.

XX AC ABX79833;

DT 17-APR-2003 (first entry)

XX EST polymorphic DNA repeat polynucleotide #158.

XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 XX Haw River syndrome; Huntington's disease; fragile-X syndrome;
 XX Friedreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 XX spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX Homo sapiens.

XX US6472154-B1.

XX 29-OCT-2002.

XX 31-DEC-1999; 99US-00475947.

XX 31-DEC-1999; 99US-00475947.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Garner HR, Wren JD, Minna JD, Fondon JW;

XX WPI; 2003-208818/20.

XX Identifying a candidate polymorphic repeat within a coding sequence, for
 XX understanding or treating genetic disease, comprises detecting tandem
 XX repeats in a target coding sequence and scoring the repeats for
 XX polymorphic probability.

XX Example; Col 747; 588pp; English.

XX The invention discloses a method for identifying a candidate polymorphic
 XX repeat within a coding sequence (expressed sequence tag, EST), which
 XX comprises detecting tandem repeats in a target coding sequence, scoring
 XX the repeats for polymorphic probability and generating a dataset
 XX correlating the repeats with polymorphic probability to identify a
 XX candidate polymorphic repeat. The computational methods (polymorphic
 XX marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 XX useful for identifying and detecting candidate polymorphic repeats in
 XX human genes, which can be used to understand, treat or eliminate genetic
 XX diseases, predispositions or adverse drug-treatment reactions. Examples
 XX of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 XX syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 XX myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 XX spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 XX the polymorphic repeats identified for a search of human ESTs

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.9%; Score 14; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 521

AAD44145/c

ID AAD44145 standard; DNA; 16 BP.

XX AC AAD44145;

DT 13-DEC-2002 (first entry)

XX Oligo-dT PCR primer #5 used to illustrate the method of the invention.

XX Sequential consensus region-directed amplification; gene expression;
 XX disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
 XX primer; ss.

XX Unidentified.

XX US6277571-B1.

XX 21-AUG-2001.

XX 30-SEP-1998; 98US-00163485.

XX 03-OCT-1997; 97US-00943162.

XX 03-OCT-1997; 97US-0108152P.

XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.

XX Fillmore H, Broadus W, Gillies G;

XX WPI; 2002-412824/44.

XX Sequential consensus region-directed amplification for sorting mixture of
 XX DNAs into 2 or more subsets or distinguishing gene expression patterns in
 XX 2 samples, useful for disease diagnosis and gene analysis.

XX Example; Fig 1C; 19pp; English.

XX The invention relates to a method of sequential consensus region-directed
 XX amplification for sorting a mixture of DNAs into 2 or more subsets or
 XX distinguishing gene expression patterns in 2 samples. The methods, kits
 XX and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 XX more subsets or distinguishing gene expression patterns in 2 samples e.g.
 XX for disease diagnosis and gene analysis. The present sequence is oligo dT
 XX PCR primer used to illustrate the method of the invention

XX SQ Sequence 16 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.9%; Score 14; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
 DB 16 AAAAAAAAAAAAAA 3

RESULT 522

AAD44147/c

ID AAD44147 standard; DNA; 16 BP.

XX AC AAD44147;

DT 13-DEC-2002 (first entry)

XX Oligo-dT PCR primer #7 used to illustrate the method of the invention.

```
XX Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX Unidentified.
XX US6277571-B1.
XX 21-AUG-2001.
XX 30-SEP-1998; 98US-00163485.
XX 03-OCT-1997; 97US-00943162.
XX 03-OCT-1997; 97US-0108152P.
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX Fillmore H, Broadus W, Gillies G;
XX WPI; 2002-412824/44.
XX Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX Example; Fig 1C; 19pp; English.
XX The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dt
CC PCR primer used to illustrate the method of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 1 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1494
DB 16 AAAAAAAAAAAAAA 3
XX
RESULT 523
AAL44149/c
ID AAL44149 standard; DNA; 16 BP.
XX
AC AAL44149;
XX
DT 13-DEC-2002 (first entry)
XX
DE Oligo-dT PCR primer #9 used to illustrate the method of the invention.
XX
KW Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX Unidentified.
XX US6277571-B1.
XX 21-AUG-2001.
XX 30-SEP-1998; 98US-00163485.
XX 03-OCT-1997; 97US-00943162.
XX 03-OCT-1997; 97US-0108152P.
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
XX Fillmore H, Broadus W, Gillies G;
XX WPI; 2002-412824/44.
XX Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX Example; Fig 1C; 19pp; English.
XX The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dt
CC PCR primer used to illustrate the method of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 1 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1494
DB 16 AAAAAAAAAAAAAA 3
XX
RESULT 523
AAD44149/c
ID AAD44149 standard; DNA; 16 BP.
XX
AC AAD44149;
XX
DT 13-DEC-2002 (first entry)
XX
DE Oligo-dT PCR primer #9 used to illustrate the method of the invention.
XX
KW Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX Unidentified.
XX US6277571-B1.
XX 21-AUG-2001.
XX 30-SEP-1998; 98US-00163485.
XX 03-OCT-1997; 97US-00943162.
XX 03-OCT-1997; 97US-0108152P.
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
XX Fillmore H, Broadus W, Gillies G;
XX WPI; 2002-412824/44.
XX Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX Example; Fig 1C; 19pp; English.
XX The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dt
CC PCR primer used to illustrate the method of the invention
XX
XX Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1494
DB 16 AAAAAAAAAAAAAA 3
XX
RESULT 524
AAL54153/c
ID AAL54153 standard; RNA; 16 BP.
XX
AC AAL54153;
XX
DT 28-MAR-2003 (first entry)
XX
DE RNA intron region #1.
XX
KW Splice junction; alternative spliced mRNA; splice variant; carcinoma;
KW sarcoma; leukaemia; lymphoma; pancreatitis; polycystic kidney disease;
KW ss.
XX Unidentified.
XX WO200293165-A1.
XX
PD 21-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-US015649.
XX
PR 17-MAY-2001; 2001US-0291598P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Dolginow D, Mertz L;
XX
DR WPI; 2003-129322/12.
XX
PT New sets of oligonucleotides with at least one that specifically
PT hybridizes to each possible splice junction in mRNA transcribed a gene,
PT useful for detecting or analyzing alternative splice variants of mRNA, or
PT diagnosing diseases.
XX Disclosure; Page 5; 37pp; English.
XX
XX The invention relates to a set of oligonucleotides, which comprise at
XX least one oligonucleotide that specifically hybridizes to each possible
XX splice junction in mRNA transcribed from at least one gene of interest.
XX The oligonucleotides are useful in solid supports for detecting
XX alternative spliced mRNA, a pathological condition in a patient, or
XX identifying an agent that modulates a pathological condition. These
```

CC oligonucleotides are particularly useful for detecting or analysing
CC alternative splice variants of mRNA, as well as for predicting disease
CC states in the diagnosis of diseases, e.g. carcinoma, sarcoma, leukaemia,
CC lymphoma, pancreatitis, or polycystic kidney disease. The splice variants
CC are useful for screening pharmaceutical agents for modulating a
CC pathological condition. This polynucleotide sequence represents an intron
CC region relating to the invention

SQ Sequence 16 BP; 1 A; 0 C; 2 G; 0 T; 12 U; 1 Other;

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAA 1493
DB 15 CTAAAAAATAAAAAA 1

RESULT 525
AA85699/C
ID AA85699 standard; DNA; 18 BP.
XX
XX AAF85699;
AC
XX
DT 13-JUL-2001 (first entry)
XX
DE Multiple repeated heat process PCR related oligonucleotide #3.
XX
KW Multiple repeated heat circulation; polymerase chain reaction; PCR;
XX target DNA production; DNA synthesis; ds.
XX
XX Unidentified.
OS
XX
XX CN1278558-A.
PN
XX
XX 03-JAN-2001.
PD
XX
XX 22-JUN-1999; 99CN-00114949.
PF
XX
XX 22-JUN-1999; 99CN-00114949.
PR
XX
XX (XIAQ/) XIA Q.
PA
XX
XX Xia Q;
PI
XX
XX WPI; 2001-245741/26.

XX Asynchronous chain-extending polymerase chain reaction for producing lots
XX of target DNA fragments, comprises a multiple repeated heat circulation
XX process.

XX Disclosure; Page 3; 4pp; Chinese.

XX The present invention relates to a kind of two chains asynchronously-
XX elongated DNA amplification technology in vitro, which is characterized
XX by that firstly, a pair of specific primers is synthesized according to
XX the target DNA sequence to be amplified, then a repetitive sequence
XX complementary oligo-repetitive sequence of 3' target DNA chain whose tail
XX end is modified and elongation vitality is lost, then the oligo-
XX repetitive sequence, chain primer, heat-resisting DNA polymerase, dNTP
XX substrate, template DNA, magnesium ion, polymerase chain reaction (PCR)
XX buffer solution and ultra-pure water are mixed uniformly and made into a
XX reaction system. The reaction system then undergoes the processes of high
XX -temp., low-temp., medium-low temp., medium-temp, and repeated heat
XX circulation treatment in the heat-circulating instrument to obtain
XX million copies of specific target DNA fragments. The invention adopts a
XX multiple repeated heat circulation process, so that it can produce lots
XX of target DNA fragments. The present sequence was used in the
XX exemplification of the invention

SQ Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 CGCCGCCGCCGCCGCC 238
DB 18 CGCCGCCGCCGCCGCC 2

RESULT 526
ABK32799
ID ABK32799 standard; DNA; 15 BP.
XX
XX
AC ABK32799;
XX

DT 23-APR-2002 (first entry)
XX

DE Human APPBP1 gene, allele-specific oligonucleotide #29.

XX Human; amyloid beta precursor protein binding protein 1; APPBP1; probe;
KW Alzheimer's disease; transgenic animal; platelet aggregation; leucide; ss.
XX single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.

OS Homo sapiens.

XX WO200202820-A1.

XX 10-JAN-2002.

XX 02-JUL-2001; 2001WO-US020951.

XX 30-JUN-2000; 2000US-0215511P.

XX (GENA-) GENAISANCE PHARM INC.

XX Anastasio AE, Chew A, Choi JY, Kazemi A, Koshy B, Sausker EA;

PI Stephens CJ;

XX WPI; 2002-164539/21.

XX Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene
XX polymorphic variants, useful e.g. in studying the expression and function
XX of APPBP1 and screening candidate drugs for treating Alzheimer's disease.

XX Claim 17; Page 13; 104pp; English.

XX The invention relates to an isolated polypeptide comprising a sequence
XX which is a polymorphic variant of a reference sequence for the amyloid
XX beta precursor protein binding protein 1, 59kD (APPBP1) protein or its
XX fragment. The polymorphic variants are useful in studying the expression
XX and function of APPBP1, in expressing APPBP1 protein for use in screening
XX for candidate drugs to treat diseases related to APPBP1 activity, in
XX studying the effect of the variation on the biological activity of
XX APPBP1, and the binding affinity of candidate drugs targeting APPBP1 for
XX the treatment of disorders such as Alzheimer's disease. The haplotyping
XX methods are useful in validating APPBP1 as a candidate target for
XX treating a specific condition or disease predicted to be associated with
XX APPBP1 activity, or in the design of clinical trials of candidate drugs
XX for treating a specific condition or disease associated with APPBP1
XX activity. The transgenic animals are useful for studying expression of
XX the APPBP1 isogenes in vivo, for in vivo screening and testing of drugs
XX targeted against APPBP1 protein, and for testing the efficacy of
XX therapeutic agents and compounds for disorders related to platelet
XX aggregation in a biological system. ABK32771-ABK32327 represent human
XX APPBP1 gene allele-specific oligonucleotides used in the method of the
XX invention

SQ Sequence 15 BP; 13 A; 1 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.9%; Score 13.6; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
 ID |||||:|
 Db 2 AAAAAAAAAAAAAA 15

RESULT 527
 ABZ04679/C
 ID ABZ04679 standard; DNA; 50 BP.
 XX
 AC ABZ04679;
 DT
 DT 09-JAN-2003 (first entry)
 XX
 DE Human leukocyte gene expression profiling probe SEQ ID NO 4670.
 XX
 KW T γ ; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200257414-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 22-OCT-2001; 2001WO-US047856.
 XX
 XX 20-OCT-2000; 2000US-0241994P.
 PR
 PR 08-JUN-2001; 2001US-0296764P.
 XX
 XX (BIOC-) BIOCARDIA INC.
 PA
 XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 PI Ly N, Woodward R, Quermous T, Johnson F;
 PI WPI; 2002-636525/68.
 XX
 XX New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.
 XX
 XX Claim 1; Page 477; Opp; English.
 XX
 CC The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 XX
 SQ Sequence 50 BP; 13 A; 17 C; 5 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.6; DB 1; Length 50;
 Best Local Similarity 67.9%; Pred. No. 3.9e+02;
 Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1127 TGATGTACATGTAGTGGCGTGTATGA 1154
 ID |||||:|
 Db 29 TGATTACAGTTGAAGCGCAGCTGTAGA 2

RESULT 528
 AAT52144/C
 ID AAT52144 standard; RNA; 15 BP.
 XX
 AC AAT52144;

XX 25-MAR-2003 (revised)
 DT 25-MAR-1997 (first entry)
 XX
 DE Human ICAM hammerhead ribozyme target sequence (nt. position 2914).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-IB000156.
 XX
 XX 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 DR
 DR Ribozymes having modified bases and methods for producing them - for use
 XX in inhibiting disease related genes.
 PT
 PT Claim 2; Page 175; 407pp; English.
 XX
 PS The present sequence represents a preferred target sequence for an
 XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
 CC nucleotide base position indicated in the DE line. Regions of the mRNA
 CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were

CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 CC inhibit ICAM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 SQ Sequence 15 BP; 1 A; 1 C; 1 G; 0 T; 12 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAA 1493
 DB 15 CTGAAAAAATAAAAAA 1

RESULT 529
 AAT56307
 ID AAT56307 standard; RNA; 15 BP.
 XX
 AC AAT56307;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-MAY-1997 (first entry)
 XX
 DE Mouse TNP-a hammerhead ribozyme target sequence (nt position 1462).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.

XX Mhs musculus.

XX OS

XX PN WO9523225-A2.

XX PD 31-AUG-1995.

XX PF 23-FEB-1995; 95WO-IB000156.

XX PR 23-FEB-1994; 94US-00201109.

PR 29-MAR-1994; 94US-00218934.

PR 04-APR-1994; 94US-00222795.

PR 07-APR-1994; 94US-00224483.

PR 15-APR-1994; 94US-00227958.

PR 18-APR-1994; 94US-00228041.

PR 18-MAY-1994; 94US-00245736.

PR 06-JUL-1994; 94US-00271280.

PR 13-AUG-1994; 94US-00291932.

PR 16-AUG-1994; 94US-00291433.

PR 17-AUG-1994; 94US-00292620.

PR 19-AUG-1994; 94US-00293520.

PR 02-SEP-1994; 94US-00300000.

PR 08-SEP-1994; 94US-00303039.

PR 23-SEP-1994; 94US-00311486.

PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Ueman N, Wincott FE, Woolf T;
 XX
 DR WPI; 1995-351090/45.

XX Ribozymes having modified bases and methods for producing them - for use
 in inhibiting disease related genes.

XX Claim 2; Page 252; 407pp; English.

XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha mRNA at
 CC the nucleotide base position indicated in the DE line. Regions of the
 CC mRNA that do not form secondary folding structures and that contain
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified
 CC by computer analysis. Ribozymes directed against these mRNA sequences
 CC were designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit TNF-alpha expression, making them
 CC potentially useful for treating rheumatoid arthritis, septic shock and
 CC other inflammatory disorders including psoriasis, as well as for
 CC treatment of AIDS. (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 15 BP; 1 A; 6 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 53.3%; Pred. No. 3.3e+02;
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1334 ACCTGTTCCTCCT 1348
 DB 1 ACCUUGUUGCCUCCU 15

RESULT 530

AAT52142/c

ID AAT52142 standard; RNA; 15 BP.

XX AC AAT52142;

XX DT 25-MAR-2003 (revised)

DT 25-MAR-1997 (first entry)

XX Human ICAM hammerhead ribozyme target sequence (nt. position 2913).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.

XX Homo sapiens.

XX WO9523225-A2.

XX PD 31-AUG-1995.

XX PF 23-FEB-1995; 95WO-IB000156.

XX PR 23-FEB-1994; 94US-00201109.


```

PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
PI Modak A, Pavco P, Belgelman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott PE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
XX in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by
XX computer analysis. Ribozymes directed against these mRNA sequences were
XX designed and synthesised with modifications that improve their nuclease
XX resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
XX inhibit ICAM-1 expression, making them useful for reducing transplant
XX rejection and alleviating symptoms in patients with rheumatoid arthritis,
XX asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
XX correct PI field.)
XX
XX Sequence 15 BP; 1 A; 1 C; 0 G; 0 T; 13 U; 0 Other;
XX
SQ
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1480 TAAAAAATAAAAAA 1494
Db 15 TGAATAAAAAA 1
XX
RESULT 531
AAT76466
ID AAT76466 standard; DNA; 15 BP.
XX
XX AAT76466;
AC
XX 16-SEP-1997 (first entry)
DT
XX Chymase antisense oligonucleotide.
DB

XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
XX chronic obstructive pulmonary disease; bronchitis; ss.
XX
XX Synthetic.
XX
XX W09640162-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009306.
XX
XX 07-JUN-1995; 95US-00474497.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW, Metzger WJ;
XX
XX WPI; 1997-051871/05.
XX
XX Treatment of airway diseases such as asthma - by topically applying
XX adenosine-free antisense oligo:nucleotide to airway epithelium of
XX subject.
XX
XX Example 5; Page 41; 71pp; English.
XX
XX A method for treating airway disease in a subject has been produced,
XX which involves the topical administration of an essentially adenosine
XX free antisense oligonucleotide (ON) to the airway epithelium of the
XX subject. The present sequence is an antisense oligonucleotide specific
XX for chymase. The method can be used to treat airway diseases such as
XX cystic fibrosis, asthma, chronic obstructive pulmonary disease,
XX bronchitis and other airway diseases characterised by an inflammatory
XX response. By eliminating adenosine from the antisense ON, its liberation
XX upon antisense degradation is prevented, thereby preventing adenosine-
XX induced bronchoconstriction in patients with hyper-reactive airways
XX
XX Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
XX
SQ
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 323 CTGGGTGTGGCCCTG 337
Db 1 CTGGGTGTGGCCCTG 15
XX
RESULT 532
AAT86420
ID AAT86420 standard; DNA; 15 BP.
XX
XX AAT86420;
AC
XX
XX 28-JAN-1998 (first entry)
DT
XX Trinucleotide simple tandem repeat (GGC)5, peptide nucleic acid probe.
XX
XX Peptide nucleic acid; PNA; hybridisation probe; polyamide backbone;
XX trinucleotide tandem repeat sequence; satellite; quantitation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..15
XX /tag= b
XX /note= "This sequence is a peptide nucleic acid, i.e. it
XX contains a polyamide backbone"
XX repeat_unit 1..3
XX /tag= a
XX /rpt_type= TANDEM
XX

```


XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 FT vasoconstriction.
 XX
 XX Disclosure; Page 60; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene initiation
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3',
 CC -end and the juxta-section between coding and non-coding regions and all
 CC segments of RNAs encoding proteins associated with one or more diseases,
 CC conditions or mixtures. The antisense oligonucleotides may be derived
 CC from sequences AAX5272-74. These multiple target oligonucleotides
 CC (specifically AAX5180-271) can be used for the antisense treatment of
 CC diseases and conditions. Typical diseases and conditions are those
 CC associated with impaired respiration and inflammation, including lung
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 CC acute asthma, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer
 XX
 SQ Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 323 CTGGGTGGGCCCG 337
 Db 1 CTGGGTGGGCCCG 15

RESULT 535
 AAX18364/c
 ID AAX18364 standard; DNA; 15 BP.
 XX
 AC AAX18364;
 XX
 XX 11-MAY-1999 (first entry)
 XX
 XX RT-PCR primer of the invention SEQ ID 5.
 XX
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX
 OS Synthetic.
 XX
 XX JPI1032765-A.
 XX
 XX 09-FEB-1999.
 XX
 XX 18-JUL-1997; 97JP-00208312.
 XX
 XX 18-JUL-1997; 97JP-00208312.
 XX
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX
 XX WPI; 1999-183822/16.
 XX
 XX Peptides having at least two new nucleotides - useful as primers in RT-
 FT PCR.
 XX
 PS Disclosure; Page 10; 19pp; Japanese.
 XX
 CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX

SQ Sequence 15 BP; 0 A; 0 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1479 CTAAAAAATAAAAAA 1493
 Db 15 CCAAAAAAATAAAAAA 1

RESULT 536
 AAX33702
 ID AAX33702 standard; DNA; 15 BP.

XX AAX33702;
 AC AAX33702;
 XX

DT 28-JUL-2000 (first entry)

DE Low adenosine antisense oligonucleotide SEQ ID NO:1391.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;
 KW anti-allergic; antiasthmatic; cytotatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

XX WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
 FT vasoconstriction, inflammation, allergies, asthma, hypertension,
 FT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 FT cancers.
 XX

XX Claim 18; Page 438; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have anti-inflammatory, anti-allergic,
 CC antiasthmatic, cytotatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive

CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONS reduces side effects. The A-containing ONS break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONS from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX
 SQ Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 323 CTGGGTGTGCCCTG 337
 |||||
 Db 1 CTGGGTGGGCCCTG 15

RESULT 537
 AAA11718/c
 ID AAA11718 standard; DNA; 15 BP.

XX AC AAA11718;

XX DT 14-JUL-2000 (first entry)

DE Human MIF gene D5k region primer #2.

XX MIF; migration inhibitory factor; D5k region; human; macrophage;
 KW diagnosis; primer; adenocarcinoma; metastasis; cancer; tumor cell; ss.

XX OS Homo sapiens.

XX PN US6043044-A.

XX PD 28-MAR-2000.

XX PF 15-JUL-1997; 97US-00893204.

XX PR 15-JUL-1997; 97US-00893204.

XX PA (HUDS/) HUDSON P B.

XX PA (HAKK/) HAKKY S I.

XX PA (SIEG/) SIEGLER K M.

XX PA (HAKK/) HAKKI A.

XX PI Hakky SI, Hudson PB, Siegler KM, Hakki A;

XX DR WPI; 2000-292363/25.

XX A new method useful for diagnosing human adenocarcinoma and measuring

PT metastatic potential comprises determining the levels of macrophage

PT migration inhibitory factor within tumor cells.

XX Claim 11; Col 7-8; 6pp; English.

XX This invention describes a novel method for diagnosing adenocarcinoma and
 CC determining metastatic ability of human cancer in an individual by
 CC determining the increased levels of macrophage migration inhibitory
 CC factor (MIF) within tumor cells. The method is useful for diagnosing
 CC human adenocarcinoma, as well as for its prognosis. The method is also
 CC useful for measuring levels of macrophage migration inhibitory factor
 CC within tumor cells. The method provides better and more accurate
 CC prognostic markers for cancer. The method is also capable of
 CC distinguishing histological tumors from clinical cancers. This sequence

CC represents a primer used to detect the human MIF gene D5k region which is
 CC described in the method of the invention

XX SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 3.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AGAAAAAAAAAAAAA 1

RESULT 538

AAFI9824

ID AAF19824 standard; DNA; 15 BP.

XX AC AAF19824;

DT 14-MAR-2001 (first entry)

XX Human chymase polynucleotide fragment #1391.

XX Low adenosine antisease oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX OS Homo sapiens.

XX PN WO2000062736-A2.

XX PD 26-OCT-2000.

XX PF 24-MAR-2000; 2000WO-US008020.

XX PR 06-APR-1999; 99US-0127958P.

XX PA (UYEC-) UNIV EAST CAROLINA.

XX PA (NYCE/) NYCE J W.

XX PI Nyce JW;

XX DR WPI; 2000-679539/66.

XX Low adenosine (A) content antisease oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.

XX Claim 14; Page 250; 1592pp; English.

XX The present invention describes low adenosine (A) content antisease
 CC oligonucleotides and compositions (I) comprising them. In the antisease
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisease oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide

transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 323 CTGGGTGGCCCTG 337
 Db 1 CTGGGTGGCCCTG 15

RESULT 539
 AAF46644
 ID AAF46644 standard; DNA; 15 BP.
 XX AAF46644;
 AC AAF46644;
 XX 30-MAR-2001 (first entry)
 DT IGFBP3 oligonucleotide #64.
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

Homo sapiens.
 OS
 XX WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wright CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 7; Page 44; 201pp; English.
 The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation,

inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Sequence 15 BP; 1 A; 9 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 65 CCTCGCGCCAGCC 79
 Db 1 CCTCGCGCCAGCC 15

RESULT 540
 AAF52137
 ID AAF52137 standard; DNA; 15 BP.
 XX AAF52137;
 AC AAF52137;
 XX 30-MAR-2001 (first entry)
 DT IGF-I oligonucleotide #3097.
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

Homo sapiens.
 OS
 XX WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wright CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 81; 201pp; English.
 The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 2 A; 2 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 665 GCCAAGGCTGTGGTG 679
 DB 1 GCCAAGGCTGTGGTG 15

RESULT 541
 AAF52138
 ID AAF52138 standard; DNA; 15 BP.

XX AC AAF52138;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE TGF-I oligonucleotide #3098.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

OS Homo sapiens.
 XX
 XX WO200078341-A1.

PN 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 81; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 3 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 666 CCAAGGCTGTGGTGA 680
 DB 1 CCAAGGCTGTGGTGA 15

RESULT 542
 AAF49438
 ID AAF49438 standard; DNA; 15 BP.

XX AC AAF49438;

DT 30-MAR-2001 (first entry)

XX TGF-I oligonucleotide #398.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.
 OS
 XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional), and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 63; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 4 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 885 TGATCTCGAGATGA 899
 DB 1 TCATCTTCGAGATGA 15

RESULT 543
 AAF46581
 ID AAF46581 standard; DNA; 15 BP.

XX AC AAF46581;
 XX 30-MAR-2001 (first entry).
 XX IGFBP3 oligonucleotide #1.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

OS Homo sapiens.
 XX WO200078341-A1.
 XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

XX Example 7; Page 44; 20lpp; English.

XX The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

XX Sequence 15 BP; 2 A; 8 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 CTCGCGCCGAGCG 80
 DB 1 CTCAGCGCCGAGCG 15

RESULT 544
 AAF49440
 ID AAF49440 standard; DNA; 15 BP.

XX AC AAF49440;
 XX 30-MAR-2001 (first entry).
 XX IGF-I oligonucleotide #400.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

OS Homo sapiens.
 XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

XX Example 8; Page 63; 20lpp; English.

XX The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

XX Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 887 ATCTTCGAGATGATC 901
 DB 1 ATCTTCGAGATGACC 15


```

RESULT 545
AAF52139
ID AAF52139 standard; DNA; 15 BP.
XX
XX
AC AAF52139;
AC
XX
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #3099.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 81; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 4 A; 1 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 667 CAAGGCTGTGTGTA 681
DB 1 CAAGGCTGTGTGTA 15
|||||
|||||

RESULT 546
AAF51849
ID AAF52139 standard; DNA; 15 BP.
XX
XX
AC AAF51849;
AC
XX
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #2809.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 79; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 614 TTCTATGACGCGCC 628
DB 1 TTCTATGTCGCGCC 15
|||||
|||||

RESULT 547
AAF53315/c
ID AAF53315 standard; DNA; 15 BP.
XX
XX
AC AAF53315;
AC
XX
XX

```


DT 30-MAR-2001 (first entry)
 XX IGF-I oligonucleotide #4275.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 XX cytotatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 XX 28-DEC-2000.
 XX
 XX 21-JUN-2000; 2000WO-AU000693.
 XX
 XX 21-JUN-1999; 99US-0140345P.
 XX
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 XX Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 XX Example 8; Page 88; 201pp; English.
 XX
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 1 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 763 TCCTCGGCGGACGAA 777
 Db 15 TCCTCGGCGGACGAA 1
 RESULT 548
 AAF46582
 ID AAF46582 standard; DNA; 15 BP.
 XX
 AC AAF46582;
 XX
 XX 30-MAR-2001 (first entry)
 DT
 XX IGFBP3 oligonucleotide #2.
 DE
 XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytotatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 XX 28-DEC-2000.
 XX
 XX 21-JUN-2000; 2000WO-AU000693.
 XX
 XX 21-JUN-1999; 99US-0140345P.
 XX
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 XX Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 XX Example 7; Page 44; 201pp; English.
 XX
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 2 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 67 TCCTCGGCGGACGCGC 81
 Db 1 TCCTCGGCGGACGCGC 15
 RESULT 549
 AAF49043/C
 ID AAF49043 standard; DNA; 15 BP.
 XX
 AC AAF49043;
 XX
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #3.
 DE
 XX
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytotatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW

KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.
 OS
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 DR

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 60; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 1 A; 0 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1479 CTAAAAAAAAAAAAA 1493
 Db 15 CTCAAAAAAAAAAAAA 1

RESULT 550
 AAF49042/C
 ID AAF49042 standard; DNA; 15 BP.
 XX AAF49042;
 AC

XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #2.
 DE

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.
 OS
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 DR

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 60; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 1 A; 0 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1480 TAAAAAAAAAAAAA 1494
 Db 15 TCAAAAAAAAAAAAAA 1

RESULT 551
 AAF80919/C
 ID AAF80919 standard; DNA; 15 BP.
 XX AAF80919;
 AC

XX 02-MAY-2001 (first entry)
 DT
 XX PTGS2 allele specific oligonucleotide probe SEQ ID 25.
 DE

XX Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
 KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
 KW inflammation; probe; ss.
 XX

XX Homo sapiens.
 OS
 XX
 PN WO200107662-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-US020114.
 XX

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PR 22-JUL-1999; 99US-0145170P.
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;
XX WPI; 2001-182805/18.
XX
XX New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
XX for gene therapy of inflammation and for establishing a genotype or
XX haplotype.
XX
XX Disclosure; Page 21; 118pp; English.
XX
XX This invention relates to a polynucleotide sequence that is a polymorphic
XX variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
XX also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
XX AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
XX AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
XX protein is represented by AAB72199. The invention includes PCR and
XX sequencing primers, and probes represented in AAF80898 - AAF81151 which
XX are used to isolate and characterise the PTGS2 gene sequence, and to
XX locate the positions of the SNPs. PTGS2 proteins and polynucleotide
XX sequences are used to express variant PTGS2 proteins, for structural
XX analysis or drug-binding studies and also in gene therapy (either
XX expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
XX useful for diagnosis, prognosis and therapy and analysis of the new, and
XX known, polymorphisms and used to determine PTGS2 haplotype and genotype,
XX especially for determining association between a particular trait, e.g. a
XX clinical response to drugs that target PTGS2 but also disease
XX susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
XX used for developing diagnostic tests and treatments for immune-related
XX disorders such as arthritis and inflammation. The polymorphisms may also
XX be used to study expression and biological function of PTGS2. Transgenic
XX animals that express PTGS2 are used to study expression of PTGS2
XX isogenes, for in vivo drug screening and testing, and for assessing
XX effects of therapeutic agents
XX
XX Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 13.4; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 3.3e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
XX
RESULT 552
AAF69483
ID AAF69483 standard; DNA; 15 BP.
XX
XX AAF69483;
XX
XX 18-APR-2001 (first entry)
XX
XX Human IL4Ralpha gene probe #123.
XX
XX Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
XX allergic disease; probe; ss.
XX
XX Homo sapiens.
XX
XX WO200104270-A1.
XX
XX 18-JAN-2001.
XX
XX 13-JUL-2000; 2000WO-US019094.
XX
XX 13-JUL-1999; 99US-0143435P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
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XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI Windemuth AK;
XX
XX WPI; 2001-103078/11.
XX
XX New isolated polynucleotide useful for the identification of therapeutics
XX in allergic diseases is new.
XX
XX Claim 15; Page 44; 188pp; English.
XX
XX The present invention relates to polymorphisms of the human interleukin 4
XX receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
XX sequence). Polynucleotides comprising polymorphic gene variants are
XX useful for therapeutic purposes. For example, where a patient may benefit
XX from expression of a particular IL4Ralpha protein isoform, an expression
XX vector encoding the isoform may be administered to the patient. It may
XX desirable to decrease or block expression of a particular IL4Ralpha
XX isogene, which may be done by turning off by transforming a targeted
XX organ, tissue or cell population with an expression vector that expresses
XX high levels of untranslatable mRNA for the isogene. Specific therapeutics
XX identified by these methods may be useful for allergic diseases. The
XX present sequence is a probe for human IL4R-alpha
XX
XX Sequence 15 BP; 3 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 13.4; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 3.3e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 383 CTGGGAGACAAAGCCC 397
Db 1 CTGGGAGGCAAGCCC 15
XX
RESULT 553
ABA97405/C
ID ABA97405 standard; DNA; 15 BP.
XX
XX ABA97405;
XX
XX 18-JUN-2002 (first entry)
XX
XX Nucleotide sequence of oligomer # 12 used to compare mismatches.
XX
XX Protein nucleic acid molecule; PNA; ds.
XX
XX Synthetic.
XX
XX WO200168673-A1.
XX
XX 20-SEP-2001.
XX
XX 13-MAR-2001; 2001WO-US008111.
XX
XX 14-MAR-2000; 2000US-0189190P.
XX
XX 30-NOV-2000; 2000US-0250334P.
XX
XX (ACTI-) ACTIVE MOTIF.
XX
XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
PI Chakmakchcheau O, Buryakova A, Choob M, Hondorp K;
XX
XX WPI; 2002-041177/05.
XX
XX Oligonucleotides analogs useful in detection, separation and purification
XX of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
XX Example 20; Page 123; 197pp; English.
XX
XX This invention relates to oligonucleotide analogues comprising a protein
XX nucleic acid molecule (PNA) monomer. They are used in the detection and
XX separation of nucleic acid molecules and as probes, primers, linkers,
XX
```

CC adapters and antisense agents on solid supports. Modifications enhance
 CC their use as capture and detection probes e.g. by the incorporation of
 CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
 CC fluorescein and reporter molecules such as alkaline phosphatase. They are
 CC also used for enhancing or inhibiting the activity of an enzyme or
 CC cellular activity. The compounds are stable to nucleases and proteases,
 CC have high affinity, binding specificity and solubility. The polyamide
 CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
 CC nucleic acid molecules with greater affinity than DNA or RNA
 CC concentration. The compounds are relatively simple to synthesize and are
 CC used in a wide variety of applications. This sequence represents a DNA
 CC oligomer which is used to represent the effect of single base mismatches
 CC on oligonucleotides

XX
 SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1

RESULT 554
 ABK98166/c
 ID ABK98166 standard; DNA; 15 BP.
 XX
 AC ABK98166;
 DT 07-OCT-2002 (first entry)
 XX
 DE Triple helix forming associated oligonucleotide #36.
 XX
 KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
 XX
 OS Synthetic.
 XX
 XX US6403302-B1.
 XX
 XX 11-JUN-2002.
 XX
 XX 16-DEC-1993; 93US-00168920.
 XX
 XX 17-SEP-1992; 92US-00946976.
 XX
 XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
 XX
 XX Dervan PB, Beal PA;
 XX WPI; 2002-536030/57.
 XX
 XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
 XX oligonucleotide which binds in parallel and antiparallel orientation,
 XX respectively, for targeting sequences on alternate strands of DHNA to
 XX control gene expression.
 XX
 XX Example 6; Fig 20A; 108pp; English.
 XX
 XX The present invention relates to methods and oligonucleotides for forming
 XX a triple-helix comprising a double helical nucleic acid comprising first
 XX and second substantially complementary strands, and an oligonucleotide
 XX bound to a purine-rich target sequence within the double helical nucleic
 XX acid, where the oligonucleotide binds in a parallel and antiparallel
 XX orientation, respectively, to target sequences on alternate strands of
 XX the double helical nucleic acid. The method has therapeutic applications,
 XX where gene expression is controlled by selective triple-helix formation
 XX within expression regulatory sequences of a target gene. The
 XX oligonucleotides can be used to form triple-helices, and are useful to

CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic double-stranded DNA including
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention

XX
 SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1

RESULT 555
 ABK98185/c
 ID ABK98185 standard; DNA; 15 BP.
 XX
 AC ABK98185;
 DT 07-OCT-2002 (first entry)
 XX
 DE Triple helix forming associated oligonucleotide #49.
 XX
 KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
 XX
 OS Synthetic.
 XX
 XX US6403302-B1.
 XX
 XX 11-JUN-2002.
 XX
 XX 16-DEC-1993; 93US-00168920.
 XX
 XX 17-SEP-1992; 92US-00946976.
 XX
 XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
 XX
 XX Dervan PB, Beal PA;
 XX WPI; 2002-536030/57.
 XX
 XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
 XX oligonucleotide which binds in parallel and antiparallel orientation,
 XX respectively, for targeting sequences on alternate strands of DHNA to
 XX control gene expression.
 XX
 XX Example 7; Fig 24A; 108pp; English.
 XX
 XX The present invention relates to methods and oligonucleotides for forming
 XX a triple-helix comprising a double helical nucleic acid comprising first
 XX and second substantially complementary strands, and an oligonucleotide
 XX bound to a purine-rich target sequence within the double helical nucleic
 XX acid, where the oligonucleotide binds in a parallel and antiparallel
 XX orientation, respectively, to target sequences on alternate strands of
 XX the double helical nucleic acid. The method has therapeutic applications,
 XX where gene expression is controlled by selective triple-helix formation
 XX within expression regulatory sequences of a target gene. The

CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic double-stranded DNA including
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or suppressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention
 XX
 SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 556
 ABZ95518
 ID ABZ95518 standard; DNA; 15 BP.
 AC ABZ95518;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human chymase antisense fragment no.1382.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 10760; 872pp; English.

XX
 PS The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 323 CTGGGTGTGGCCCTG 337
 DB 1 CTGGGTGTGGCCCTG 15

RESULT 557
 ABX79839/C
 ID ABX79839 standard; CDNA; 15 BP.
 AC ABX79839;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE EST polymorphic DNA repeat polynucleotide #164.
 XX

XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
 XX
 OS Homo sapiens.
 XX
 PN US6472154-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 31-DEC-1999; 99US-00475947.
 XX
 PR 31-DEC-1999; 99US-00475947.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.

XX Garner HR, Wren JD, Minna JD, Fondon JW;
 XX WPI; 2003-208818/20.
 XX

XX Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.
 XX

XX Example; Col 779; 588pp; English.

XX The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic

CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to undertake, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
 CC myotonic dystrophy, hyperandrogenemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs

XX SQ Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 558
 ADB68522/c
 ID ADB68522 standard; DNA; 15 BP.

XX AC ADB68522;

XX DT 04-DEC-2003 (first entry)

XX DE Single-base mismatch oligonucleotide SEQ ID 12 DNA.

XX KW hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
 KW gene expression; respiration; secretion; signalling;
 KW ion-channel activity; cell motility; developmental phenotype;
 KW tumour regression; single-base mismatch; ss;
 KW phosphono-peptide nucleic acid; pPNA.

XX OS Synthetic.

XX PN WO2003068798-A2.

XX PD 21-AUG-2003.

XX PF 07-FEB-2003; 2003WO-US003904.

XX PR 09-FEB-2002; 2002US-00072975.

XX PA (ACT1-) ACTIVE MOTIF.

XX PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;

XX DR WPI; 2003-689653/65.

XX PT Method of inhibiting expression of genes or RNA transcripts, useful for
 PT therapy and determining effects of genes, by administering oligomers
 PT containing hydroxyproline nucleic acid.

XX PS Disclosure; Page 234; 240pp; English.

XX The invention relates to a novel method of inhibiting the expression of
 CC one or more genes or RNA transcripts by administering at least one
 CC oligonucleotide analogue that includes at least one hydroxyproline
 CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
 CC oligonucleotides of the invention may be used to monitor properties
 CC including gene expression, respiration, secretion, signalling, ion-
 CC channel activity, cell motility, developmental phenotype and tumour
 CC regression. Furthermore, they may be utilised to determine the effects of
 CC particular genes, as antisense or homologous recombination constructs
 CC e.g. for creating animal models of disease and finally, for increasing
 CC the activity of some enzymes, such as polymerases. The current sequence
 CC is that of the single-base mismatch oligonucleotide SEQ ID 12 DNA of the
 CC invention. This sequence may also comprise a peptide nucleic acid (PNA),
 CC a phosphono-PNA (pPNA) or a HypNA.

XX SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 559

AAV48216/c
 ID AAV48216 standard; DNA; 14 BP.

XX AC AAV48216;

XX DT 09-NOV-1998 (first entry)

XX DE 3' poly-A-anchoring primer.

XX KW ds; aortic preferentially expressed protein 1; smooth muscle;
 KW cell proliferation; developmental stage; tissue plasminogen activator;
 KW p21 cell cycle; nitric oxide synthetase; gamma-interferon.

XX OS Synthetic.

XX PN WO9835040-A2.

XX PD 13-AUG-1998.

XX PF 06-FEB-1998; 98WO-US002441.

XX PR 06-FEB-1997; 97US-00795868.

XX PA (HARD) HARVARD COLLEGE.

XX PI Lee M, Hsieh C;

XX DR WPI; 1998-447237/38.

XX PT Novel human, rat or mouse aorta or striated-muscle preferentially
 PT expressed proteins - useful for treating e.g. atherosclerosis.

XX PS Disclosure; Page 17; 88pp; English.

XX The 3' poly-A-anchoring primer was used in the production of an aortic
 CC preferentially expressed protein 1 (APEG-1) which is used to derive an
 CC enhancer/promoter. This linked to a polypeptide coding sequence which
 CC regulates smooth muscle cell-specific expression of the polypeptide
 CC coding sequence can be used as a method of inhibiting vascular smooth
 CC muscle cell proliferation. The nucleic acids are used to direct
 CC developmental stage-specific expression of a heterologous polypeptide
 CC which is especially selected from tissue plasminogen activator (tPA), p21
 CC cell cycle inhibitor, nitric oxide synthetase, gamma-interferon, atrial
 CC natriuretic proteins. These are used to inhibit the proliferation of
 CC smooth muscle cells, e.g. for the treatment of atherosclerosis

XX SQ Sequence 14 BP; 0 A; 0 C; 1 G; 12 T; 0 U; 1 Other;

Query Match 0.9%; Score 13.2; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 3.2e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAAAAAAAA 1492
 DB 14 CBAAAAAAAAAAAAA 1

RESULT 560
 AAZ51049/c
 ID AAZ51049 standard; DNA; 14 BP.

```

XX AC AAZ51049;
XX DT 05-JUN-2000 (first entry)
XX DE 3' poly-A-anchoring primer to synthesise rat APEG-1 gene.
XX KW Rat; aortic-preferentially-expressed gene-1; APEG-1; primer; aorta;
XX KW striated muscle cell; vascular smooth muscle cell; VSMC;
XX KW antiarteriosclerotic; vasotropic; cis-acting transcriptional repressor;
XX KW treatment; diagnosis; vascular disease; atherosclerosis; restenosis; ss.
XX OS Rattus sp.
XX PN W0200009689-A2.
XX PD 24-FEB-2000.
XX PF 11-MAY-1999; 99WO-US010298.
XX PR 14-AUG-1998; 98US-00134250.
XX PR 30-APR-1999; 99US-00303069.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Lee M, Hsieh C;
XX PS WPI; 2000-224334/19.
XX PT New gene useful for treating and diagnosing vascular diseases comprises a
XX PT single gene encoding aortic-specific and striated-specific muscle cell
XX PT isoforms.
XX PS Disclosure; Page 20; 89pp; English.
XX CC The present sequence is a 3' poly-A-anchoring primer used in differential
XX CC mRNA display technique to synthesise rat aortic-preferentially-expressed
XX CC gene-1 (APEG-1) cDNA. APEG-1 gene encodes two muscle cell protein
XX CC isoforms, one specific to aortic smooth muscle cells designated APEG-1
XX CC protein and the other specific to striated muscle cells designated SPEG
XX CC protein. APEG-1 protein can be administered to vascular smooth muscle
XX CC cells (VSMC) to inhibit their proliferation or migration at the site of
XX CC vascular injury. APEG-1 enhancer sequence is used to direct VSMC-specific
XX CC expression. A cis-acting transcriptional repressor sequence found in the
XX CC 5' region of APEG-1 gene is useful to detect compounds that bind to the
XX CC repressor and increase APEG-1 expression in VSMC. APEG-1 is useful for
XX CC treating and diagnosing vascular diseases such as atherosclerosis and
XX CC restenosis
XX SQ Sequence 14 BP; 0 A; 0 C; 1 G; 12 T; 0 U; 1 Other;

Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTAAGAAAAA 1492
Db 14 CBAAGAAAAA 1

RESULT 561
AAZ36741/C
ID AAZ36741 standard; DNA; 14 BP.
XX AC AAZ36741;
XX DT 13-MAR-2000 (first entry)
XX DE Anchored oligo(dT) primer T13V used for modified differential display.
XX KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
XX KW differentially expressed nucleic acid; disease state; cancer;
XX KW autoimmune disease; infectious disease; aging; developmental disorder;

KW KW proliferative disorder; neurological disorder; toxicity; primer;
KW KW treatment resistance; differential expression; drug discovery;
KW KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX OS Synthetic.
XX PN W09955913-A2.
XX PD 04-NOV-1999.
XX PF 27-APR-1999; 99WO-US009119.
XX PR 27-APR-1998; 98US-0083331P.
XX PR 27-AUG-1998; 98US-0098070P.
XX PR 04-FEB-1999; 99US-0118624P.
XX PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX PI McClelland M, Welsh J, Trenkle T;
XX PS WPI; 2000-086388/07.
XX PT Measuring expression of low abundance reduced complexity target nucleic
XX PT acid molecules.
XX PS Example 3; Page 91; 187pp; English.
XX CC AAZ36739-41 represent oligo(dT) primers used for modified differential
XX CC display, in the method of the invention. The specification describes a
XX CC method for measuring the level of two or more nucleic acid molecules in a
XX CC target. The method comprises contacting a probe with an arbitrarily or
XX CC statistically sampled target and detecting the amount of specific binding
XX CC of the target to the probe. The methods can be used to identify
XX CC differentially expressed nucleic acid molecules associated with disease
XX CC states, such as cancer, autoimmune disease, infectious disease, aging,
XX CC developmental disorder, proliferative disorder or neurological disorder.
XX CC Alternatively the methods can be used to assess the efficacy or toxicity
XX CC of a resistance to a treatment. Also the methods can be used to
XX CC determine differential expression of nucleic acid molecules in response
XX CC to a stimulus, e.g. a chemical, drug or growth factor (especially
XX CC epidermal growth factor), radiation, stress or a pathogen. The methods
XX CC can also be used to determine co-regulated genes that can be potential
XX CC targets for drug discovery
XX SQ Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 0 U; 1 Other;

Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1480 TAAAAA 1493
Db 14 BAAAAA 1

RESULT 562
AAD44142
ID AAD44142 standard; DNA; 14 BP.
XX AC AAD44142;
XX DT 13-DEC-2002 (first entry)
XX DE Oligo-dT PCR primer #2 used to illustrate the method of the invention.
XX KW Sequential consensus region-directed amplification; gene expression;
XX KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
XX KW primer; ss.
XX OS Unidentified.
XX PN US6277571-B1.

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PD 21-AUG-2001.
XX
XX 30-SEP-1998; 98US-00163485.
XX
PR 03-OCT-1997; 97US-00943162.
PR 03-OCT-1997; 97US-0108152P.
XX
XX (UVVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
XX Fillmore H, Broadus W, Gillies G;
XX
XX WPI; 2002-412824/44.
XX
XX Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX
XX Example; Fig 1C; 19pp; English.
XX
XX The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dT
CC PCR primer used to illustrate the method of the invention
XX
XX Sequence 14 BP; 13 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
XX
Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1494
DB 1 AAAAAAAAAAAAAA 14

RESULT 563
AAD44148
ID AAD44148 standard; DNA; 14 BP.
XX
XX AAD44148;
XX
DT 13-DEC-2002 (first entry)
XX
XX Oligo-dT PCR primer #8 used to illustrate the method of the invention.
XX
XX Sequential consensus region-directed amplification; gene expression;
XX disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
XX primer; ss.
XX
XX Unidentified.
XX
XX US6277571-B1.
XX
XX 21-AUG-2001.
XX
XX 30-SEP-1998; 98US-00163485.
XX
XX 03-OCT-1997; 97US-00943162.
XX 03-OCT-1997; 97US-0108152P.
XX
XX (UVVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
XX Fillmore H, Broadus W, Gillies G;
XX
XX WPI; 2002-412824/44.
XX
XX Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX
XX Example; Fig 1C; 19pp; English.
XX
XX The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dT
CC PCR primer used to illustrate the method of the invention
XX
XX Sequence 14 BP; 13 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
XX
Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1494
DB 1 AAAAAAAAAAAAAA 14

RESULT 564
ADC51416/c
ID ADC51416 standard; DNA; 14 BP.
XX
XX ADC51416;
XX
XX 18-DEC-2003 (first entry)
XX
XX Rat LTRF protein-related PCR primer, SEQ ID 3.
XX
XX Rat; LTRF; cranial-nerve cell promoter; long term potentiation;
XX cranial-nerve cell; nootropic; PCR; primer; ss.
XX
XX Unidentified.
XX
XX JP2003116564-A.
XX
XX 22-APR-2003.
XX
XX 12-OCT-2001; 2001JP-00314830.
XX
XX 12-OCT-2001; 2001JP-00314830.
XX
XX (MITS-) MITSUBISHI KAGAKU SEIMEI KAGAKU KENKYUSH.
XX
XX WPI; 2003-601823/57.
XX
XX Novel protein having cranial-nerve cell promoter activity and that
XX induces long term potentiation, useful for screening for cranial-nerve
XX cell regulating agent.
XX
XX Example 1; SEQ ID NO 3; 16pp; Japanese.
XX
XX The present invention relates to rat LTRF protein (I; ADC51414), which
XX has cranial-nerve cell promoter activity and induces long term
XX potentiation (LTP). (I) is useful for screening for cranial-nerve cell
XX regulating agent for inducing LTP. (I) is useful for promoting the
XX activity of a cranial-nerve cell or has a cranial-nerve cell promoting
XX activity. The present sequence is a PCR primer, which was used in an
XX example from invention.
XX
XX Sequence 14 BP; 0 A; 0 C; 1 G; 12 T; 0 U; 1 Other;
XX
Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CBAATAAAAAAAAAA 1


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RESULT 565
AAI18386/c
ID AAX18386 standard; DNA; 15 BP.
XX
AC AAX18386;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 27.
XX
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JF11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
XX Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Example 1; Page 12; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 0 U; 2 Other;
XX
Query Match 0.9%; Score 13.2; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA
Db 14 BAAAAA
Search completed: April 21, 2004, 10:48:56
Job time : 11 secs

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